

PCTWORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/00	A1	(11) International Publication Number: WO 96/40893 (43) International Publication Date: 19 December 1996 (19.12.96)
--	-----------	---

(21) International Application Number: PCT/US96/09122

(22) International Filing Date: 6 June 1996 (06.06.96)

(30) Priority Data:

08/487,032	7 June 1995 (07.06.95)	US
08/630,405	1 April 1996 (01.04.96)	US

(60) Parent Applications or Grants

(63) Related by Continuation

US	08/487,032 (CIP)
Filed on	7 June 1995 (07.06.95)
US	08/561,469 (CIP)
Filed on	17 November 1995 (17.11.95)
US	08/630,405 (CIP)
Filed on	1 April 1996 (01.04.96)

(71) Applicant (for all designated States except US): ASTRA
AKTIEBOLAG [SE/SE]; S-151 85 Södertälje (SE).

(72) Inventors; and

(75) Inventors/Applicants (for US only): SMITH, Douglas
[US/US]; 2 Mayflower Lane, Gloucester, MA 01930
(US). BERGLINDH, O., Thomas [SE/SE]; Ripvägen 5,S-756 53 Uppsala (SE). MELLGÅRD, Björn, L. [SE/SE];
Reutersgatan 4, S-413 20 Göteborg (SE).(74) Agents: MANDRAGOURAS, Amy, E. et al.; Lahive &
Cockfield, 60 State Street, Boston, MA 02109 (US).(81) Designated States: AL, AM, AT, AU, AZ, BB, BG, BR, BY,
CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL,
IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV,
MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU,
SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ,
VN, ARIPO patent (KE, LS, MW, SD, SZ, UG), Eurasian
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European
patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT,
LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI,
CM, GA, GN, ML, MR, NE, SN, TD, TG).**Published***With international search report.*(54) Title: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *HELICOBACTER PYLORI* FOR DIAGNOSTICS
AND THERAPEUTICS

(57) Abstract

Recombinant or substantially pure preparations of *H. pylori* polypeptides are described. The nucleic acids encoding the polypeptides also are described. The *H. pylori* polypeptides are useful for diagnostics and vaccine compositions.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AM	Armenia	GB	United Kingdom	MW	Malawi
AT	Austria	GE	Georgia	MX	Mexico
AU	Australia	GN	Guinea	NE	Niger
BB	Barbados	GR	Greece	NL	Netherlands
BE	Belgium	HU	Hungary	NO	Norway
BF	Burkina Faso	IE	Ireland	NZ	New Zealand
BG	Bulgaria	IT	Italy	PL	Poland
BJ	Benin	JP	Japan	PT	Portugal
BR	Brazil	KE	Kenya	RO	Romania
BY	Belarus	KG	Kyrgyzstan	RU	Russian Federation
CA	Canada	KP	Democratic People's Republic of Korea	SD	Sudan
CF	Central African Republic	KR	Republic of Korea	SE	Sweden
CG	Congo	KZ	Kazakhstan	SG	Singapore
CH	Switzerland	LI	Liechtenstein	SI	Slovenia
CI	Côte d'Ivoire	LK	Sri Lanka	SK	Slovakia
CM	Cameroon	LR	Liberia	SN	Senegal
CN	China	LT	Lithuania	SZ	Swaziland
CS	Czechoslovakia	LU	Luxembourg	TD	Chad
CZ	Czech Republic	LV	Latvia	TG	Togo
DE	Germany	MC	Monaco	TJ	Tajikistan
DK	Denmark	MD	Republic of Moldova	TT	Trinidad and Tobago
EE	Estonia	MG	Madagascar	UA	Ukraine
ES	Spain	ML	Mali	UG	Uganda
FI	Finland	MN	Mongolia	US	United States of America
FR	France	MR	Mauritania	UZ	Uzbekistan
GA	Gabon			VN	Viet Nam

**NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS**

Background of the Invention

5 *Helicobacter pylori* is a gram-negative, S-shaped, microaerophilic bacterium that was discovered and cultured from a human gastric biopsy specimen. (Warren, J.R. and B. Marshall, (1983) *Lancet* 1: 1273-1275; and Marshall et al., (1984) *Microbios Lett.* 25: 83-88). *H. pylori* has been strongly linked to chronic gastritis and duodenal ulcer disease. (Rathbone et. al., (1986) *Gut* 27: 635-641). Moreover, evidence is accumulating for an
10 etiologic role of *H. pylori* in nonulcer dyspepsia, gastric ulcer disease, and gastric adenocarcinoma. (Blaser M. J., (1993) *Trends Microbiol.* 1: 255-260). Transmission of the bacteria occurs via the oral route, and the risk of infection increases with age. (Taylor, D.N. and M. J. Blaser, (1991) *Epidemiol. Rev* 13: 42-50). *H. pylori* colonizes the human gastric mucosa, establishing an infection that usually persists for decades. Infection by *H.*
15 *pylori* is prevalent worldwide. Developed countries have infection rates over 50% of the adult population, while developing countries have infection rates reaching 90% of the adults over the age of 20. (Hopkins R. J. and J. G. Morris (1994) *Am. J. Med.* 97: 265-277).

 The bacterial factors necessary for colonization of the gastric environment, and for virulence of this pathogen, are poorly understood. Examples of the putative virulence
20 factors include the following: urease, an enzyme that may play a role in neutralizing gastric acid pH (Eaton et al., (1991) *Infect. Immunol.* 59: 2470-2475; Ferrero, R.L. and A. Lee (1991) *Microb. Ecol. Hlth. Dis.* 4: 121-134; Labigne et al., (1991) *J. Bacteriol.* 173: 1920-1931); the bacterial flagellar proteins responsible for motility across the mucous layer. (Hazell et al., (1986) *J. Inf. Dis.* 153: 658-663; Leying et al., (1992) *Mol. Microbiol.* 6:
25 2863-2874; and Haas et al., (1993) *Mol. Microbiol.* 8: 753-760); Vac A, a bacterial toxin that induces the formation of intracellular vacuoles in epithelial cells (Schmitt, W. and R. Haas, (1994) *Molecular Microbiol.* 12(2): 307-319); and several gastric tissue-specific adhesins. (Boren et al., (1993) *Science* 262: 1892-1895; Evans et al., (1993) *J. Bacteriol.* 175: 674-683; and Falk et al., (1993) *Proc. Natl. Acad. Sci. USA* 90: 2035-203).

30 Numerous therapeutic agents are currently available that eradicate *H. pylori* infections *in vitro*. (Huesca et. al., (1993) *Zbl. Bakt.* 280: 244-252; Hopkins, R. J. and J. G. Morris, supra). However, many of these treatments are suboptimally effective *in vivo* because of bacterial resistance, altered drug distribution, patient non-compliance or poor drug availability. (Hopkins, R. J. and J. G. Morris, supra). Treatment with antibiotics
35 combined with bismuth are part of the standard regime used to treat *H. pylori* infection. (Malfertheiner, P. and J. E. Dominguez-Munoz (1993) *Clinical Therapeutics* 15 Supp. B: 37-48). Recently, combinations of a proton pump inhibitors and a single antibiotic have been shown to ameliorate duodenal ulcer disease. (Malfertheiner, P. and J. E. Dominguez-Munoz supra). However, methods employing antibiotic agents can have the problem of the

-2-

emergence of bacterial strains which are resistant to these agents. (Hopkins, R. J. and J. G. Morris, *supra*). These limitations demonstrate that new more effective methods are needed to combat *H. pylori* infections *in vivo*. In particular, the design of new vaccines that may prevent infection by this bacterium is highly desirable.

5

Summary of the Invention

This invention relates to novel genes, e.g., genes encoding polypeptides such as bacterial surface proteins, from the organism *Helicobacter pylori* (*H. pylori*), and other related genes, their products, and uses thereof. The nucleic acids and peptides of the present invention have utility for diagnostic and therapeutics for *H. pylori* and other *Helicobacter* species. They can also be used to detect the presence of *H. pylori* and other *Helicobacter* species in a sample; and for use in screening compounds for the ability to interfere with the *H. pylori* life cycle or to inhibit *H. pylori* infection. More specifically, this invention features compositions of nucleic acids corresponding to entire coding sequences of *H. pylori* proteins, including surface or secreted proteins or parts thereof, nucleic acids capable of binding mRNA from *H. pylori* proteins to block protein translation, and methods for producing *H. pylori* proteins or parts thereof using peptide synthesis and recombinant DNA techniques. This invention also features antibodies and nucleic acids useful as probes to detect *H. pylori* infection. In addition, vaccine compositions and methods for the protection or treatment of infection by *H. pylori* are within the scope of this invention.

10
15
20

Detailed Description of the Drawings

Figure 1 is a bar graph that depicts the antibody titer in serum of mice following immunization with specific *H. pylori* antigens.

25

Figure 2 is a bar graph that depicts the antibody titer in mucous of mice following immunization with specific *H. pylori* antigens.

30

Figure 3 is a bar graph that depicts therapeutic immunization of *H. pylori* infected mice with specific antigens dissolved in HEPES buffer.

Figure 4 is a bar graph that depicts therapeutic immunization of *H. pylori* infected mice with specific antigens dissolved in buffer containing DOC.

35

Detailed Description of the Invention

In one aspect, the invention features a recombinant or substantially pure preparation of *H. pylori* polypeptide of SEQ ID NO: 384. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide of SEQ ID NO: 384, such nucleic acid

-3-

is contained in SEQ ID NO: 1. The *H. pylori* polypeptide sequences of the invention described herein are contained in the Sequence Listing, and the nucleic acids encoding *H. pylori* polypeptides of the invention are contained in the Sequence Listing.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 384 through SEQ ID NO: 389, SEQ ID NO: 391 through SEQ ID NO: 400, SEQ ID NO: 402 through SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 411 through SEQ ID NO: 412, SEQ ID NO: 414 through SEQ ID NO: 430, SEQ ID NO: 432 through SEQ ID NO: 434, SEQ ID NO: 436 through SEQ ID NO: 441, and SEQ ID NO: 443. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 384 through SEQ ID NO: 389, SEQ ID NO: 391 through SEQ ID NO: 400, SEQ ID NO: 402 through SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 411 through SEQ ID NO: 412, SEQ ID NO: 414 through SEQ ID NO: 430, SEQ ID NO: 432 through SEQ ID NO: 434, SEQ ID NO: 436 through SEQ ID NO: 441, and SEQ ID NO: 443, such nucleic acids are contained in SEQ ID NO: 1 through SEQ ID NO: 50.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 444, SEQ ID NO: 446 through SEQ ID NO: 448, SEQ ID NO: 450 through SEQ ID NO: 462, SEQ ID NO: 465 through SEQ ID NO: 466, SEQ ID NO: 468 through SEQ ID NO: 469, SEQ ID NO: 471 through SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 478 through SEQ ID NO: 479, SEQ ID NO: 481 through SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488 through SEQ ID NO: 501, and SEQ ID NO: 503 through SEQ ID NO: 506. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 444, SEQ ID NO: 446 through SEQ ID NO: 448, SEQ ID NO: 450 through SEQ ID NO: 462, SEQ ID NO: 465 through SEQ ID NO: 466, SEQ ID NO: 468 through SEQ ID NO: 469, SEQ ID NO: 471 through SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 478 through SEQ ID NO: 479, SEQ ID NO: 481 through SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488 through SEQ ID NO: 501, and SEQ ID NO: 503 through SEQ ID NO: 506, such nucleic acids are contained in SEQ ID NO: 51 through SEQ ID NO: 100.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 509 through SEQ ID NO: 510, SEQ ID NO: 512 through SEQ ID NO: 514, SEQ ID NO: 516, SEQ ID NO: 518 through SEQ ID NO: 520, SEQ ID NO: 522 through SEQ ID NO: 525, SEQ ID NO: 527 through SEQ ID NO: 533, SEQ ID NO: 535 through SEQ ID NO: 537, SEQ ID NO: 539 through SEQ ID NO: 540, SEQ ID NO: 542 through SEQ ID NO: 544, SEQ ID NO: 546 through SEQ ID NO: 548, SEQ ID NO:

550, SEQ ID NO: 553 through SEQ ID NO: 556, SEQ ID NO: 558, SEQ ID NO: 560, SEQ ID NO: 562 through SEQ ID NO: 568, SEQ ID NO: 570, and SEQ ID NO: 572 through SEQ ID NO: 575. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 509 through SEQ ID NO: 510, SEQ ID NO: 512 through SEQ ID NO: 514, SEQ ID NO: 516, SEQ ID NO: 518 through SEQ ID NO: 520, SEQ ID NO: 522 through SEQ ID NO: 525, SEQ ID NO: 527 through SEQ ID NO: 533, SEQ ID NO: 535 through SEQ ID NO: 537, SEQ ID NO: 539 through SEQ ID NO: 540, SEQ ID NO: 542 through SEQ ID NO: 544, SEQ ID NO: 546 through SEQ ID NO: 548, SEQ ID NO: 550, SEQ ID NO: 553 through SEQ ID NO: 556, SEQ ID NO: 558, SEQ ID NO: 560, SEQ ID NO: 562 through SEQ ID NO: 568, SEQ ID NO: 570, and SEQ ID NO: 572 through SEQ ID NO: 575, such nucleic acids are contained in SEQ ID NO: 101 through SEQ ID NO: 150.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 576 through SEQ ID NO: 579, SEQ ID NO: 581 through SEQ ID NO: 583, SEQ ID NO: 585 through SEQ ID NO: 593, SEQ ID NO: 596 through SEQ ID NO: 614, SEQ ID NO: 617 through SEQ ID NO: 623, SEQ ID NO: 625, SEQ ID NO: 627, SEQ ID NO: 629 through SEQ ID NO: 631, SEQ ID NO: 633, and SEQ ID NO: 635 through SEQ ID NO: 636. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 576 through SEQ ID NO: 579, SEQ ID NO: 581 through SEQ ID NO: 583, SEQ ID NO: 585 through SEQ ID NO: 593, SEQ ID NO: 596 through SEQ ID NO: 614, SEQ ID NO: 617 through SEQ ID NO: 623, SEQ ID NO: 625, SEQ ID NO: 627, SEQ ID NO: 629 through SEQ ID NO: 631, SEQ ID NO: 633, and SEQ ID NO: 635 through SEQ ID NO: 636, such nucleic acids are contained in SEQ ID NO: 151 through SEQ ID NO: 200.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 638 through SEQ ID NO: 640, SEQ ID NO: 642 through SEQ ID NO: 643, SEQ ID NO: 647, SEQ ID NO: 649 through SEQ ID NO: 651, SEQ ID NO: 653 through SEQ ID NO: 661, SEQ ID NO: 663 through SEQ ID NO: 670, SEQ ID NO: 673 through SEQ ID NO: 674, SEQ ID NO: 676, SEQ ID NO: 678 through SEQ ID NO: 683, SEQ ID NO: 687 through SEQ ID NO: 692, and SEQ ID NO: 694 through SEQ ID NO: 702. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 638 through SEQ ID NO: 640, SEQ ID NO: 642 through SEQ ID NO: 643, SEQ ID NO: 647, SEQ ID NO: 649 through SEQ ID NO: 651, SEQ ID NO: 653 through SEQ ID NO: 661, SEQ ID NO: 663 through SEQ ID NO: 670, SEQ ID NO: 673 through SEQ ID NO: 674, SEQ ID NO: 676, SEQ ID NO: 678 through SEQ ID NO: 683, SEQ ID NO: 687

through SEQ ID NO: 692, and SEQ ID NO: 694 through SEQ ID NO: 702, such nucleic acids are contained in SEQ ID NO: 201 through SEQ ID NO: 250.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 705 through SEQ ID NO: 708, SEQ ID NO: 712 through SEQ ID NO: 714, SEQ ID NO: 716 through SEQ ID NO: 722, SEQ ID NO: 725 through SEQ ID NO: 730, SEQ ID NO: 732 through SEQ ID NO: 733, SEQ ID NO: 735 through SEQ ID NO: 744, SEQ ID NO: 746 through SEQ ID NO: 752, SEQ ID NO: 755 through SEQ ID NO: 757, SEQ ID NO: 759, SEQ ID NO: 761 through SEQ ID NO: 763, and SEQ ID NO: 767 through SEQ ID NO: 770. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 705 through SEQ ID NO: 708, SEQ ID NO: 712 through SEQ ID NO: 714, SEQ ID NO: 716 through SEQ ID NO: 722, SEQ ID NO: 725 through SEQ ID NO: 730, SEQ ID NO: 732 through SEQ ID NO: 733, SEQ ID NO: 735 through SEQ ID NO: 744, SEQ ID NO: 746 through SEQ ID NO: 752, SEQ ID NO: 755 through SEQ ID NO: 757, SEQ ID NO: 759, SEQ ID NO: 761 through SEQ ID NO: 763, and SEQ ID NO: 767 through SEQ ID NO: 770, such nucleic acids are contained in SEQ ID NO: 251 through SEQ ID NO: 300.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 771 through SEQ ID NO: 773, SEQ ID NO: 775, SEQ ID NO: 777, SEQ ID NO: 779 through SEQ ID NO: 784, SEQ ID NO: 786 through SEQ ID NO: 787, SEQ ID NO: 789 through SEQ ID NO: 792, SEQ ID NO: 794, SEQ ID NO: 796, SEQ ID NO: 798 through SEQ ID NO: 805, SEQ ID NO: 807 through SEQ ID NO: 811, SEQ ID NO: 813 through SEQ ID NO: 819, SEQ ID NO: 821 through SEQ ID NO: 822, SEQ ID NO: 824 through SEQ ID NO: 826, SEQ ID NO: 828 through SEQ ID NO: 832, and SEQ ID NO: 835. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 771 through SEQ ID NO: 773, SEQ ID NO: 775, SEQ ID NO: 777, SEQ ID NO: 779 through SEQ ID NO: 784, SEQ ID NO: 786 through SEQ ID NO: 787, SEQ ID NO: 789 through SEQ ID NO: 792, SEQ ID NO: 794, SEQ ID NO: 796, SEQ ID NO: 798 through SEQ ID NO: 805, SEQ ID NO: 807 through SEQ ID NO: 811, SEQ ID NO: 813 through SEQ ID NO: 819, SEQ ID NO: 821 through SEQ ID NO: 822, SEQ ID NO: 824 through SEQ ID NO: 826, SEQ ID NO: 828 through SEQ ID NO: 832, and SEQ ID NO: 835, such nucleic acids are contained in SEQ ID NO: 301 through SEQ ID NO: 350.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 836 through SEQ ID NO: 841, SEQ ID NO: 843 through SEQ ID NO: 851, SEQ ID NO: 853, SEQ ID NO: 855 through SEQ ID NO: 857, SEQ ID NO:

-6-

859 through SEQ ID NO: 862, SEQ ID NO: 866, SEQ ID NO: 868 through SEQ ID NO: 871, SEQ ID NO: 873 through SEQ ID NO: 876, and SEQ ID NO: 879. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 836 through SEQ ID NO: 841, SEQ ID NO: 843 through SEQ ID NO: 851, SEQ ID NO: 853, SEQ ID NO: 855 through SEQ ID NO: 857, SEQ ID NO: 859 through SEQ ID NO: 862, SEQ ID NO: 866, SEQ ID NO: 868 through SEQ ID NO: 871, SEQ ID NO: 873 through SEQ ID NO: 876, and SEQ ID NO: 879, such nucleic acids are contained in SEQ ID NO: 351 through SEQ ID NO: 383.

10 In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 385, SEQ ID NO: 390, SEQ ID NO: 401, SEQ ID NO: 407, SEQ ID NO: 409 through SEQ ID NO: 410, SEQ ID NO: 413, SEQ ID NO: 431, SEQ ID NO: 435, SEQ ID NO: 442, SEQ ID NO: 445, SEQ ID NO: 449, SEQ ID NO: 463 through
15 SEQ ID NO: 464, SEQ ID NO: 467, SEQ ID NO: 470, SEQ ID NO: 474, SEQ ID NO: 476 through SEQ ID NO: 477, SEQ ID NO: 480, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 502, SEQ ID NO: 507 through SEQ ID NO: 508, SEQ ID NO: 511, SEQ ID NO: 515, SEQ ID NO: 517, SEQ ID NO: 521, SEQ ID NO: 526, SEQ ID NO: 534, SEQ ID NO: 538, SEQ ID NO: 541, SEQ ID NO: 545, SEQ ID NO: 549, SEQ ID NO: 551 through SEQ
20 ID NO: 552, SEQ ID NO: 557, SEQ ID NO: 559, SEQ ID NO: 561, SEQ ID NO: 569, SEQ ID NO: 571, SEQ ID NO: 580, SEQ ID NO: 584, SEQ ID NO: 594 through SEQ ID NO: 595, SEQ ID NO: 615 through SEQ ID NO: 616, SEQ ID NO: 624, and SEQ ID NO: 626. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO:
25 385, SEQ ID NO: 390, SEQ ID NO: 401, SEQ ID NO: 407, SEQ ID NO: 409 through SEQ ID NO: 410, SEQ ID NO: 413, SEQ ID NO: 431, SEQ ID NO: 435, SEQ ID NO: 442, SEQ ID NO: 445, SEQ ID NO: 449, SEQ ID NO: 463 through SEQ ID NO: 464, SEQ ID NO: 467, SEQ ID NO: 470, SEQ ID NO: 474, SEQ ID NO: 476 through SEQ ID NO: 477, SEQ ID NO: 480, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 502, SEQ ID NO: 507
30 through SEQ ID NO: 508, SEQ ID NO: 511, SEQ ID NO: 515, SEQ ID NO: 517, SEQ ID NO: 521, SEQ ID NO: 526, SEQ ID NO: 534, SEQ ID NO: 538, SEQ ID NO: 541, SEQ ID NO: 545, SEQ ID NO: 549, SEQ ID NO: 551 through SEQ ID NO: 552, SEQ ID NO: 557, SEQ ID NO: 559, SEQ ID NO: 561, SEQ ID NO: 569, SEQ ID NO: 571, SEQ ID NO: 580, SEQ ID NO: 584, SEQ ID NO: 594 through SEQ ID NO: 595, SEQ ID NO: 615
35 through SEQ ID NO: 616, SEQ ID NO: 624, and SEQ ID NO: 626, such nucleic acids are contained in SEQ ID NO: 881 through SEQ ID NO: 930.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 628, SEQ ID NO: 632, SEQ ID NO: 634, SEQ ID NO: 637,

-7-

SEQ ID NO: 641, SEQ ID NO: 644 through SEQ ID NO: 646, SEQ ID NO: 648, SEQ ID NO: 652, SEQ ID NO: 662, SEQ ID NO: 671 through SEQ ID NO: 672, SEQ ID NO: 675, SEQ ID NO: 677, SEQ ID NO: 684 through SEQ ID NO: 686, SEQ ID NO: 693, SEQ ID NO: 703 through SEQ ID NO: 704, SEQ ID NO: 709 through SEQ ID NO: 711, SEQ ID NO: 715, SEQ ID NO: 723 through SEQ ID NO: 724, SEQ ID NO: 731, SEQ ID NO: 734, SEQ ID NO: 745, SEQ ID NO: 753 through SEQ ID NO: 754, SEQ ID NO: 758, SEQ ID NO: 760, SEQ ID NO: 764 through SEQ ID NO: 766, SEQ ID NO: 774, SEQ ID NO: 776, SEQ ID NO: 778, SEQ ID NO: 785, SEQ ID NO: 788, SEQ ID NO: 793, SEQ ID NO: 795, SEQ ID NO: 797, SEQ ID NO: 806, SEQ ID NO: 812, SEQ ID NO: 820, SEQ ID NO: 823, and SEQ ID NO: 827. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 628, SEQ ID NO: 632, SEQ ID NO: 634, SEQ ID NO: 637, SEQ ID NO: 641, SEQ ID NO: 644 through SEQ ID NO: 646, SEQ ID NO: 648, SEQ ID NO: 652, SEQ ID NO: 662, SEQ ID NO: 671 through SEQ ID NO: 672, SEQ ID NO: 675, SEQ ID NO: 677, SEQ ID NO: 684 through SEQ ID NO: 686, SEQ ID NO: 693, SEQ ID NO: 703 through SEQ ID NO: 704, SEQ ID NO: 709 through SEQ ID NO: 711, SEQ ID NO: 715, SEQ ID NO: 723 through SEQ ID NO: 724, SEQ ID NO: 731, SEQ ID NO: 734, SEQ ID NO: 745, SEQ ID NO: 753 through SEQ ID NO: 754, SEQ ID NO: 758, SEQ ID NO: 760, SEQ ID NO: 764 through SEQ ID NO: 766, SEQ ID NO: 774, SEQ ID NO: 776, SEQ ID NO: 778, SEQ ID NO: 785, SEQ ID NO: 788, SEQ ID NO: 793, SEQ ID NO: 795, SEQ ID NO: 797, SEQ ID NO: 806, SEQ ID NO: 812, SEQ ID NO: 820, SEQ ID NO: 823, and SEQ ID NO: 827, such nucleic acids are contained in SEQ ID NO: 931 through SEQ ID NO: 980.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 833 through SEQ ID NO: 834, SEQ ID NO: 842, SEQ ID NO: 852, SEQ ID NO: 854, SEQ ID NO: 858, SEQ ID NO: 863, SEQ ID NO: 864 through SEQ ID NO: 865, SEQ ID NO: 867, SEQ ID NO: 872, SEQ ID NO: 877 through SEQ ID NO: 878, and SEQ ID NO: 880. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 833 through SEQ ID NO: 834, SEQ ID NO: 842, SEQ ID NO: 852, SEQ ID NO: 854, SEQ ID NO: 858, SEQ ID NO: 863, SEQ ID NO: 864 through SEQ ID NO: 865, SEQ ID NO: 867, SEQ ID NO: 872, SEQ ID NO: 877 through SEQ ID NO: 878, and SEQ ID NO: 880, such nucleic acids are contained in SEQ ID NO: 981 through SEQ ID NO: 994.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1446 through SEQ ID NO: 1461, SEQ ID NO: 1463, and SEQ ID NO: 1465 through SEQ ID NO: 1495. The invention also includes substantially

pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1446 through SEQ ID NO: 1461, SEQ ID NO: 1463, and SEQ ID NO: 1465 through SEQ ID NO: 1495, such nucleic acids are contained in SEQ ID NO: 995 through SEQ ID NO: 1010, SEQ ID NO: 1012, and SEQ ID NO: 1014 through SEQ ID NO: 1044.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1497 through SEQ ID NO: 1515, and SEQ ID NO: 1517 through SEQ ID NO: 1545. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1497 through SEQ ID NO: 1515, and SEQ ID NO: 1517 through SEQ ID NO: 1545, such nucleic acids are contained in SEQ ID NO: 1046 through SEQ ID NO: 1064, and SEQ ID NO: 1066 through SEQ ID NO: 1094.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1546 through SEQ ID NO: 1595. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1546 through SEQ ID NO: 1595, such nucleic acids are contained in SEQ ID NO: 1095 through SEQ ID NO: 1144.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1596 through SEQ ID NO: 1617, SEQ ID NO: 1620 through SEQ ID NO: 1645. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1596 through SEQ ID NO: 1617, SEQ ID NO: 1620 through SEQ ID NO: 1645, such nucleic acids are contained in SEQ ID NO: 1145 through SEQ ID NO: 1166, and SEQ ID NO: 1169 through SEQ ID NO: 1194.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1646 through SEQ ID NO: 1681, and SEQ ID NO: 1683 through SEQ ID NO: 1695. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1646 through SEQ ID NO: 1681, and SEQ ID NO: 1683 through SEQ ID NO: 1695, such nucleic acids are contained in SEQ ID NO: 1195 through SEQ ID NO: 1230, and SEQ ID NO: 1232 through SEQ ID NO: 1244.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1696 through SEQ ID NO: 1745. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group

consisting of *H. pylori* polypeptides SEQ ID NO: 1696 through SEQ ID NO: 1745, such nucleic acids are contained in SEQ ID NO: 1245 through SEQ ID NO: 1294.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1746 through SEQ ID NO: 1783, and SEQ ID NO: 1786 through SEQ ID NO: 1795. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1746 through SEQ ID NO: 1783, and SEQ ID NO: 1786 through SEQ ID NO: 1795, such nucleic acids are contained in SEQ ID NO: 1295 through SEQ ID NO: 1332, and SEQ ID NO: 1335 through SEQ ID NO: 1344.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1796 through SEQ ID NO: 1817, SEQ ID NO: 1819, SEQ ID NO: 1821, SEQ ID NO: 1823 through SEQ ID NO: 1836, and SEQ ID NO: 1838 through SEQ ID NO: 1845. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1796 through SEQ ID NO: 1817, SEQ ID NO: 1819, SEQ ID NO: 1821, SEQ ID NO: 1823 through SEQ ID NO: 1836, and SEQ ID NO: 1838 through SEQ ID NO: 1845, such nucleic acids are contained in SEQ ID NO: 1345 through SEQ ID NO: 1366, SEQ ID NO: 1368, SEQ ID NO: 1370, SEQ ID NO: 1372 through SEQ ID NO: 1385, and SEQ ID NO: 1387 through SEQ ID NO: 1394.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 1846 through SEQ ID NO: 1896. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 1846 through SEQ ID NO: 1896, such nucleic acids are contained in SEQ ID NO: 1395 through SEQ ID NO: 1445.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of the invention as set forth in the Sequence Listing. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of the invention as set forth in the Sequence Listing. It should be understood that this invention encompasses each of the *H. pylori* polypeptides and nucleic acids encoding such polypeptides as identified in the Sequence Listing by a given sequence identification number. For example, a representative *H. pylori* polypeptide is contained in SEQ ID NO: 1450. Therefore, this invention encompasses a recombinant or substantially pure preparation of an *H. pylori* polypeptide of SEQ ID NO: 1450. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide of SEQ ID NO: 1450.

In another aspect, the invention pertains to any individual *H. pylori* polypeptide member or nucleic acid encoding such member from the above-identified groups of *H. pylori* polypeptides (e.g., SEQ ID NO: 1546 through SEQ ID NO: 1595) or nucleic acids (e.g., SEQ ID NO: 1095-SEQ ID NO: 1144), as well as any subgroups from within the
 5 above-identified groups. Furthermore, the subgroups can preferably consists of 1, 3, 5, 10, 15, 20, 30 or 40 members of any of the groups identified above, as well as any combinations thereof. For example, the group consisting of *H. pylori* polypeptides SEQ ID NO: 1846 through SEQ ID NO: 1896 can be divided into one or more subgroups as follows: SEQ ID NO: 1846-SEQ ID NO: 1860; SEQ ID NO: 1861-SEQ ID NO: 1875;
 10 SEQ ID NO: 1876-SEQ ID NO: 1885; SEQ ID NO: 1886-SEQ ID NO: 1896; or any combinations thereof.

Particularly preferred is an isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* cell envelope polypeptide or a fragment thereof. Such nucleic acid is selected from the group consisting of SEQ ID NO: 1020, SEQ ID NO: 1021, SEQ ID NO:
 15 1036, SEQ ID NO: 1050, SEQ ID NO: 1071, SEQ ID NO: 1101, SEQ ID NO: 1135, SEQ ID NO: 1276, SEQ ID NO: 1150, SEQ ID NO: 1187, SEQ ID NO: 1192, SEQ ID NO: 1361, SEQ ID NO: 1379, SEQ ID NO: 1399, SEQ ID NO: 1403, SEQ ID NO: 1400, SEQ ID NO: 1189, SEQ ID NO: 1002, SEQ ID NO: 1213, SEQ ID NO: 1214, SEQ ID NO: 1215, SEQ ID NO: 1234, SEQ ID NO: 1236, SEQ ID NO: 1237, SEQ ID NO: 1224, SEQ
 20 ID NO: 1251, SEQ ID NO: 1262, SEQ ID NO: 1149, SEQ ID NO: 1220, SEQ ID NO: 1240, SEQ ID NO: 1164, SEQ ID NO: 1165, SEQ ID NO: 1404, SEQ ID NO: 1144, SEQ ID NO: 1182, SEQ ID NO: 1157, SEQ ID NO: 1160, SEQ ID NO: 1300, SEQ ID NO: 1321, SEQ ID NO: 1323, SEQ ID NO: 1329, SEQ ID NO: 1332, SEQ ID NO: 1345, SEQ ID NO: 1358, SEQ ID NO: 1375, SEQ ID NO: 1417, SEQ ID NO: 1283, SEQ ID NO:
 25 1335, SEQ ID NO: 1368, SEQ ID NO: 1179, SEQ ID NO: 1255, SEQ ID NO: 1258, SEQ ID NO: 1044, SEQ ID NO: 1273, SEQ ID NO: 1219, SEQ ID NO: 1274, SEQ ID NO: 1210, SEQ ID NO: 1422, SEQ ID NO: 1302, SEQ ID NO: 1308, SEQ ID NO: 1310, SEQ ID NO: 1331, SEQ ID NO: 1432, SEQ ID NO: 1052, SEQ ID NO: 1091, SEQ ID NO: 1421, SEQ ID NO: 1069, SEQ ID NO: 1005, SEQ ID NO: 1007, SEQ ID NO: 1166, SEQ
 30 ID NO: 1177, SEQ ID NO: 1193, SEQ ID NO: 1206, SEQ ID NO: 1207, SEQ ID NO: 1304, SEQ ID NO: 1305, SEQ ID NO: 1346, SEQ ID NO: 1348, SEQ ID NO: 1350, SEQ ID NO: 1032, SEQ ID NO: 1053, SEQ ID NO: 1081, SEQ ID NO: 1124, SEQ ID NO: 1382, SEQ ID NO: 1437, SEQ ID NO: 1263, SEQ ID NO: 1173, SEQ ID NO: 1405, SEQ ID NO: 1406, SEQ ID NO: 1410, SEQ ID NO: 1086, SEQ ID NO: 1322, SEQ ID NO:
 35 1266, SEQ ID NO: 1282, SEQ ID NO: 1271, SEQ ID NO: 1208, SEQ ID NO: 1126, SEQ ID NO: 1270, SEQ ID NO: 1278, SEQ ID NO: 1419, SEQ ID NO: 1125, SEQ ID NO: 1181, SEQ ID NO: 1416, SEQ ID NO: 1096, SEQ ID NO: 1082, SEQ ID NO: 1146, SEQ ID NO: 1145, SEQ ID NO: 1108, SEQ ID NO: 1148, SEQ ID NO: 1337, SEQ ID NO: 1338, SEQ ID NO: 1424, SEQ ID NO: 1000, SEQ ID NO: 1027, SEQ ID NO: 1175, SEQ

-11-

ID NO: 1330, SEQ ID NO: 217, SEQ ID NO: 217, SEQ ID NO: 367, SEQ ID NO:
 911, SEQ ID NO: 944, SEQ ID NO: 18, SEQ ID NO: 107, SEQ ID NO: 894, SEQ ID NO:
 943, SEQ ID NO: 203, SEQ ID NO: 85, SEQ ID NO: 290, SEQ ID NO: 5, SEQ ID NO:
 199, SEQ ID NO: 992, SEQ ID NO: 934, SEQ ID NO: 899, SEQ ID NO: 302, SEQ ID
 5 NO: 215, SEQ ID NO: 893, SEQ ID NO: 984, SEQ ID NO: 97, SEQ ID NO: 22, SEQ ID
 NO: 49, SEQ ID NO: 309, SEQ ID NO: 150, SEQ ID NO: 240, SEQ ID NO: 957, SEQ ID
 NO: 57, SEQ ID NO: 2, SEQ ID NO: 92, SEQ ID NO: 255, SEQ ID NO: 164, SEQ ID NO:
 201, SEQ ID NO: 278, SEQ ID NO: 245, SEQ ID NO: 921, SEQ ID NO: 896, SEQ ID
 NO: 248, SEQ ID NO: 159, SEQ ID NO: 979, SEQ ID NO: 194, SEQ ID NO: 194, SEQ
 10 ID NO: 946, SEQ ID NO: 916, SEQ ID NO: 76, SEQ ID NO: 905, SEQ ID NO: 914, SEQ
 ID NO: 931, SEQ ID NO: 50, SEQ ID NO: 250, SEQ ID NO: 969, SEQ ID NO: 66, SEQ
 ID NO: 275, SEQ ID NO: 330, SEQ ID NO: 204, SEQ ID NO: 383, SEQ ID NO: 303,
 SEQ ID NO: 70, SEQ ID NO: 983, SEQ ID NO: 972, SEQ ID NO: 929, SEQ ID NO: 972,
 SEQ ID NO: 936, SEQ ID NO: 267, SEQ ID NO: 197, SEQ ID NO: 55, SEQ ID NO: 54,
 15 SEQ ID NO: 210, SEQ ID NO: 90, SEQ ID NO: 15, SEQ ID NO: 913, SEQ ID NO: 227,
 SEQ ID NO: 79, SEQ ID NO: 191, SEQ ID NO: 238, SEQ ID NO: 274, SEQ ID NO: 27,
 SEQ ID NO: 258, SEQ ID NO: 295, SEQ ID NO: 10, SEQ ID NO: 160, SEQ ID NO: 225,
 SEQ ID NO: 964, SEQ ID NO: 166, SEQ ID NO: 56, SEQ ID NO: 980, SEQ ID NO: 903,
 SEQ ID NO: 261, SEQ ID NO: 71, SEQ ID NO: 955, SEQ ID NO: 361, SEQ ID NO: 58,
 20 SEQ ID NO: 114, SEQ ID NO: 940, SEQ ID NO: 960, SEQ ID NO: 144, SEQ ID NO:
 362, SEQ ID NO: 40, SEQ ID NO: 285, SEQ ID NO: 11, SEQ ID NO: 161, SEQ ID NO:
 974, SEQ ID NO: 111, SEQ ID NO: 316, SEQ ID NO: 257, SEQ ID NO: 78, SEQ ID NO:
 966, SEQ ID NO: 352, SEQ ID NO: 981, SEQ ID NO: 158, SEQ ID NO: 989, SEQ ID
 NO: 963, SEQ ID NO: 48, SEQ ID NO: 68, SEQ ID NO: 135, SEQ ID NO: 910, SEQ ID
 25 NO: 236, SEQ ID NO: 241, SEQ ID NO: 949, SEQ ID NO: 945, SEQ ID NO: 207, SEQ
 ID NO: 977, SEQ ID NO: 978, SEQ ID NO: 994, SEQ ID NO: 163, SEQ ID NO: 256,
 SEQ ID NO: 287, SEQ ID NO: 184, SEQ ID NO: 45, SEQ ID NO: 136, SEQ ID NO: 214,
 SEQ ID NO: 16, SEQ ID NO: 192, SEQ ID NO: 373, SEQ ID NO: 892, SEQ ID NO: 239,
 SEQ ID NO: 34, SEQ ID NO: 340, SEQ ID NO: 41, SEQ ID NO: 332, SEQ ID NO: 134,
 30 and SEQ ID NO: 330.

In one embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is
 an *H. pylori* flagella-associated polypeptide or a fragment thereof encoded by the nucleic
 acid selected from the group consisting of SEQ ID NO: 1020, SEQ ID NO: 1021, SEQ ID
 NO: 1036, SEQ ID NO: 1050, SEQ ID NO: 1071, SEQ ID NO: 1101, SEQ ID NO: 1135,
 35 SEQ ID NO: 1276, SEQ ID NO: 1150, SEQ ID NO: 1187, SEQ ID NO: 1192, SEQ ID
 NO: 1361, SEQ ID NO: 1379, SEQ ID NO: 1399, SEQ ID NO: 1403, SEQ ID NO: 1400,
 SEQ ID NO: 1189, SEQ ID NO: 217, SEQ ID NO: 367, SEQ ID NO: 911, SEQ ID NO:
 944, SEQ ID NO: 18, SEQ ID NO: 107, SEQ ID NO: 894, SEQ ID NO: 943, SEQ ID NO:

203, SEQ ID NO: 85, SEQ ID NO: 290, SEQ ID NO: 5, SEQ ID NO: 199, SEQ ID NO: 992, SEQ ID NO: 934, SEQ ID NO: 899, SEQ ID NO: 302, and SEQ ID NO: 215.

In another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* inner membrane polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1002, SEQ ID NO: 1213, SEQ ID NO: 1214, SEQ ID NO: 1215, SEQ ID NO: 1234, SEQ ID NO: 1236, SEQ ID NO: 1237, SEQ ID NO: 1224, SEQ ID NO: 1251, SEQ ID NO: 1262, SEQ ID NO: 1149, SEQ ID NO: 1220, SEQ ID NO: 1240, SEQ ID NO: 1164, SEQ ID NO: 1165, SEQ ID NO: 1404, SEQ ID NO: 1144, SEQ ID NO: 1182, SEQ ID NO: 1157, SEQ ID NO: 1160, SEQ ID NO: 1300, SEQ ID NO: 1321, SEQ ID NO: 1323, SEQ ID NO: 1329, SEQ ID NO: 1332, SEQ ID NO: 1345, SEQ ID NO: 1358, SEQ ID NO: 1375, SEQ ID NO: 1417, SEQ ID NO: 1283, SEQ ID NO: 1335, SEQ ID NO: 1368, SEQ ID NO: 1179, SEQ ID NO: 1255, SEQ ID NO: 1258, SEQ ID NO: 1044, SEQ ID NO: 1273, SEQ ID NO: 893, SEQ ID NO: 984, SEQ ID NO: 97, SEQ ID NO: 22, SEQ ID NO: 49, SEQ ID NO: 309, SEQ ID NO: 150, SEQ ID NO: 240, SEQ ID NO: 957, SEQ ID NO: 57, SEQ ID NO: 2, SEQ ID NO: 92, SEQ ID NO: 255, SEQ ID NO: 164, SEQ ID NO: 201, SEQ ID NO: 278, SEQ ID NO: 245, SEQ ID NO: 921, SEQ ID NO: 896, SEQ ID NO: 248, SEQ ID NO: 159, SEQ ID NO: 979, SEQ ID NO: 194, SEQ ID NO: 194, SEQ ID NO: 946, SEQ ID NO: 916, SEQ ID NO: 76, SEQ ID NO: 905, SEQ ID NO: 914, SEQ ID NO: 931, SEQ ID NO: 50, SEQ ID NO: 250, SEQ ID NO: 969, SEQ ID NO: 66, SEQ ID NO: 275, SEQ ID NO: 330, SEQ ID NO: 204, SEQ ID NO: 383, SEQ ID NO: 303, SEQ ID NO: 70, SEQ ID NO: 983, SEQ ID NO: 972, SEQ ID NO: 929, SEQ ID NO: 972, SEQ ID NO: 936, SEQ ID NO: 267, SEQ ID NO: 197, SEQ ID NO: 55, SEQ ID NO: 54, and SEQ ID NO: 210.

In yet another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* transporter polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1219, SEQ ID NO: 1274, SEQ ID NO: 1210, SEQ ID NO: 1422, SEQ ID NO: 1302, SEQ ID NO: 1308, SEQ ID NO: 1310, SEQ ID NO: 1331, SEQ ID NO: 1432, SEQ ID NO: 1052, SEQ ID NO: 1091, SEQ ID NO: 1421, SEQ ID NO: 1069, SEQ ID NO: 1005, SEQ ID NO: 1007, SEQ ID NO: 1166, SEQ ID NO: 1177, SEQ ID NO: 1193, SEQ ID NO: 1206, SEQ ID NO: 1207, SEQ ID NO: 1304, SEQ ID NO: 1305, SEQ ID NO: 1346, SEQ ID NO: 1348, SEQ ID NO: 1350, SEQ ID NO: 1032, SEQ ID NO: 1053, SEQ ID NO: 1081, SEQ ID NO: 1124, SEQ ID NO: 1382, SEQ ID NO: 1437, SEQ ID NO: 1263, SEQ ID NO: 90, SEQ ID NO: 15, SEQ ID NO: 913, SEQ ID NO: 227, SEQ ID NO: 79, SEQ ID NO: 191, SEQ ID NO: 238, SEQ ID NO: 274, SEQ ID NO: 27, SEQ ID NO: 258, SEQ ID NO: 295, SEQ ID NO: 10, SEQ ID NO: 160, SEQ ID NO: 225, SEQ ID NO: 964, SEQ ID NO: 166, SEQ ID NO: 56, SEQ ID NO: 980, SEQ ID NO: 903, SEQ ID NO: 261, SEQ ID NO: 71, SEQ ID NO: 955, SEQ ID NO: 361, SEQ ID NO: 58, SEQ ID NO: 114, SEQ ID NO: 940, SEQ ID NO: 960, SEQ ID NO: 144, SEQ ID NO: 362, SEQ ID NO: 40, SEQ ID NO: 285, SEQ ID NO: 11, SEQ

ID NO: 161, SEQ ID NO: 974, SEQ ID NO: 111, SEQ ID NO: 316, SEQ ID NO: 257, SEQ ID NO: 78, and SEQ ID NO: 966.

In yet a further embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* outer membrane polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1173, SEQ ID NO: 1405, SEQ ID NO: 1406, SEQ ID NO: 1410, SEQ ID NO: 1086, SEQ ID NO: 1322, SEQ ID NO: 1266, SEQ ID NO: 1282, SEQ ID NO: 1271, SEQ ID NO: 1208, SEQ ID NO: 1126, SEQ ID NO: 1270, SEQ ID NO: 1278, SEQ ID NO: 1419, SEQ ID NO: 1125, SEQ ID NO: 1181, SEQ ID NO: 1416, SEQ ID NO: 1096, SEQ ID NO: 1082, SEQ ID NO: 1146, SEQ ID NO: 1145, SEQ ID NO: 1108, SEQ ID NO: 1148, SEQ ID NO: 1337, SEQ ID NO: 1338, SEQ ID NO: 1424, SEQ ID NO: 1000, SEQ ID NO: 1027, SEQ ID NO: 1175, SEQ ID NO: 1330, SEQ ID NO: 352, SEQ ID NO: 981, SEQ ID NO: 158, SEQ ID NO: 989, SEQ ID NO: 963, SEQ ID NO: 48, SEQ ID NO: 68, SEQ ID NO: 135, SEQ ID NO: 910, SEQ ID NO: 236, SEQ ID NO: 241, SEQ ID NO: 949, SEQ ID NO: 945, SEQ ID NO: 207, and SEQ ID NO: 977.

Particularly preferred is an isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* cytoplasmic polypeptide or a fragment thereof. Such nucleic acid is selected from the group consisting of SEQ ID NO: 1147, SEQ ID NO: 1288, SEQ ID NO: 1324, SEQ ID NO: 1363, SEQ ID NO: 997, SEQ ID NO: 1015, SEQ ID NO: 1084, SEQ ID NO: 1094, SEQ ID NO: 1099, SEQ ID NO: 1229, SEQ ID NO: 1250, SEQ ID NO: 1268, SEQ ID NO: 1293, SEQ ID NO: 1339, SEQ ID NO: 1408, SEQ ID NO: 1429, SEQ ID NO: 1434, SEQ ID NO: 1228, SEQ ID NO: 1031, SEQ ID NO: 1034, SEQ ID NO: 1008, SEQ ID NO: 1061, SEQ ID NO: 1064, SEQ ID NO: 1191, SEQ ID NO: 1217, SEQ ID NO: 1365, SEQ ID NO: 1394, SEQ ID NO: 1414, SEQ ID NO: 1415, SEQ ID NO: 1435, SEQ ID NO: 1058, SEQ ID NO: 1059, SEQ ID NO: 1080, SEQ ID NO: 1128, SEQ ID NO: 1133, SEQ ID NO: 1211, SEQ ID NO: 1252, SEQ ID NO: 1253, SEQ ID NO: 1286, SEQ ID NO: 1289, SEQ ID NO: 1291, SEQ ID NO: 1303, SEQ ID NO: 1396, SEQ ID NO: 996, SEQ ID NO: 1095, SEQ ID NO: 1156, SEQ ID NO: 1158, SEQ ID NO: 1159, SEQ ID NO: 1277, SEQ ID NO: 1038, SEQ ID NO: 1257, SEQ ID NO: 1357, SEQ ID NO: 1436, SEQ ID NO: 1047, SEQ ID NO: 1055, SEQ ID NO: 1141, SEQ ID NO: 1227, SEQ ID NO: 1327, SEQ ID NO: 1412, SEQ ID NO: 1003, SEQ ID NO: 1087, SEQ ID NO: 1116, SEQ ID NO: 1130, SEQ ID NO: 1132, SEQ ID NO: 1185, SEQ ID NO: 1188, SEQ ID NO: 1198, SEQ ID NO: 1218, SEQ ID NO: 1244, SEQ ID NO: 1306, SEQ ID NO: 1325, SEQ ID NO: 1397, SEQ ID NO: 1398, SEQ ID NO: 1407, SEQ ID NO: 1433, SEQ ID NO: 1216, SEQ ID NO: 1239, SEQ ID NO: 1362, SEQ ID NO: 1017, SEQ ID NO: 1019, SEQ ID NO: 1360, SEQ ID NO: 1423, SEQ ID NO: 1425, SEQ ID NO: 1374, SEQ ID NO: 1028, SEQ ID NO: 1037, SEQ ID NO: 1077, SEQ ID NO: 1115, SEQ ID NO: 1232, SEQ ID NO: 1241, SEQ ID NO: 1267, SEQ ID NO: 1163, SEQ ID NO: 1068, SEQ ID NO: 1025, SEQ ID NO: 1042, SEQ ID NO: 1046, SEQ ID NO:

1056, SEQ ID NO: 1039, SEQ ID NO: 1072, SEQ ID NO: 1073, SEQ ID NO: 1092, SEQ ID NO: 1100, SEQ ID NO: 1102, SEQ ID NO: 1103, SEQ ID NO: 1104, SEQ ID NO: 1111, SEQ ID NO: 1119, SEQ ID NO: 1136, SEQ ID NO: 1137, SEQ ID NO: 1140, SEQ ID NO: 1142, SEQ ID NO: 1233, SEQ ID NO: 1238, SEQ ID NO: 1243, SEQ ID NO: 1245, SEQ ID NO: 1247, SEQ ID NO: 1249, SEQ ID NO: 1261, SEQ ID NO: 1269, SEQ ID NO: 1279, SEQ ID NO: 1284, SEQ ID NO: 1290, SEQ ID NO: 1297, SEQ ID NO: 1328, SEQ ID NO: 1370, SEQ ID NO: 1372, SEQ ID NO: 1377, SEQ ID NO: 1383, SEQ ID NO: 1384, SEQ ID NO: 1385, SEQ ID NO: 1388, SEQ ID NO: 1401, SEQ ID NO: 1402, SEQ ID NO: 1418, SEQ ID NO: 1420, SEQ ID NO: 1427, SEQ ID NO: 1070, SEQ ID NO: 1151, SEQ ID NO: 1176, SEQ ID NO: 999, SEQ ID NO: 1006, SEQ ID NO: 1012, SEQ ID NO: 1018, SEQ ID NO: 1030, SEQ ID NO: 1033, SEQ ID NO: 1041, SEQ ID NO: 1049, SEQ ID NO: 1054, SEQ ID NO: 1057, SEQ ID NO: 1090, SEQ ID NO: 1097, SEQ ID NO: 1129, SEQ ID NO: 1139, SEQ ID NO: 1143, SEQ ID NO: 1152, SEQ ID NO: 1153, SEQ ID NO: 1155, SEQ ID NO: 1161, SEQ ID NO: 1162, SEQ ID NO: 1169, SEQ ID NO: 1170, SEQ ID NO: 1171, SEQ ID NO: 1180, SEQ ID NO: 1194, SEQ ID NO: 1195, SEQ ID NO: 1199, SEQ ID NO: 1200, SEQ ID NO: 1201, SEQ ID NO: 1202, SEQ ID NO: 1205, SEQ ID NO: 1312, SEQ ID NO: 1336, SEQ ID NO: 1349, SEQ ID NO: 1355, SEQ ID NO: 1359, SEQ ID NO: 1413, SEQ ID NO: 1426, SEQ ID NO: 1430, SEQ ID NO: 882, SEQ ID NO: 382, SEQ ID NO: 130, SEQ ID NO: 230, SEQ ID NO: 269, SEQ ID NO: 312, SEQ ID NO: 211, SEQ ID NO: 959, SEQ ID NO: 938, SEQ ID NO: 110, SEQ ID NO: 244, SEQ ID NO: 328, SEQ ID NO: 235, SEQ ID NO: 315, SEQ ID NO: 296, SEQ ID NO: 976, SEQ ID NO: 321, SEQ ID NO: 43, SEQ ID NO: 281, SEQ ID NO: 326, SEQ ID NO: 272, SEQ ID NO: 344, SEQ ID NO: 139, SEQ ID NO: 30, SEQ ID NO: 220, SEQ ID NO: 364, SEQ ID NO: 369, SEQ ID NO: 372, SEQ ID NO: 991, SEQ ID NO: 128, SEQ ID NO: 347, SEQ ID NO: 52, SEQ ID NO: 12, SEQ ID NO: 247, SEQ ID NO: 64, SEQ ID NO: 101, SEQ ID NO: 338, SEQ ID NO: 83, SEQ ID NO: 46, SEQ ID NO: 348, SEQ ID NO: 223, SEQ ID NO: 39, SEQ ID NO: 232, SEQ ID NO: 168, SEQ ID NO: 65, SEQ ID NO: 952, SEQ ID NO: 341, SEQ ID NO: 69, SEQ ID NO: 924, SEQ ID NO: 4, SEQ ID NO: 197, SEQ ID NO: 313, SEQ ID NO: 119, SEQ ID NO: 188, SEQ ID NO: 956, SEQ ID NO: 935, SEQ ID NO: 246, SEQ ID NO: 196, SEQ ID NO: 376, SEQ ID NO: 172, SEQ ID NO: 25, SEQ ID NO: 126, SEQ ID NO: 951, SEQ ID NO: 147, SEQ ID NO: 895, SEQ ID NO: 14, SEQ ID NO: 154, SEQ ID NO: 277, SEQ ID NO: 363, SEQ ID NO: 342, SEQ ID NO: 378, SEQ ID NO: 130, SEQ ID NO: 198, SEQ ID NO: 243, SEQ ID NO: 19, SEQ ID NO: 9, SEQ ID NO: 149, SEQ ID NO: 167, SEQ ID NO: 349, SEQ ID NO: 209, SEQ ID NO: 990, SEQ ID NO: 185, SEQ ID NO: 883, SEQ ID NO: 8, SEQ ID NO: 887, SEQ ID NO: 350, SEQ ID NO: 987, SEQ ID NO: 63, SEQ ID NO: 249, SEQ ID NO: 118, SEQ ID NO: 132, SEQ ID NO: 47, SEQ ID NO: 106, SEQ ID NO: 324, SEQ ID NO: 155, SEQ ID NO: 121, SEQ ID NO: 153, SEQ ID NO: 87, SEQ ID NO: 986, SEQ ID NO: 262, SEQ ID NO: 333, SEQ ID NO: 36, SEQ ID NO: 982, SEQ ID

NO: 180, SEQ ID NO: 84, SEQ ID NO: 900, SEQ ID NO: 20, SEQ ID NO: 7, SEQ ID NO: 61, SEQ ID NO: 253, SEQ ID NO: 120, SEQ ID NO: 268, SEQ ID NO: 299, SEQ ID NO: 942, SEQ ID NO: 173, SEQ ID NO: 187, SEQ ID NO: 187, SEQ ID NO: 234, SEQ ID NO: 112, SEQ ID NO: 324, SEQ ID NO: 971, SEQ ID NO: 62, SEQ ID NO: 308, SEQ ID NO: 74, SEQ ID NO: 1, SEQ ID NO: 266, SEQ ID NO: 337, SEQ ID NO: 93, SEQ ID NO: 44, SEQ ID NO: 335, SEQ ID NO: 368, SEQ ID NO: 208, SEQ ID NO: 358, SEQ ID NO: 923, SEQ ID NO: 310, SEQ ID NO: 26, SEQ ID NO: 279, SEQ ID NO: 890, SEQ ID NO: 325, SEQ ID NO: 109, SEQ ID NO: 143, SEQ ID NO: 918, SEQ ID NO: 252, SEQ ID NO: 953, SEQ ID NO: 902, SEQ ID NO: 174, SEQ ID NO: 73, SEQ ID NO: 898, SEQ ID NO: 300, SEQ ID NO: 356, SEQ ID NO: 298, SEQ ID NO: 354, SEQ ID NO: 138, SEQ ID NO: 319, SEQ ID NO: 80, SEQ ID NO: 933, SEQ ID NO: 891, SEQ ID NO: 366, SEQ ID NO: 113, SEQ ID NO: 320, SEQ ID NO: 915, SEQ ID NO: 351, SEQ ID NO: 162, SEQ ID NO: 965, SEQ ID NO: 67, SEQ ID NO: 314, SEQ ID NO: 904, SEQ ID NO: 345, SEQ ID NO: 374, SEQ ID NO: 962, SEQ ID NO: 270, SEQ ID NO: 186, SEQ ID NO: 60, SEQ ID NO: 379, SEQ ID NO: 889, SEQ ID NO: 967, SEQ ID NO: 973, SEQ ID NO: 280, SEQ ID NO: 170, SEQ ID NO: 985, and SEQ ID NO: 932.

In one embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in energy conversion encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1147, SEQ ID NO: 1288, SEQ ID NO: 1324, SEQ ID NO: 1363, SEQ ID NO: 882, SEQ ID NO: 382, SEQ ID NO: 130, and SEQ ID NO: 230.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in amino acid metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 997, SEQ ID NO: 1015, SEQ ID NO: 1084, SEQ ID NO: 1094, SEQ ID NO: 1099, SEQ ID NO: 1229, SEQ ID NO: 1250, SEQ ID NO: 1268, SEQ ID NO: 1293, SEQ ID NO: 1339, SEQ ID NO: 1408, SEQ ID NO: 1429, SEQ ID NO: 1434, SEQ ID NO: 1228, SEQ ID NO: 1031, SEQ ID NO: 1034, SEQ ID NO: 1008, SEQ ID NO: 269, SEQ ID NO: 312, SEQ ID NO: 211, SEQ ID NO: 959, SEQ ID NO: 938, SEQ ID NO: 110, SEQ ID NO: 244, SEQ ID NO: 328, SEQ ID NO: 235, SEQ ID NO: 315, SEQ ID NO: 296, SEQ ID NO: 976, SEQ ID NO: 321, SEQ ID NO: 43, SEQ ID NO: 281, SEQ ID NO: 326, and SEQ ID NO: 272.

In yet another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in nucleotide metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1061, SEQ ID NO: 1064, SEQ ID NO: 1191, SEQ ID NO: 1217, SEQ ID NO: 1365, SEQ ID NO: 1394, SEQ ID NO: 1414, SEQ ID NO: 1415, SEQ ID NO: 1435, SEQ ID NO: 1058, SEQ ID NO: 1059, SEQ ID NO: 344, SEQ ID NO: 139, SEQ ID NO: 30, SEQ ID NO: 220,

SEQ ID NO: 364, SEQ ID NO: 369, SEQ ID NO: 372, SEQ ID NO: 991, SEQ ID NO: 128, SEQ ID NO: 347, and SEQ ID NO: 52.

In yet a further embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in carbohydrate metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1080, SEQ ID NO: 1128, SEQ ID NO: 1133, SEQ ID NO: 1211, SEQ ID NO: 1252, SEQ ID NO: 1253, SEQ ID NO: 1286, SEQ ID NO: 1289, SEQ ID NO: 1291, SEQ ID NO: 1303, SEQ ID NO: 1396, SEQ ID NO: 996, SEQ ID NO: 12, SEQ ID NO: 247, SEQ ID NO: 64, SEQ ID NO: 101, SEQ ID NO: 338, SEQ ID NO: 83, SEQ ID NO: 46, SEQ ID NO: 348, SEQ ID NO: 223, SEQ ID NO: 39, SEQ ID NO: 232, and SEQ ID NO: 168.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in cofactor metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1095, SEQ ID NO: 1156, SEQ ID NO: 1158, SEQ ID NO: 1159, SEQ ID NO: 1277, SEQ ID NO: 1038, SEQ ID NO: 65, SEQ ID NO: 952, SEQ ID NO: 341, SEQ ID NO: 69, SEQ ID NO: 924, and SEQ ID NO: 4.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in lipid metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1257, SEQ ID NO: 1357, SEQ ID NO: 1436, SEQ ID NO: 197, SEQ ID NO: 313, and SEQ ID NO: 119.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in mRNA translation and ribosome biogenesis encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1047, SEQ ID NO: 1055, SEQ ID NO: 1141, SEQ ID NO: 1227, SEQ ID NO: 1327, SEQ ID NO: 1412, SEQ ID NO: 188, SEQ ID NO: 956, SEQ ID NO: 935, SEQ ID NO: 246, SEQ ID NO: 196, and SEQ ID NO: 376.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in genome replication, transcription, recombination and repair encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1003, SEQ ID NO: 1087, SEQ ID NO: 1116, SEQ ID NO: 1130, SEQ ID NO: 1132, SEQ ID NO: 1185, SEQ ID NO: 1188, SEQ ID NO: 1198, SEQ ID NO: 1218, SEQ ID NO: 1244, SEQ ID NO: 1306, SEQ ID NO: 1325, SEQ ID NO: 1397, SEQ ID NO: 1398, SEQ ID NO: 1407, SEQ ID NO: 1433, SEQ ID NO: 172, SEQ ID NO: 25, SEQ ID NO: 126, SEQ ID NO: 951, SEQ ID NO: 147, SEQ ID NO: 895, SEQ ID NO: 14, SEQ ID NO: 154, SEQ ID NO: 277, SEQ ID NO: 363, SEQ ID NO: 342, SEQ ID NO: 378, SEQ ID NO: 130, SEQ ID NO: 198, SEQ ID NO: 243, SEQ ID NO: 19, and SEQ ID NO: 9.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in outer membrane or cell wall

biosynthesis encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1216, SEQ ID NO: 1239, SEQ ID NO: 1362, SEQ ID NO: 1017, SEQ ID NO: 1019, SEQ ID NO: 1360, SEQ ID NO: 149, SEQ ID NO: 167, SEQ ID NO: 349, SEQ ID NO: 209, SEQ ID NO: 990, SEQ ID NO: 185, SEQ ID NO: 883, and SEQ ID NO: 8.

- 5 In yet another embodiment, the *H. pylori* cytoplasmic polypeptide is an *H. pylori* chaperone polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1423, SEQ ID NO: 1425, SEQ ID NO: 1374, SEQ ID NO: 887, SEQ ID NO: 350, and SEQ ID NO: 987.

- 10 Particularly preferred is an isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* secreted or periplasmic polypeptide or a fragment thereof. Such nucleic acid is selected from the group consisting of SEQ ID NO: 1004, SEQ ID NO: 1138, SEQ ID NO: 1067, SEQ ID NO: 1078, SEQ ID NO: 1314, SEQ ID NO: 1319, SEQ ID NO: 1378, SEQ ID NO: 1105, SEQ ID NO: 1114, SEQ ID NO: 1118, SEQ ID NO: 1120, SEQ ID NO: 1123, SEQ ID NO: 1127, SEQ ID NO: 1212, SEQ ID NO: 1223, SEQ ID NO: 1225, SEQ ID NO: 1246, SEQ ID NO: 1248, SEQ ID NO: 1259, SEQ ID NO: 1264, SEQ ID NO: 1265, SEQ ID NO: 1281, SEQ ID NO: 1285, SEQ ID NO: 1294, SEQ ID NO: 1298, SEQ ID NO: 1299, SEQ ID NO: 1315, SEQ ID NO: 1316, SEQ ID NO: 1317, SEQ ID NO: 1318, SEQ ID NO: 1344, SEQ ID NO: 1351, SEQ ID NO: 1353, SEQ ID NO: 1373, SEQ ID NO: 1380, SEQ ID NO: 1387, SEQ ID NO: 1389, SEQ ID NO: 1393, SEQ ID NO: 1411, SEQ ID NO: 1428, SEQ ID NO: 1431, SEQ ID NO: 1439, SEQ ID NO: 1043, SEQ ID NO: 1183, SEQ ID NO: 1184, SEQ ID NO: 1196, SEQ ID NO: 1197, SEQ ID NO: 1203, SEQ ID NO: 995, SEQ ID NO: 998, SEQ ID NO: 1001, SEQ ID NO: 1022, SEQ ID NO: 1023, SEQ ID NO: 1029, SEQ ID NO: 1040, SEQ ID NO: 1051, SEQ ID NO: 1062, SEQ ID NO: 1154, SEQ ID NO: 1320, SEQ ID NO: 1075, SEQ ID NO: 1106, SEQ ID NO: 1109, SEQ ID NO: 1134, SEQ ID NO: 1221, SEQ ID NO: 1226, SEQ ID NO: 1235, SEQ ID NO: 1301, SEQ ID NO: 1311, SEQ ID NO: 1326, SEQ ID NO: 1341, SEQ ID NO: 1354, SEQ ID NO: 1364, SEQ ID NO: 1366, SEQ ID NO: 1376, SEQ ID NO: 1391, SEQ ID NO: 1395, SEQ ID NO: 1445, SEQ ID NO: 1079, SEQ ID NO: 1186, SEQ ID NO: 1010, SEQ ID NO: 1016, SEQ ID NO: 1172, SEQ ID NO: 1174, SEQ ID NO: 117, SEQ ID NO: 254, SEQ ID NO: 24, SEQ ID NO: 242, SEQ ID NO: 950, SEQ ID NO: 263, SEQ ID NO: 286, SEQ ID NO: 947, SEQ ID NO: 51, SEQ ID NO: 177, SEQ ID NO: 156, SEQ ID NO: 190, SEQ ID NO: 375, SEQ ID NO: 222, SEQ ID NO: 21, SEQ ID NO: 912, SEQ ID NO: 148, SEQ ID NO: 202, SEQ ID NO: 224, SEQ ID NO: 112, SEQ ID NO: 32, SEQ ID NO: 339, SEQ ID NO: 182, SEQ ID NO: 228, SEQ ID NO: 152, SEQ ID NO: 219, SEQ ID NO: 137, SEQ ID NO: 318, SEQ ID NO: 141, SEQ ID NO: 165, SEQ ID NO: 334, SEQ ID NO: 13, SEQ ID NO: 297, SEQ ID NO: 35, SEQ ID NO: 216, SEQ ID NO: 908, SEQ ID NO: 124, SEQ ID NO: 75, SEQ ID NO: 927, SEQ ID NO: 221, SEQ ID NO: 178, SEQ ID NO: 169, SEQ ID NO: 293, SEQ ID NO: 289, SEQ ID NO: 926, SEQ ID NO: 948, SEQ ID NO: 115, SEQ ID NO: 251, SEQ ID NO: 345, SEQ

- ID NO: 17, SEQ ID NO: 920, SEQ ID NO: 95, SEQ ID NO: 86, SEQ ID NO: 360, SEQ ID NO: 271, SEQ ID NO: 970, SEQ ID NO: 288, SEQ ID NO: 282, SEQ ID NO: 98, SEQ ID NO: 29, SEQ ID NO: 317, SEQ ID NO: 343, SEQ ID NO: 291, SEQ ID NO: 108, SEQ ID NO: 377, SEQ ID NO: 305, SEQ ID NO: 305, SEQ ID NO: 100, SEQ ID NO: 988, SEQ ID NO: 212, SEQ ID NO: 884, SEQ ID NO: 37, SEQ ID NO: 968, SEQ ID NO: 975, SEQ ID NO: 237, SEQ ID NO: 335, SEQ ID NO: 260, SEQ ID NO: 370, SEQ ID NO: 91, SEQ ID NO: 276, SEQ ID NO: 311, SEQ ID NO: 173, SEQ ID NO: 102, SEQ ID NO: 304, SEQ ID NO: 380, SEQ ID NO: 127, SEQ ID NO: 993, SEQ ID NO: 925, SEQ ID NO: 181, and SEQ ID NO: 171.
- 10 Particularly preferred is an isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* surface or membrane polypeptide or a fragment thereof. Such nucleic acid is selected from the group consisting of SEQ ID NO: 1060, SEQ ID NO: 1110, SEQ ID NO: 1112, SEQ ID NO: 1230, SEQ ID NO: 1260, SEQ ID NO: 1280, SEQ ID NO: 1292, SEQ ID NO: 1296, SEQ ID NO: 1307, SEQ ID NO: 1442, SEQ ID NO: 1444,
- 15 SEQ ID NO: 1122, SEQ ID NO: 1254, SEQ ID NO: 1256, SEQ ID NO: 1272, SEQ ID NO: 1275, SEQ ID NO: 1309, SEQ ID NO: 1313, SEQ ID NO: 1347, SEQ ID NO: 1352, SEQ ID NO: 1356, SEQ ID NO: 1438, SEQ ID NO: 1441, SEQ ID NO: 1009, SEQ ID NO: 1026, SEQ ID NO: 1048, SEQ ID NO: 1063, SEQ ID NO: 1190, SEQ ID NO: 1083, SEQ ID NO: 1113, SEQ ID NO: 1222, SEQ ID NO: 1295, SEQ ID NO: 1343, SEQ ID NO: 1392, SEQ ID NO: 1443, SEQ ID NO: 1085, SEQ ID NO: 1093, SEQ ID NO: 1117,
- 20 SEQ ID NO: 1121, SEQ ID NO: 1131, SEQ ID NO: 1287, SEQ ID NO: 1440, SEQ ID NO: 1209, SEQ ID NO: 1342, SEQ ID NO: 1381, SEQ ID NO: 1390, SEQ ID NO: 1409, SEQ ID NO: 1035, SEQ ID NO: 1014, SEQ ID NO: 1088, SEQ ID NO: 1242, SEQ ID NO: 1178, SEQ ID NO: 1089, SEQ ID NO: 1340, SEQ ID NO: 1074, SEQ ID NO: 1107, SEQ ID NO: 1204, SEQ ID NO: 1066, SEQ ID NO: 381, SEQ ID NO: 229, SEQ ID NO: 323, SEQ ID NO: 371, SEQ ID NO: 284, SEQ ID NO: 116, SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 907, SEQ ID NO: 193, SEQ ID NO: 145, SEQ ID NO: 59, SEQ ID NO: 322, SEQ ID NO: 94, SEQ ID NO: 306, SEQ ID NO: 939, SEQ ID NO: 205, SEQ ID NO: 123, SEQ ID NO: 906, SEQ ID NO: 928, SEQ ID NO: 346, SEQ ID NO: 129, SEQ ID NO: 307, SEQ ID NO: 133, SEQ ID NO: 131, SEQ ID NO: 886, SEQ ID NO: 179, SEQ ID NO: 104, SEQ ID NO: 213, SEQ ID NO: 359, SEQ ID NO: 140, SEQ ID NO: 146, SEQ ID NO: 327, SEQ ID NO: 365, SEQ ID NO: 33, SEQ ID NO: 331, SEQ ID NO: 175, SEQ ID NO: 200, SEQ ID NO: 292, SEQ ID NO: 23, SEQ ID NO: 336, SEQ ID NO: 301, SEQ ID NO: 28, SEQ ID NO: 941, SEQ ID NO: 103, SEQ ID NO: 231, SEQ ID NO: 176,
- 35 SEQ ID NO: 31, SEQ ID NO: 917, SEQ ID NO: 151, SEQ ID NO: 922, SEQ ID NO: 265, SEQ ID NO: 142, SEQ ID NO: 259, SEQ ID NO: 122, SEQ ID NO: 206, SEQ ID NO: 96, SEQ ID NO: 353, SEQ ID NO: 38, SEQ ID NO: 89, SEQ ID NO: 77, SEQ ID NO: 954, SEQ ID NO: 264, SEQ ID NO: 937, SEQ ID NO: 226, SEQ ID NO: 283, SEQ ID NO: 88,

SEQ ID NO: 125, SEQ ID NO: 183, SEQ ID NO: 195, SEQ ID NO: 81, SEQ ID NO: 901, SEQ ID NO: 82, SEQ ID NO: 42, SEQ ID NO: 881, and SEQ ID NO: 885.

In one embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least one membrane spanning region encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1060, SEQ ID NO: 1110, SEQ ID NO: 1112, SEQ ID NO: 1230, SEQ ID NO: 1260, SEQ ID NO: 1280, SEQ ID NO: 1292, SEQ ID NO: 1296, SEQ ID NO: 1307, SEQ ID NO: 1442, SEQ ID NO: 1444, SEQ ID NO: 381, SEQ ID NO: 229, SEQ ID NO: 323, SEQ ID NO: 371, SEQ ID NO: 284, SEQ ID NO: 116, SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 907, SEQ ID NO: 193, SEQ ID NO: 145, SEQ ID NO: 59, SEQ ID NO: 322, SEQ ID NO: 94, SEQ ID NO: 306, and SEQ ID NO: 881.

In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least two membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1122, SEQ ID NO: 1254, SEQ ID NO: 1256, SEQ ID NO: 1272, SEQ ID NO: 1275, SEQ ID NO: 1309, SEQ ID NO: 1313, SEQ ID NO: 1347, SEQ ID NO: 1352, SEQ ID NO: 1356, SEQ ID NO: 1438, SEQ ID NO: 1441, SEQ ID NO: 1009, SEQ ID NO: 1026, SEQ ID NO: 1048, SEQ ID NO: 1063, SEQ ID NO: 1190, SEQ ID NO: 939, SEQ ID NO: 205, SEQ ID NO: 123, SEQ ID NO: 906, SEQ ID NO: 928, SEQ ID NO: 346, SEQ ID NO: 129, SEQ ID NO: 307, SEQ ID NO: 133, SEQ ID NO: 131, SEQ ID NO: 886, SEQ ID NO: 179, SEQ ID NO: 104, SEQ ID NO: 213, SEQ ID NO: 359, SEQ ID NO: 140, SEQ ID NO: 146, SEQ ID NO: 327, and SEQ ID NO: 365.

In yet another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least three membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1083, SEQ ID NO: 1113, SEQ ID NO: 1222, SEQ ID NO: 1295, SEQ ID NO: 1343, SEQ ID NO: 1392, SEQ ID NO: 1443, SEQ ID NO: 33, SEQ ID NO: 331, SEQ ID NO: 175, SEQ ID NO: 200, SEQ ID NO: 292, SEQ ID NO: 23, and SEQ ID NO: 336.

In yet a further embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least four membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1085, SEQ ID NO: 1093, SEQ ID NO: 1117, SEQ ID NO: 1121, SEQ ID NO: 1131, SEQ ID NO: 1287, SEQ ID NO: 1440, SEQ ID NO: 1209, SEQ ID NO: 301, SEQ ID NO: 28, SEQ ID NO: 941, SEQ ID NO: 103, SEQ ID NO: 231, SEQ ID NO: 176, SEQ ID NO: 31, SEQ ID NO: 917, SEQ ID NO: 151, and SEQ ID NO: 922.

In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least five membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1342, SEQ ID NO: 1381, SEQ ID NO: 1390, SEQ ID NO: 1409, SEQ ID

NO: 1035, SEQ ID NO: 265, SEQ ID NO: 142, SEQ ID NO: 259, SEQ ID NO: 122, SEQ ID NO: 206, and SEQ ID NO: 885.

In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least six
5 membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1014, SEQ ID NO: 1088, SEQ ID NO: 1242, SEQ ID NO: 1178, SEQ ID NO: 96, SEQ ID NO: 353, SEQ ID NO: 38, SEQ ID NO: 89, SEQ ID NO: 77, SEQ ID NO: 954, SEQ ID NO: 264.

In another embodiment, the *H. pylori* surface or membrane polypeptide or a
10 fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least seven membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1089, SEQ ID NO: 1340, SEQ ID NO: 1074, SEQ ID NO: 1107, SEQ ID NO: 1204, SEQ ID NO: 1066, SEQ ID NO: 937, SEQ ID NO: 226, SEQ ID NO: 283, SEQ ID NO: 88, SEQ ID NO: 125, SEQ ID NO: 183, SEQ ID NO: 195, SEQ ID NO: 81, SEQ
15 ID NO: 901, SEQ ID NO: 82, and SEQ ID NO: 42.

Particularly preferred is a purified or isolated *H. pylori* cell envelope polypeptide or a fragment thereof, wherein the polypeptide is selected from the group consisting of SEQ ID NO: 1471, SEQ ID NO: 1472, SEQ ID NO: 1487, SEQ ID NO: 1501, SEQ ID NO: 1522, SEQ ID NO: 1552, SEQ ID NO: 1586, SEQ ID NO: 1727, SEQ ID NO: 1601, SEQ
20 ID NO: 1638, SEQ ID NO: 1643, SEQ ID NO: 1812, SEQ ID NO: 1830, SEQ ID NO: 1850, SEQ ID NO: 1854, SEQ ID NO: 1851, SEQ ID NO: 1640, SEQ ID NO: 1453, SEQ ID NO: 1664, SEQ ID NO: 1665, SEQ ID NO: 1666, SEQ ID NO: 1685, SEQ ID NO: 1687, SEQ ID NO: 1688, SEQ ID NO: 1675, SEQ ID NO: 1702, SEQ ID NO: 1713, SEQ ID NO: 1600, SEQ ID NO: 1671, SEQ ID NO: 1691, SEQ ID NO: 1615, SEQ ID NO:
25 1616, SEQ ID NO: 1855, SEQ ID NO: 1595, SEQ ID NO: 1633, SEQ ID NO: 1608, SEQ ID NO: 1611, SEQ ID NO: 1751, SEQ ID NO: 1772, SEQ ID NO: 1774, SEQ ID NO: 1780, SEQ ID NO: 1783, SEQ ID NO: 1796, SEQ ID NO: 1809, SEQ ID NO: 1826, SEQ ID NO: 1868, SEQ ID NO: 1734, SEQ ID NO: 1786, SEQ ID NO: 1819, SEQ ID NO: 1630, SEQ ID NO: 1706, SEQ ID NO: 1709, SEQ ID NO: 1495, SEQ ID NO: 1724, SEQ
30 ID NO: 1670, SEQ ID NO: 1725, SEQ ID NO: 1661, SEQ ID NO: 1873, SEQ ID NO: 1753, SEQ ID NO: 1759, SEQ ID NO: 1761, SEQ ID NO: 1782, SEQ ID NO: 1883, SEQ ID NO: 1503, SEQ ID NO: 1542, SEQ ID NO: 1872, SEQ ID NO: 1520, SEQ ID NO: 1456, SEQ ID NO: 1458, SEQ ID NO: 1617, SEQ ID NO: 1628, SEQ ID NO: 1644, SEQ ID NO: 1657, SEQ ID NO: 1658, SEQ ID NO: 1755, SEQ ID NO: 1756, SEQ ID NO:
35 1797, SEQ ID NO: 1799, SEQ ID NO: 1801, SEQ ID NO: 1483, SEQ ID NO: 1504, SEQ ID NO: 1532, SEQ ID NO: 1575, SEQ ID NO: 1833, SEQ ID NO: 1888, SEQ ID NO: 1714, SEQ ID NO: 1624, SEQ ID NO: 1856, SEQ ID NO: 1857, SEQ ID NO: 1861, SEQ ID NO: 1537, SEQ ID NO: 1773, SEQ ID NO: 1717, SEQ ID NO: 1733, SEQ ID NO: 1722, SEQ ID NO: 1659, SEQ ID NO: 1577, SEQ ID NO: 1721, SEQ ID NO: 1729, SEQ

-21-

ID NO: 1870, SEQ ID NO: 1576, SEQ ID NO: 1632, SEQ ID NO: 1867, SEQ ID NO:
 1547, SEQ ID NO: 1533, SEQ ID NO: 1597, SEQ ID NO: 1596, SEQ ID NO: 1559, SEQ
 ID NO: 1599, SEQ ID NO: 1788, SEQ ID NO: 1789, SEQ ID NO: 1875, SEQ ID NO:
 1451, SEQ ID NO: 1478, SEQ ID NO: 1626, SEQ ID NO: 1781, SEQ ID NO: 660, SEQ
 5 ID NO: 660, SEQ ID NO: 855, SEQ ID NO: 534, SEQ ID NO: 675, SEQ ID NO: 404,
 SEQ ID NO: 518, SEQ ID NO: 464, SEQ ID NO: 672, SEQ ID NO: 640, SEQ ID NO:
 490, SEQ ID NO: 755, SEQ ID NO: 389, SEQ ID NO: 635, SEQ ID NO: 877, SEQ ID
 NO: 637, SEQ ID NO: 477, SEQ ID NO: 772, SEQ ID NO: 658, SEQ ID NO: 463, SEQ
 ID NO: 852, SEQ ID NO: 503, SEQ ID NO: 411, SEQ ID NO: 441, SEQ ID NO: 782,
 10 SEQ ID NO: 575, SEQ ID NO: 691, SEQ ID NO: 724, SEQ ID NO: 452, SEQ ID NO:
 386, SEQ ID NO: 497, SEQ ID NO: 712, SEQ ID NO: 591, SEQ ID NO: 638, SEQ ID
 NO: 740, SEQ ID NO: 697, SEQ ID NO: 569, SEQ ID NO: 470, SEQ ID NO: 700, SEQ
 ID NO: 586, SEQ ID NO: 823, SEQ ID NO: 627, SEQ ID NO: 627, SEQ ID NO: 684,
 SEQ ID NO: 551, SEQ ID NO: 478, SEQ ID NO: 508, SEQ ID NO: 545, SEQ ID NO:
 15 628, SEQ ID NO: 443, SEQ ID NO: 702, SEQ ID NO: 776, SEQ ID NO: 461, SEQ ID
 NO: 737, SEQ ID NO: 809, SEQ ID NO: 642, SEQ ID NO: 879, SEQ ID NO: 773, SEQ
 ID NO: 468, SEQ ID NO: 842, SEQ ID NO: 788, SEQ ID NO: 624, SEQ ID NO: 788,
 SEQ ID NO: 644, SEQ ID NO: 727, SEQ ID NO: 631, SEQ ID NO: 450, SEQ ID NO:
 448, SEQ ID NO: 653, SEQ ID NO: 495, SEQ ID NO: 400, SEQ ID NO: 541, SEQ ID
 20 NO: 673, SEQ ID NO: 482, SEQ ID NO: 622, SEQ ID NO: 689, SEQ ID NO: 736, SEQ
 ID NO: 417, SEQ ID NO: 716, SEQ ID NO: 762, SEQ ID NO: 395, SEQ ID NO: 587,
 SEQ ID NO: 669, SEQ ID NO: 758, SEQ ID NO: 593, SEQ ID NO: 451, SEQ ID NO:
 827, SEQ ID NO: 502, SEQ ID NO: 719, SEQ ID NO: 469, SEQ ID NO: 715, SEQ ID
 NO: 847, SEQ ID NO: 453, SEQ ID NO: 527, SEQ ID NO: 652, SEQ ID NO: 745, SEQ
 25 ID NO: 567, SEQ ID NO: 848, SEQ ID NO: 430, SEQ ID NO: 748, SEQ ID NO: 396,
 SEQ ID NO: 588, SEQ ID NO: 795, SEQ ID NO: 523, SEQ ID NO: 791, SEQ ID NO:
 714, SEQ ID NO: 481, SEQ ID NO: 765, SEQ ID NO: 837, SEQ ID NO: 833, SEQ ID
 NO: 585, SEQ ID NO: 865, SEQ ID NO: 764, SEQ ID NO: 440, SEQ ID NO: 465, SEQ
 ID NO: 555, SEQ ID NO: 526, SEQ ID NO: 687, SEQ ID NO: 692, SEQ ID NO: 693,
 30 SEQ ID NO: 677, SEQ ID NO: 649, SEQ ID NO: 812, SEQ ID NO: 820, SEQ ID NO:
 880, SEQ ID NO: 590, SEQ ID NO: 713, SEQ ID NO: 750, SEQ ID NO: 613, SEQ ID NO:
 437, SEQ ID NO: 556, SEQ ID NO: 657, SEQ ID NO: 402, SEQ ID NO: 623, SEQ ID
 NO: 862, SEQ ID NO: 449, SEQ ID NO: 690, SEQ ID NO: 424, SEQ ID NO: 821, SEQ
 ID NO: 432, SEQ ID NO: 811, SEQ ID NO: 554, and SEQ ID NO: 809.

35 In one embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is
 an *H. pylori* flagella-associated polypeptide or a fragment thereof selected from the group
 consisting of SEQ ID NO: 1471, SEQ ID NO: 1472, SEQ ID NO: 1487, SEQ ID NO: 1501,
 SEQ ID NO: 1522, SEQ ID NO: 1552, SEQ ID NO: 1586, SEQ ID NO: 1727, SEQ ID
 NO: 1601, SEQ ID NO: 1638, SEQ ID NO: 1643, SEQ ID NO: 1812, SEQ ID NO: 1830,

-22-

SEQ ID NO: 1850, SEQ ID NO: 1854, SEQ ID NO: 1851, SEQ ID NO: 1640, SEQ ID NO: 660, SEQ ID NO: 660, SEQ ID NO: 855, SEQ ID NO: 534, SEQ ID NO: 675, SEQ ID NO: 404, SEQ ID NO: 518, SEQ ID NO: 464, SEQ ID NO: 672, SEQ ID NO: 640, SEQ ID NO: 490, SEQ ID NO: 755, SEQ ID NO: 389, SEQ ID NO: 635, SEQ ID NO: 877, SEQ ID NO: 637, SEQ ID NO: 477, SEQ ID NO: 772, and SEQ ID NO: 658.

In another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* inner membrane polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1453, SEQ ID NO: 1664, SEQ ID NO: 1665, SEQ ID NO: 1666, SEQ ID NO: 1685, SEQ ID NO: 1687, SEQ ID NO: 1688, SEQ ID NO: 1675, SEQ ID NO: 1702, SEQ ID NO: 1713, SEQ ID NO: 1600, SEQ ID NO: 1671, SEQ ID NO: 1691, SEQ ID NO: 1615, SEQ ID NO: 1616, SEQ ID NO: 1855, SEQ ID NO: 1595, SEQ ID NO: 1633, SEQ ID NO: 1608, SEQ ID NO: 1611, SEQ ID NO: 1751, SEQ ID NO: 1772, SEQ ID NO: 1774, SEQ ID NO: 1780, SEQ ID NO: 1783, SEQ ID NO: 1796, SEQ ID NO: 1809, SEQ ID NO: 1826, SEQ ID NO: 1868, SEQ ID NO: 1734, SEQ ID NO: 1786, SEQ ID NO: 1819, SEQ ID NO: 1630, SEQ ID NO: 1706, SEQ ID NO: 1709, SEQ ID NO: 1495, SEQ ID NO: 1724, SEQ ID NO: 463, SEQ ID NO: 852, SEQ ID NO: 503, SEQ ID NO: 411, SEQ ID NO: 441, SEQ ID NO: 782, SEQ ID NO: 575, SEQ ID NO: 691, SEQ ID NO: 724, SEQ ID NO: 452, SEQ ID NO: 386, SEQ ID NO: 497, SEQ ID NO: 712, SEQ ID NO: 591, SEQ ID NO: 638, SEQ ID NO: 740, SEQ ID NO: 697, SEQ ID NO: 569, SEQ ID NO: 470, SEQ ID NO: 700, SEQ ID NO: 586, SEQ ID NO: 823, SEQ ID NO: 627, SEQ ID NO: 627, SEQ ID NO: 684, SEQ ID NO: 551, SEQ ID NO: 478, SEQ ID NO: 508, SEQ ID NO: 545, SEQ ID NO: 628, SEQ ID NO: 443, SEQ ID NO: 702, SEQ ID NO: 776, SEQ ID NO: 461, SEQ ID NO: 737, SEQ ID NO: 809, SEQ ID NO: 642, SEQ ID NO: 879, SEQ ID NO: 773, SEQ ID NO: 468, SEQ ID NO: 842, SEQ ID NO: 788, SEQ ID NO: 624, SEQ ID NO: 788, SEQ ID NO: 644, SEQ ID NO: 727, SEQ ID NO: 631, SEQ ID NO: 450, SEQ ID NO: 448, and SEQ ID NO: 653.

In yet another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* transporter polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1670, SEQ ID NO: 1725, SEQ ID NO: 1661, SEQ ID NO: 1873, SEQ ID NO: 1753, SEQ ID NO: 1759, SEQ ID NO: 1761, SEQ ID NO: 1782, SEQ ID NO: 1883, SEQ ID NO: 1503, SEQ ID NO: 1542, SEQ ID NO: 1872, SEQ ID NO: 1520, SEQ ID NO: 1456, SEQ ID NO: 1458, SEQ ID NO: 1617, SEQ ID NO: 1628, SEQ ID NO: 1644, SEQ ID NO: 1657, SEQ ID NO: 1658, SEQ ID NO: 1755, SEQ ID NO: 1756, SEQ ID NO: 1797, SEQ ID NO: 1799, SEQ ID NO: 1801, SEQ ID NO: 1483, SEQ ID NO: 1504, SEQ ID NO: 1532, SEQ ID NO: 1575, SEQ ID NO: 1833, SEQ ID NO: 1888, SEQ ID NO: 1714, SEQ ID NO: 495, SEQ ID NO: 400, SEQ ID NO: 541, SEQ ID NO: 673, SEQ ID NO: 482, SEQ ID NO: 622, SEQ ID NO: 689, SEQ ID NO: 736, SEQ ID NO: 417, SEQ ID NO: 716, SEQ ID NO: 762, SEQ ID NO: 395, SEQ ID NO: 587, SEQ ID NO: 669, SEQ ID NO: 758, SEQ ID NO: 593, SEQ ID NO: 451, SEQ ID NO: 827,

SEQ ID NO: 502, SEQ ID NO: 719, SEQ ID NO: 469, SEQ ID NO: 715, SEQ ID NO: 847, SEQ ID NO: 453, SEQ ID NO: 527, SEQ ID NO: 652, SEQ ID NO: 745, SEQ ID NO: 567, SEQ ID NO: 848, SEQ ID NO: 430, SEQ ID NO: 748, SEQ ID NO: 396, SEQ ID NO: 588, SEQ ID NO: 795, SEQ ID NO: 523, SEQ ID NO: 791, SEQ ID NO: 714, 5 SEQ ID NO: 481, and SEQ ID NO: 765.

In another embodiment, the *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* outer membrane polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1624, SEQ ID NO: 1856, SEQ ID NO: 1857, SEQ ID NO: 1861, SEQ ID NO: 1537, SEQ ID NO: 1773, SEQ ID NO: 1717, SEQ ID NO: 1733, 10 SEQ ID NO: 1722, SEQ ID NO: 1659, SEQ ID NO: 1577, SEQ ID NO: 1721, SEQ ID NO: 1729, SEQ ID NO: 1870, SEQ ID NO: 1576, SEQ ID NO: 1632, SEQ ID NO: 1867, SEQ ID NO: 1547, SEQ ID NO: 1533, SEQ ID NO: 1597, SEQ ID NO: 1596, SEQ ID NO: 1559, SEQ ID NO: 1599, SEQ ID NO: 1788, SEQ ID NO: 1789, SEQ ID NO: 1875, SEQ ID NO: 1451, SEQ ID NO: 1478, SEQ ID NO: 1626, SEQ ID NO: 1781, SEQ ID NO: 837, SEQ ID NO: 833, SEQ ID NO: 585, SEQ ID NO: 865, SEQ ID NO: 764, SEQ 15 ID NO: 440, SEQ ID NO: 465, SEQ ID NO: 555, SEQ ID NO: 526, SEQ ID NO: 687, SEQ ID NO: 692, SEQ ID NO: 693, SEQ ID NO: 677, SEQ ID NO: 649, and SEQ ID NO: 812.

Particularly preferred is a purified or isolated *H. pylori* cytoplasmic polypeptide or a 20 fragment thereof, wherein the polypeptide is selected from the group consisting of SEQ ID NO: 1598, SEQ ID NO: 1739, SEQ ID NO: 1775, SEQ ID NO: 1814, SEQ ID NO: 1448, SEQ ID NO: 1466, SEQ ID NO: 1535, SEQ ID NO: 1545, SEQ ID NO: 1550, SEQ ID NO: 1680, SEQ ID NO: 1701, SEQ ID NO: 1719, SEQ ID NO: 1744, SEQ ID NO: 1790, SEQ ID NO: 1859, SEQ ID NO: 1880, SEQ ID NO: 1885, SEQ ID NO: 1679, SEQ ID NO: 1482, SEQ ID NO: 1485, SEQ ID NO: 1459, SEQ ID NO: 1512, SEQ ID NO: 1515, 25 SEQ ID NO: 1642, SEQ ID NO: 1668, SEQ ID NO: 1816, SEQ ID NO: 1845, SEQ ID NO: 1865, SEQ ID NO: 1866, SEQ ID NO: 1886, SEQ ID NO: 1509, SEQ ID NO: 1510, SEQ ID NO: 1531, SEQ ID NO: 1579, SEQ ID NO: 1584, SEQ ID NO: 1662, SEQ ID NO: 1703, SEQ ID NO: 1704, SEQ ID NO: 1737, SEQ ID NO: 1740, SEQ ID NO: 1742, 30 SEQ ID NO: 1754, SEQ ID NO: 1847, SEQ ID NO: 1447, SEQ ID NO: 1546, SEQ ID NO: 1607, SEQ ID NO: 1609, SEQ ID NO: 1610, SEQ ID NO: 1728, SEQ ID NO: 1489, SEQ ID NO: 1708, SEQ ID NO: 1808, SEQ ID NO: 1887, SEQ ID NO: 1498, SEQ ID NO: 1506, SEQ ID NO: 1592, SEQ ID NO: 1678, SEQ ID NO: 1778, SEQ ID NO: 1863, SEQ ID NO: 1454, SEQ ID NO: 1538, SEQ ID NO: 1567, SEQ ID NO: 1581, SEQ ID NO: 1583, SEQ ID NO: 1636, SEQ ID NO: 1639, SEQ ID NO: 1649, SEQ ID NO: 1669, 35 SEQ ID NO: 1695, SEQ ID NO: 1757, SEQ ID NO: 1776, SEQ ID NO: 1848, SEQ ID NO: 1849, SEQ ID NO: 1858, SEQ ID NO: 1884, SEQ ID NO: 1667, SEQ ID NO: 1690, SEQ ID NO: 1813, SEQ ID NO: 1468, SEQ ID NO: 1470, SEQ ID NO: 1811, SEQ ID NO: 1874, SEQ ID NO: 1876, SEQ ID NO: 1825, SEQ ID NO: 1479, SEQ ID NO: 1488,

-24-

SEQ ID NO: 1528, SEQ ID NO: 1566, SEQ ID NO: 1683, SEQ ID NO: 1692, SEQ ID NO: 1718, SEQ ID NO: 1614, SEQ ID NO: 1519, SEQ ID NO: 1476, SEQ ID NO: 1493, SEQ ID NO: 1497, SEQ ID NO: 1507, SEQ ID NO: 1490, SEQ ID NO: 1523, SEQ ID NO: 1524, SEQ ID NO: 1543, SEQ ID NO: 1551, SEQ ID NO: 1553, SEQ ID NO: 1554, 5 SEQ ID NO: 1555, SEQ ID NO: 1562, SEQ ID NO: 1570, SEQ ID NO: 1587, SEQ ID NO: 1588, SEQ ID NO: 1591, SEQ ID NO: 1593, SEQ ID NO: 1684, SEQ ID NO: 1689, SEQ ID NO: 1694, SEQ ID NO: 1696, SEQ ID NO: 1698, SEQ ID NO: 1700, SEQ ID NO: 1712, SEQ ID NO: 1720, SEQ ID NO: 1730, SEQ ID NO: 1735, SEQ ID NO: 1741, SEQ ID NO: 1748, SEQ ID NO: 1779, SEQ ID NO: 1821, SEQ ID NO: 1823, SEQ ID 10 NO: 1828, SEQ ID NO: 1834, SEQ ID NO: 1835, SEQ ID NO: 1836, SEQ ID NO: 1839, SEQ ID NO: 1852, SEQ ID NO: 1853, SEQ ID NO: 1869, SEQ ID NO: 1871, SEQ ID NO: 1878, SEQ ID NO: 1521, SEQ ID NO: 1602, SEQ ID NO: 1627, SEQ ID NO: 1450, SEQ ID NO: 1457, SEQ ID NO: 1463, SEQ ID NO: 1469, SEQ ID NO: 1481, SEQ ID NO: 1484, SEQ ID NO: 1492, SEQ ID NO: 1500, SEQ ID NO: 1505, SEQ ID NO: 1508, 15 SEQ ID NO: 1541, SEQ ID NO: 1548, SEQ ID NO: 1580, SEQ ID NO: 1590, SEQ ID NO: 1594, SEQ ID NO: 1603, SEQ ID NO: 1604, SEQ ID NO: 1606, SEQ ID NO: 1612, SEQ ID NO: 1613, SEQ ID NO: 1620, SEQ ID NO: 1621, SEQ ID NO: 1622, SEQ ID NO: 1631, SEQ ID NO: 1645, SEQ ID NO: 1646, SEQ ID NO: 1650, SEQ ID NO: 1651, SEQ ID NO: 1652, SEQ ID NO: 1653, SEQ ID NO: 1656, SEQ ID NO: 1763, SEQ ID 20 NO: 1787, SEQ ID NO: 1800, SEQ ID NO: 1806, SEQ ID NO: 1810, SEQ ID NO: 1864, SEQ ID NO: 1877, SEQ ID NO: 1881, SEQ ID NO: 390, SEQ ID NO: 876, SEQ ID NO: 547, SEQ ID NO: 678, SEQ ID NO: 729, SEQ ID NO: 786, SEQ ID NO: 654, SEQ ID NO: 734, SEQ ID NO: 646, SEQ ID NO: 522, SEQ ID NO: 696, SEQ ID NO: 807, SEQ ID NO: 683, SEQ ID NO: 790, SEQ ID NO: 763, SEQ ID NO: 806, SEQ ID NO: 799, 25 SEQ ID NO: 434, SEQ ID NO: 743, SEQ ID NO: 804, SEQ ID NO: 733, SEQ ID NO: 826, SEQ ID NO: 562, SEQ ID NO: 420, SEQ ID NO: 664, SEQ ID NO: 850, SEQ ID NO: 857, SEQ ID NO: 861, SEQ ID NO: 872, SEQ ID NO: 544, SEQ ID NO: 830, SEQ ID NO: 446, SEQ ID NO: 397, SEQ ID NO: 699, SEQ ID NO: 459, SEQ ID NO: 509, SEQ ID NO: 818, SEQ ID NO: 488, SEQ ID NO: 438, SEQ ID NO: 831, SEQ ID NO: 30 667, SEQ ID NO: 429, SEQ ID NO: 680, SEQ ID NO: 597, SEQ ID NO: 460, SEQ ID NO: 709, SEQ ID NO: 822, SEQ ID NO: 466, SEQ ID NO: 584, SEQ ID NO: 388, SEQ ID NO: 631, SEQ ID NO: 787, SEQ ID NO: 532, SEQ ID NO: 619, SEQ ID NO: 723, SEQ ID NO: 641, SEQ ID NO: 698, SEQ ID NO: 630, SEQ ID NO: 869, SEQ ID NO: 601, SEQ ID NO: 415, SEQ ID NO: 542, SEQ ID NO: 704, SEQ ID NO: 572, SEQ ID 35 NO: 467, SEQ ID NO: 399, SEQ ID NO: 579, SEQ ID NO: 739, SEQ ID NO: 849, SEQ ID NO: 824, SEQ ID NO: 871, SEQ ID NO: 547, SEQ ID NO: 633, SEQ ID NO: 695, SEQ ID NO: 405, SEQ ID NO: 394, SEQ ID NO: 761, SEQ ID NO: 574, SEQ ID NO: 596, SEQ ID NO: 832, SEQ ID NO: 651, SEQ ID NO: 867, SEQ ID NO: 614, SEQ ID NO: 401, SEQ ID NO: 393, SEQ ID NO: 413, SEQ ID NO: 835, SEQ ID NO: 863, SEQ

ID NO: 458, SEQ ID NO: 701, SEQ ID NO: 531, SEQ ID NO: 550, SEQ ID NO: 439, SEQ ID NO: 516, SEQ ID NO: 802, SEQ ID NO: 581, SEQ ID NO: 535, SEQ ID NO: 578, SEQ ID NO: 492, SEQ ID NO: 858, SEQ ID NO: 720, SEQ ID NO: 813, SEQ ID NO: 426, SEQ ID NO: 834, SEQ ID NO: 609, SEQ ID NO: 489, SEQ ID NO: 480, SEQ ID NO: 406, SEQ ID NO: 392, SEQ ID NO: 456, SEQ ID NO: 707, SEQ ID NO: 533, SEQ ID NO: 728, SEQ ID NO: 769, SEQ ID NO: 671, SEQ ID NO: 602, SEQ ID NO: 618, SEQ ID NO: 618, SEQ ID NO: 682, SEQ ID NO: 524, SEQ ID NO: 802, SEQ ID NO: 785, SEQ ID NO: 457, SEQ ID NO: 781, SEQ ID NO: 473, SEQ ID NO: 384, SEQ ID NO: 726, SEQ ID NO: 817, SEQ ID NO: 498, SEQ ID NO: 436, SEQ ID NO: 815, SEQ ID NO: 856, SEQ ID NO: 650, SEQ ID NO: 844, SEQ ID NO: 580, SEQ ID NO: 783, SEQ ID NO: 416, SEQ ID NO: 741, SEQ ID NO: 442, SEQ ID NO: 803, SEQ ID NO: 520, SEQ ID NO: 566, SEQ ID NO: 557, SEQ ID NO: 706, SEQ ID NO: 710, SEQ ID NO: 487, SEQ ID NO: 603, SEQ ID NO: 472, SEQ ID NO: 476, SEQ ID NO: 770, SEQ ID NO: 841, SEQ ID NO: 768, SEQ ID NO: 839, SEQ ID NO: 560, SEQ ID NO: 796, SEQ ID NO: 483, SEQ ID NO: 634, SEQ ID NO: 445, SEQ ID NO: 853, SEQ ID NO: 525, SEQ ID NO: 798, SEQ ID NO: 549, SEQ ID NO: 836, SEQ ID NO: 589, SEQ ID NO: 760, SEQ ID NO: 462, SEQ ID NO: 789, SEQ ID NO: 507, SEQ ID NO: 828, SEQ ID NO: 866, SEQ ID NO: 754, SEQ ID NO: 730, SEQ ID NO: 617, SEQ ID NO: 455, SEQ ID NO: 873, SEQ ID NO: 435, SEQ ID NO: 766, SEQ ID NO: 793, SEQ ID NO: 742, SEQ ID NO: 599, SEQ ID NO: 854, and SEQ ID NO: 632.

In one embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in energy conversion selected from the group consisting of SEQ ID NO: 1598, SEQ ID NO: 1739, SEQ ID NO: 1775, SEQ ID NO: 1814, SEQ ID NO: 390, SEQ ID NO: 876, SEQ ID NO: 547, and SEQ ID NO: 678.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in amino acid metabolism selected from the group consisting of SEQ ID NO: 1448, SEQ ID NO: 1466, SEQ ID NO: 1535, SEQ ID NO: 1545, SEQ ID NO: 1550, SEQ ID NO: 1680, SEQ ID NO: 1701, SEQ ID NO: 1719, SEQ ID NO: 1744, SEQ ID NO: 1790, SEQ ID NO: 1859, SEQ ID NO: 1880, SEQ ID NO: 1885, SEQ ID NO: 1679, SEQ ID NO: 1482, SEQ ID NO: 1485, SEQ ID NO: 1459, SEQ ID NO: 729, SEQ ID NO: 786, SEQ ID NO: 654, SEQ ID NO: 734, SEQ ID NO: 646, SEQ ID NO: 522, SEQ ID NO: 696, SEQ ID NO: 807, SEQ ID NO: 683, SEQ ID NO: 790, SEQ ID NO: 763, SEQ ID NO: 806, SEQ ID NO: 799, SEQ ID NO: 434, SEQ ID NO: 743, SEQ ID NO: 804, and SEQ ID NO: 733.

In yet another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in nucleotide metabolism selected from the group consisting of SEQ ID NO: 1512, SEQ ID NO: 1515, SEQ ID NO: 1642, SEQ ID NO: 1668, SEQ ID NO: 1816, SEQ ID NO: 1845, SEQ ID NO: 1865, SEQ ID NO: 1866, SEQ ID NO: 1886, SEQ ID NO: 1509, SEQ ID NO: 1510, SEQ ID NO: 826,

SEQ ID NO: 562, SEQ ID NO: 420, SEQ ID NO: 664, SEQ ID NO: 850, SEQ ID NO: 857, SEQ ID NO: 861, SEQ ID NO: 872, SEQ ID NO: 544, SEQ ID NO: 830, and SEQ ID NO: 446.

5 In yet a further embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in carbohydrate metabolism selected from the group consisting of SEQ ID NO: 1531, SEQ ID NO: 1579, SEQ ID NO: 1584, SEQ ID NO: 1662, SEQ ID NO: 1703, SEQ ID NO: 1704, SEQ ID NO: 1737, SEQ ID NO: 1740, SEQ ID NO: 1742, SEQ ID NO: 1754, SEQ ID NO: 1847, SEQ ID NO: 1447, SEQ ID NO: 397, SEQ ID NO: 699, SEQ ID NO: 459, SEQ ID NO: 10 509, SEQ ID NO: 818, SEQ ID NO: 488, SEQ ID NO: 438, SEQ ID NO: 831, SEQ ID NO: 667, SEQ ID NO: 429, SEQ ID NO: 680, and SEQ ID NO: 597.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in cofactor metabolism selected from the group consisting of SEQ ID NO: 1546, SEQ ID NO: 1607, SEQ ID NO: 1609, 15 1610, SEQ ID NO: 1728, SEQ ID NO: 1489, SEQ ID NO: 460, SEQ ID NO: 709, SEQ ID NO: 822, SEQ ID NO: 466, SEQ ID NO: 584, and SEQ ID NO: 388.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in lipid metabolism selected from the group consisting of SEQ ID NO: 1708, SEQ ID NO: 1808, SEQ ID NO: 1887, 20 SEQ ID NO: 631, SEQ ID NO: 787, and SEQ ID NO: 532.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in mRNA translation and ribosome biogenesis selected from the group consisting of SEQ ID NO: 1498, SEQ ID NO: 1506, SEQ ID NO: 1592, SEQ ID NO: 1678, SEQ ID NO: 1778, SEQ ID NO: 1863, SEQ 25 ID NO: 619, SEQ ID NO: 723, SEQ ID NO: 641, SEQ ID NO: 698, SEQ ID NO: 630, and SEQ ID NO: 869.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in genome replication, transcription, recombination and repair selected from the group consisting of SEQ ID NO: 30 1454, SEQ ID NO: 1538, SEQ ID NO: 1567, SEQ ID NO: 1581, SEQ ID NO: 1583, SEQ ID NO: 1636, SEQ ID NO: 1639, SEQ ID NO: 1649, SEQ ID NO: 1669, SEQ ID NO: 1695, SEQ ID NO: 1757, SEQ ID NO: 1776, SEQ ID NO: 1848, SEQ ID NO: 1849, SEQ ID NO: 1858, SEQ ID NO: 1884, SEQ ID NO: 601, SEQ ID NO: 415, SEQ ID NO: 542, SEQ ID NO: 704, SEQ ID NO: 572, SEQ ID NO: 467, SEQ ID NO: 399, SEQ ID NO: 35 579, SEQ ID NO: 739, SEQ ID NO: 849, SEQ ID NO: 824, SEQ ID NO: 871, SEQ ID NO: 547, SEQ ID NO: 633, SEQ ID NO: 695, SEQ ID NO: 405, SEQ ID NO: 394, and SEQ ID NO: 761.

In another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in outer membrane or cell wall

-27-

biosynthesis selected from the group consisting of SEQ ID NO: 1667, SEQ ID NO: 1690, SEQ ID NO: 1813, SEQ ID NO: 1468, SEQ ID NO: 1470, SEQ ID NO: 1811, SEQ ID NO: 574, SEQ ID NO: 596, SEQ ID NO: 832, SEQ ID NO: 651, SEQ ID NO: 867, SEQ ID NO: 614, SEQ ID NO: 401, and SEQ ID NO: 393.

- 5 In yet another embodiment, the *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* chaperone polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1874, SEQ ID NO: 1876, SEQ ID NO: 1825, SEQ ID NO: 413, SEQ ID NO: 835, and SEQ ID NO: 863.

- Particularly preferred is a purified or isolated *H. pylori* secreted or periplasmic polypeptide or a fragment thereof, wherein the polypeptide is selected from the group consisting of SEQ ID NO: 1455, SEQ ID NO: 1589, SEQ ID NO: 1518, SEQ ID NO: 1529, SEQ ID NO: 1765, SEQ ID NO: 1770, SEQ ID NO: 1829, SEQ ID NO: 1556, SEQ ID NO: 1565, SEQ ID NO: 1569, SEQ ID NO: 1571, SEQ ID NO: 1574, SEQ ID NO: 1578, SEQ ID NO: 1663, SEQ ID NO: 1674, SEQ ID NO: 1676, SEQ ID NO: 1697, SEQ ID NO: 1699, SEQ ID NO: 1710, SEQ ID NO: 1715, SEQ ID NO: 1716, SEQ ID NO: 1732, SEQ ID NO: 1736, SEQ ID NO: 1745, SEQ ID NO: 1749, SEQ ID NO: 1750, SEQ ID NO: 1766, SEQ ID NO: 1767, SEQ ID NO: 1768, SEQ ID NO: 1769, SEQ ID NO: 1795, SEQ ID NO: 1802, SEQ ID NO: 1804, SEQ ID NO: 1824, SEQ ID NO: 1831, SEQ ID NO: 1838, SEQ ID NO: 1840, SEQ ID NO: 1844, SEQ ID NO: 1862, SEQ ID NO: 1879, SEQ ID NO: 1882, SEQ ID NO: 1890, SEQ ID NO: 1494, SEQ ID NO: 1634, SEQ ID NO: 1635, SEQ ID NO: 1647, SEQ ID NO: 1648, SEQ ID NO: 1654, SEQ ID NO: 1446, SEQ ID NO: 1449, SEQ ID NO: 1452, SEQ ID NO: 1473, SEQ ID NO: 1474, SEQ ID NO: 1480, SEQ ID NO: 1491, SEQ ID NO: 1502, SEQ ID NO: 1513, SEQ ID NO: 1605, SEQ ID NO: 1771, SEQ ID NO: 1526, SEQ ID NO: 1557, SEQ ID NO: 1560, SEQ ID NO: 1585, SEQ ID NO: 1672, SEQ ID NO: 1677, SEQ ID NO: 1686, SEQ ID NO: 1752, SEQ ID NO: 1762, SEQ ID NO: 1777, SEQ ID NO: 1792, SEQ ID NO: 1805, SEQ ID NO: 1815, SEQ ID NO: 1817, SEQ ID NO: 1827, SEQ ID NO: 1842, SEQ ID NO: 1846, SEQ ID NO: 1896, SEQ ID NO: 1530, SEQ ID NO: 1637, SEQ ID NO: 1461, SEQ ID NO: 1467, SEQ ID NO: 1623, SEQ ID NO: 1625, SEQ ID NO: 530, SEQ ID NO: 708, SEQ ID NO: 414, SEQ ID NO: 694, SEQ ID NO: 703, SEQ ID NO: 721, SEQ ID NO: 749, SEQ ID NO: 685, SEQ ID NO: 444, SEQ ID NO: 606, SEQ ID NO: 582, SEQ ID NO: 621, SEQ ID NO: 868, SEQ ID NO: 666, SEQ ID NO: 408, SEQ ID NO: 538, SEQ ID NO: 573, SEQ ID NO: 639, SEQ ID NO: 668, SEQ ID NO: 524, SEQ ID NO: 422, SEQ ID NO: 819, SEQ ID NO: 611, SEQ ID NO: 674, SEQ ID NO: 577, SEQ ID NO: 663, SEQ ID NO: 558, SEQ ID NO: 794, SEQ ID NO: 564, SEQ ID NO: 592, SEQ ID NO: 814, SEQ ID NO: 398, SEQ ID NO: 767, SEQ ID NO: 425, SEQ ID NO: 659, SEQ ID NO: 517, SEQ ID NO: 539, SEQ ID NO: 475, SEQ ID NO: 615, SEQ ID NO: 665, SEQ ID NO: 607, SEQ ID NO: 598, SEQ ID NO: 759, SEQ ID NO: 752, SEQ ID NO: 595, SEQ ID NO: 686, SEQ ID NO: 528, SEQ ID NO: 705, SEQ ID NO: 828, SEQ ID

-28-

NO: 403, SEQ ID NO: 561, SEQ ID NO: 500, SEQ ID NO: 491, SEQ ID NO: 846, SEQ ID NO: 732, SEQ ID NO: 778, SEQ ID NO: 751, SEQ ID NO: 744, SEQ ID NO: 504, SEQ ID NO: 419, SEQ ID NO: 792, SEQ ID NO: 825, SEQ ID NO: 756, SEQ ID NO: 519, SEQ ID NO: 870, SEQ ID NO: 777, SEQ ID NO: 808, SEQ ID NO: 506, SEQ ID NO: 864, SEQ ID NO: 655, SEQ ID NO: 407, SEQ ID NO: 427, SEQ ID NO: 774, SEQ ID NO: 797, SEQ ID NO: 688, SEQ ID NO: 815, SEQ ID NO: 718, SEQ ID NO: 859, SEQ ID NO: 775, SEQ ID NO: 874, SEQ ID NO: 543, SEQ ID NO: 878, SEQ ID NO: 594, SEQ ID NO: 610, and SEQ ID NO: 600.

Particularly preferred is a purified or isolated *H. pylori* surface or membrane polypeptide or a fragment thereof, wherein the polypeptide is selected from the group consisting of SEQ ID NO: 1511, SEQ ID NO: 1561, SEQ ID NO: 1563, SEQ ID NO: 1681, SEQ ID NO: 1711, SEQ ID NO: 1731, SEQ ID NO: 1743, SEQ ID NO: 1747, SEQ ID NO: 1758, SEQ ID NO: 1893, SEQ ID NO: 1895, SEQ ID NO: 1573, SEQ ID NO: 1705, SEQ ID NO: 1707, SEQ ID NO: 1723, SEQ ID NO: 1726, SEQ ID NO: 1760, SEQ ID NO: 1764, SEQ ID NO: 1798, SEQ ID NO: 1803, SEQ ID NO: 1807, SEQ ID NO: 1889, SEQ ID NO: 1892, SEQ ID NO: 1460, SEQ ID NO: 1477, SEQ ID NO: 1499, SEQ ID NO: 1514, SEQ ID NO: 1641, SEQ ID NO: 1534, SEQ ID NO: 1564, SEQ ID NO: 1673, SEQ ID NO: 1746, SEQ ID NO: 1794, SEQ ID NO: 1843, SEQ ID NO: 1894, SEQ ID NO: 1536, SEQ ID NO: 1544, SEQ ID NO: 1568, SEQ ID NO: 1572, SEQ ID NO: 1582, SEQ ID NO: 1738, SEQ ID NO: 1891, SEQ ID NO: 1660, SEQ ID NO: 1793, SEQ ID NO: 1832, SEQ ID NO: 1841, SEQ ID NO: 1860, SEQ ID NO: 1486, SEQ ID NO: 1465, SEQ ID NO: 1539, SEQ ID NO: 1693, SEQ ID NO: 1629, SEQ ID NO: 1540, SEQ ID NO: 1791, SEQ ID NO: 1525, SEQ ID NO: 1558, SEQ ID NO: 1655, SEQ ID NO: 1517, SEQ ID NO: 875, SEQ ID NO: 676, SEQ ID NO: 801, SEQ ID NO: 860, SEQ ID NO: 747, SEQ ID NO: 529, SEQ ID NO: 387, SEQ ID NO: 391, SEQ ID NO: 515, SEQ ID NO: 625, SEQ ID NO: 568, SEQ ID NO: 454, SEQ ID NO: 800, SEQ ID NO: 499, SEQ ID NO: 779, SEQ ID NO: 648, SEQ ID NO: 643, SEQ ID NO: 537, SEQ ID NO: 511, SEQ ID NO: 616, SEQ ID NO: 829, SEQ ID NO: 546, SEQ ID NO: 780, SEQ ID NO: 553, SEQ ID NO: 549, SEQ ID NO: 410, SEQ ID NO: 608, SEQ ID NO: 513, SEQ ID NO: 656, SEQ ID NO: 845, SEQ ID NO: 563, SEQ ID NO: 570, SEQ ID NO: 805, SEQ ID NO: 851, SEQ ID NO: 423, SEQ ID NO: 810, SEQ ID NO: 604, SEQ ID NO: 636, SEQ ID NO: 757, SEQ ID NO: 412, SEQ ID NO: 816, SEQ ID NO: 771, SEQ ID NO: 418, SEQ ID NO: 662, SEQ ID NO: 512, SEQ ID NO: 679, SEQ ID NO: 605, SEQ ID NO: 421, SEQ ID NO: 552, SEQ ID NO: 576, SEQ ID NO: 571, SEQ ID NO: 725, SEQ ID NO: 565, SEQ ID NO: 717, SEQ ID NO: 536, SEQ ID NO: 647, SEQ ID NO: 501, SEQ ID NO: 838, SEQ ID NO: 428, SEQ ID NO: 494, SEQ ID NO: 479, SEQ ID NO: 711, SEQ ID NO: 722, SEQ ID NO: 645, SEQ ID NO: 670, SEQ ID NO: 746, SEQ ID NO: 493, SEQ ID NO: 540, SEQ ID NO: 612, SEQ ID NO: 629, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 433, SEQ ID NO: 385, and SEQ ID NO: 409.

In one embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least one membrane spanning region selected from the group consisting of SEQ ID NO: 1511, SEQ ID NO: 1561, SEQ ID NO: 1563, SEQ ID NO: 1681, SEQ ID NO: 1711, SEQ ID NO: 1731, SEQ ID NO: 1743, SEQ ID NO: 1747, SEQ ID NO: 1758, SEQ ID NO: 1893, SEQ ID NO: 1895, SEQ ID NO: 875, SEQ ID NO: 676, SEQ ID NO: 801, SEQ ID NO: 860, SEQ ID NO: 747, SEQ ID NO: 529, SEQ ID NO: 387, SEQ ID NO: 391, SEQ ID NO: 515, SEQ ID NO: 625, SEQ ID NO: 568, SEQ ID NO: 454, SEQ ID NO: 800, SEQ ID NO: 499, SEQ ID NO: 779, and SEQ ID NO: 385.

10 In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least two membrane spanning regions selected from the group consisting of SEQ ID NO: 1573, SEQ ID NO: 1705, SEQ ID NO: 1707, SEQ ID NO: 1723, SEQ ID NO: 1726, SEQ ID NO: 1760, SEQ ID NO: 1764, SEQ ID NO: 1798, SEQ ID NO: 1803, SEQ ID NO: 1807, SEQ ID NO: 1889, SEQ ID NO: 1892, SEQ ID NO: 1460, SEQ ID NO: 1477, SEQ ID NO: 1499, SEQ ID NO: 1514, SEQ ID NO: 1641, SEQ ID NO: 648, SEQ ID NO: 643, SEQ ID NO: 537, SEQ ID NO: 511, SEQ ID NO: 616, SEQ ID NO: 829, SEQ ID NO: 546, SEQ ID NO: 780, SEQ ID NO: 553, SEQ ID NO: 549, SEQ ID NO: 410, SEQ ID NO: 608, SEQ ID NO: 513, SEQ ID NO: 656, SEQ ID NO: 845, SEQ ID NO: 563, SEQ ID NO: 570, SEQ ID NO: 805, and SEQ ID NO: 851.

20 In yet another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least three membrane spanning regions selected from the group consisting of SEQ ID NO: 1534, SEQ ID NO: 1564, SEQ ID NO: 1673, SEQ ID NO: 1746, SEQ ID NO: 1794, SEQ ID NO: 1843, SEQ ID NO: 1894, SEQ ID NO: 423, SEQ ID NO: 810, SEQ ID NO: 604, SEQ ID NO: 636, SEQ ID NO: 757, SEQ ID NO: 412, and SEQ ID NO: 816.

30 In yet a further embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least four membrane spanning regions selected from the group consisting of SEQ ID NO: 1536, SEQ ID NO: 1544, SEQ ID NO: 1568, SEQ ID NO: 1572, SEQ ID NO: 1582, SEQ ID NO: 1738, SEQ ID NO: 1891, SEQ ID NO: 1660, SEQ ID NO: 771, SEQ ID NO: 418, SEQ ID NO: 662, SEQ ID NO: 512, SEQ ID NO: 679, SEQ ID NO: 605, SEQ ID NO: 421, SEQ ID NO: 552, SEQ ID NO: 576, SEQ ID NO: 571.

35 In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least five membrane spanning regions selected from the group consisting of SEQ ID NO: 1793, SEQ ID NO: 1832, SEQ ID NO: 1841, SEQ ID NO: 1860, SEQ ID NO: 1486, SEQ ID NO: 725, SEQ ID NO: 565, SEQ ID NO: 717, SEQ ID NO: 536, SEQ ID NO: 647, and SEQ ID NO: 409.

In another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least six membrane spanning regions selected from the group consisting of SEQ ID NO: 1465, SEQ ID NO: 1539, SEQ ID NO: 1693, SEQ ID NO: 1629, SEQ ID NO: 501, SEQ ID NO: 838, SEQ ID NO: 428, SEQ ID NO: 494, SEQ ID NO: 479, SEQ ID NO: 711, and SEQ ID NO: 722.

In yet another embodiment, the *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least seven membrane spanning regions selected from the group consisting of SEQ ID NO: 1540, SEQ ID NO: 1791, SEQ ID NO: 1525, SEQ ID NO: 1558, SEQ ID NO: 1655, SEQ ID NO: 1517, SEQ ID NO: 645, SEQ ID NO: 670, SEQ ID NO: 746, SEQ ID NO: 493, SEQ ID NO: 540, SEQ ID NO: 612, SEQ ID NO: 629, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, and SEQ ID NO: 433.

In another aspect, the invention pertains to any individual *H. pylori* polypeptide member or nucleic acid encoding such a member from the above-identified groups of *H. pylori* polypeptides.

In another aspect, the invention features nucleic acids capable of binding mRNA of *H. pylori*. Such nucleic acid is capable of acting as antisense nucleic acid to control the translation of mRNA of *H. pylori*. A further aspect features a nucleic acid which is capable of binding specifically to an *H. pylori* nucleic acid. These nucleic acids are also referred to herein as complements and have utility as probes and as capture reagents.

In another aspect, the invention features an expression system comprising an open reading frame corresponding to *H. pylori* nucleic acid. The nucleic acid further comprises a control sequence compatible with an intended host. The expression system is useful for making polypeptides corresponding to *H. pylori* nucleic acid.

In another aspect, the invention features a cell transformed with the expression system to produce *H. pylori* polypeptides.

In another aspect, the invention features a method of generating antibodies against *H. pylori* polypeptides which are capable of binding specifically to *H. pylori* polypeptides. Such antibodies have utility as reagents for immunoassays to evaluate the abundance and distribution of *H. pylori*-specific antigens.

In another aspect, the invention features a method of generating vaccines for immunizing an individual against *H. pylori*. The method includes: immunizing a subject with an *H. pylori* polypeptide, e.g., a surface or secreted polypeptide, or active portion thereof, and a pharmaceutically acceptable carrier. Such vaccines have therapeutic and prophylactic utilities.

In another aspect, the invention provides a method for generating a vaccine comprising a modified immunogenic *H. pylori* polypeptide, e.g., a surface or secreted polypeptide, or active portion thereof, and a pharmacologically acceptable carrier.

In another aspect, the invention features a method of evaluating a compound, e.g. a polypeptide, e.g., a fragment of a host cell polypeptide, for the ability to bind an *H. pylori* polypeptide. The method includes: contacting the candidate compound with an *H. pylori* polypeptide and determining if the compound binds or otherwise interacts with an *H. pylori* polypeptide. Compounds which bind *H. pylori* are candidates as activators or inhibitors of the bacterial life cycle. These assays can be performed *in vitro* or *in vivo*.

In another aspect, the invention features a method of evaluating a compound, e.g. a polypeptide, e.g., a fragment of a host cell polypeptide, for the ability to bind an *H. pylori* nucleic acid, e.g., DNA or RNA. The method includes: contacting the candidate compound with an *H. pylori* nucleic acid and determining if the compound binds or otherwise interacts with an *H. pylori* polypeptide. Compounds which bind *H. pylori* are candidates as activators or inhibitors of the bacterial life cycle. These assays can be performed *in vitro* or *in vivo*.

The invention features *H. pylori* polypeptides, preferably a substantially pure preparation of an *H. pylori* polypeptide, or a recombinant *H. pylori* polypeptide. In preferred embodiments: the polypeptide has biological activity; the polypeptide has an amino acid sequence at least 60%, 70%, 80%, 90%, 95%, 98%, or 99% identical to an amino acid sequence of the invention contained in the Sequence Listing, preferably it has about 65% sequence identity with an amino acid sequence of the invention contained in the Sequence Listing, and most preferably it has about 92% to about 99% sequence identity with an amino acid sequence of the invention contained in the Sequence Listing; the polypeptide has an amino acid sequence essentially the same as an amino acid sequence of the invention contained in the Sequence Listing; the polypeptide is at least 5, 10, 20, 50, 100, or 150 amino acid residues in length; the polypeptide includes at least 5, preferably at least 10, more preferably at least 20, more preferably at least 50, 100, or 150 contiguous amino acid residues of the invention contained in the Sequence Listing. In yet another preferred embodiment, the amino acid sequence which differs in sequence identity by about 7% to about 8% from the *H. pylori* amino acid sequences of the invention contained in the Sequence Listing is also encompassed by the invention.

In preferred embodiments: the *H. pylori* polypeptide is encoded by a nucleic acid of the invention contained in the Sequence Listing, or by a nucleic acid having at least 60%, 70%, 80%, 90%, 95%, 98%, or 99% homology with a nucleic acid of the invention contained in the Sequence Listing.

In a preferred embodiment, the subject *H. pylori* polypeptide differs in amino acid sequence at 1, 2, 3, 5, 10 or more residues from a sequence of the invention contained in the Sequence Listing. The differences, however, are such that the *H. pylori* polypeptide exhibits an *H. pylori* biological activity, e.g., the *H. pylori* polypeptide retains a biological activity of a naturally occurring *H. pylori* enzyme.

In preferred embodiments, the polypeptide includes all or a fragment of an amino acid sequence of the invention contained in the Sequence Listing; fused, in reading frame, to additional amino acid residues, preferably to residues encoded by genomic DNA 5' or 3' to the genomic DNA which encodes a sequence of the invention contained in the Sequence Listing.

In yet other preferred embodiments, the *H. pylori* polypeptide is a recombinant fusion protein having a first *H. pylori* polypeptide portion and a second polypeptide portion, e.g., a second polypeptide portion having an amino acid sequence unrelated to *H. pylori*. The second polypeptide portion can be, e.g., any of glutathione-S-transferase, a DNA binding domain, or a polymerase activating domain. In preferred embodiment the fusion protein can be used in a two-hybrid assay.

Polypeptides of the invention include those which arise as a result of alternative transcription events, alternative RNA splicing events, and alternative translational and postranslational events.

The invention also encompasses an immunogenic component which includes an *H. pylori* polypeptide in an immunogenic preparation; the immunogenic component being capable of eliciting an immune response specific for the *H. pylori* polypeptide, e.g., a humoral response, an antibody response, or a cellular response. In preferred embodiments, the immunogenic component comprises at least one antigenic determinant from a polypeptide of the invention contained in the Sequence Listing.

In another aspect, the invention provides a substantially pure nucleic acid having a nucleotide sequence which encodes an *H. pylori* polypeptide. In preferred embodiments: the encoded polypeptide has biological activity; the encoded polypeptide has an amino acid sequence at least 60%, 70%, 80%, 90%, 95%, 98%, or 99% homologous to an amino acid sequence of the invention contained in the Sequence Listing; the encoded polypeptide has an amino acid sequence essentially the same as an amino acid sequence of the invention contained in the Sequence Listing; the encoded polypeptide is at least 5, 10, 20, 50, 100, or 150 amino acids in length; the encoded polypeptide comprises at least 5, preferably at least 10, more preferably at least 20, more preferably at least 50, 100, or 150 contiguous amino acids of the invention contained in the Sequence Listing.

In preferred embodiments: the nucleic acid of the invention is that contained in the Sequence Listing; the nucleic acid is at least 60%, 70%, 80%, 90%, 95%, 98%, or 99% homologous with a nucleic acid sequence of the invention contained in the Sequence Listing.

In a preferred embodiment, the encoded *H. pylori* polypeptide differs (e.g., by amino acid substitution, addition or deletion of at least one amino acid residue) in amino acid sequence at 1, 2, 3, 5, 10 or more residues, from a sequence of the invention contained in the Sequence Listing. The differences, however, are such that: the *H. pylori* encoded

polypeptide exhibits a *H. pylori* biological activity, e.g., the encoded *H. pylori* enzyme retains a biological activity of a naturally occurring *H. pylori*.

In preferred embodiments, the encoded polypeptide includes all or a fragment of an amino acid sequence of the invention contained in the Sequence Listing; fused, in reading
5 frame, to additional amino acid residues, preferably to residues encoded by genomic DNA 5' or 3' to the genomic DNA which encodes a sequence of the invention contained in the Sequence Listing.

In preferred embodiments, the subject *H. pylori* nucleic acid will include a transcriptional regulatory sequence, e.g. at least one of a transcriptional promoter or
10 transcriptional enhancer sequence, operably linked to the *H. pylori* gene sequence, e.g., to render the *H. pylori* gene sequence suitable for expression in a recombinant host cell.

In yet a further preferred embodiment, the nucleic acid which encodes an *H. pylori* polypeptide of the invention, hybridizes under stringent conditions to a nucleic acid probe corresponding to at least 8 consecutive nucleotides of the invention contained in the
15 Sequence Listing; more preferably to at least 12 consecutive nucleotides of the invention contained in the Sequence Listing; more preferably to at least 20 consecutive nucleotides of the invention contained in the Sequence Listing; more preferably to at least 40 consecutive nucleotides of the invention contained in the Sequence Listing.

In a preferred embodiment, the nucleic acid encodes a peptide which differs by at
20 least one amino acid residue from the sequences of the invention contained in the Sequence Listing.

In a preferred embodiment, the nucleic acid differs by at least one nucleotide from a nucleotide sequence of the invention contained in the Sequence Listing which encodes amino acids of the invention contained in the Sequence Listing.

In another aspect, the invention encompasses: a vector including a nucleic acid
25 which encodes an *H. pylori* polypeptide or an *H. pylori* polypeptide variant as described herein; a host cell transfected with the vector; and a method of producing a recombinant *H. pylori* polypeptide or *H. pylori* polypeptide variant; including culturing the cell, e.g., in a cell culture medium, and isolating the *H. pylori* or *H. pylori* polypeptide variant, e.g., from
30 the cell or from the cell culture medium.

In another aspect, the invention features, a purified recombinant nucleic acid having at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, or 99% homology with a sequence of the invention contained in the Sequence Listing.

The invention also provides a probe or primer which includes a substantially
35 purified oligonucleotide. The oligonucleotide includes a region of nucleotide sequence which hybridizes under stringent conditions to at least 10 consecutive nucleotides of sense or antisense sequence of the invention contained in the Sequence Listing, or naturally occurring mutants thereof. In preferred embodiments, the probe or primer further includes a label group attached thereto. The label group can be, e.g., a radioisotope, a fluorescent

compound, an enzyme, and/or an enzyme co-factor. Preferably the oligonucleotide is at least 10 and less than 20, 30, 50, 100, or 150 nucleotides in length.

The invention further provides nucleic acids, e.g., RNA or DNA, encoding a polypeptide of the invention. This includes double stranded nucleic acids as well as coding
5 and antisense single strands.

The *H. pylori* strain, from which genomic sequences have been sequenced, has been deposited in the American Type Culture Collection(ATCC # 55679) as strain HP-J99.

Included in the invention are: allelic variations; natural mutants; induced mutants; proteins encoded by DNA that hybridizes under high or low stringency conditions to a
10 nucleic acid which encodes a polypeptide of the invention contained in the Sequence Listing (for definitions of high and low stringency see Current Protocols in Molecular Biology, John Wiley & Sons, New York, 1989, 6.3.1 - 6.3.6, hereby incorporated by reference); and, polypeptides specifically bound by antisera to *H. pylori* polypeptides, especially by antisera to an active site or binding domain of *H. pylori* polypeptide. The
15 invention also includes fragments, preferably biologically active fragments. These and other polypeptides are also referred to herein as *H. pylori* polypeptide analogs or variants.

Putative functions have been determined for several of the *H. pylori* polypeptides of the invention, as shown in Table 1.

Accordingly, uses of the claimed *H. pylori* polypeptides in these identified functions
20 are also within the scope of the invention.

In addition, the present invention encompasses *H. pylori* polypeptides characterized as shown in Table 1 below, including: *H. pylori* cell envelope proteins, *H. pylori* periplasmic/secreted proteins, *H. pylori* cytoplasmic proteins, and other *H. pylori* surface and membrane proteins. Members of these groups were identified by BLAST homology
25 searches and by searches for secretion signal or transmembrane protein motifs. (Polypeptides in the same row of Table 1, i.e., rows 1 and 3, or rows 2 and 4, are related to one another as described in Table 3 below.)

TABLE 1

TABLE OF FUNCTIONAL GROUPS					
ORF Name	nt	aa	ORF Name	nt	aa
	SeqID	SeqID		SeqID	SeqID
	#	#		#	#
Row	1	2		3	4
A. CELL ENVELOPE					
A.1. Flagella-associated					
01gp10401orf1	1020	1471	26588588.aa	217	660
01gp10401orf5	1021	1472	26588588.aa	217	660
02ael1612orf21	1036	1487	6288949.aa	367	855
02cel0213orf7	1050	1501	22692187.aa	911	534
02ge20116orf34	1071	1522	29454837.aa	944	675
04gel1713orf5	1101	1552	1171928.aa	18	404
04gel1713orf5	1101	1552	21699087.aa	107	518
05ep20322orf11	1135	1586	16219090.aa	894	464
12ge20305orf11	1276	1727	29298130.aa	943	672
06cp20302orf12	1150	1601	25525277.aa	203	640
07ge20415orf27	1187	1638	19557055.aa	85	490
07ge20415orf27	1187	1638	36111066.aa	290	755
07ge31107orf2	1192	1643	104792.aa	5	389
29zp10241orf6	1361	1812	24882763.aa	199	635
hp2e10911orf5	1379	1830	917152.aa	992	877
hp3e11122orf1	1399	1850	25478375.aa	934	637
hp3e11168orf2	1403	1854	16984442.aa	899	477
hpe11122orf5	1400	1851	3942217.aa	302	772
07ge20415orf34	1189	1640	26380318.aa	215	658
A.2. Inner membrane proteins					
01cel11016orf1	1002	1453			
09ap11406orf14	1213	1664	16131887.aa	893	463
09ap11406orf15	1214	1665	6093906.aa	984	852
09ap11406orf5	1215	1666	2082012.aa	97	503
11cel1603orf16	1234	1685	1204418.aa	22	411
11cel1603orf16	1234	1685	14455461.aa	49	441
11cel1603orf25	1236	1687	4035783.aa	309	782
11cel1603orf6	1237	1688	23915877.aa	150	575
09cp10502orf22	1224	1675	30730068.aa	240	691
09cp10502orf22	1224	1675	3385833.aa	957	724
11gp10904orf29	1251	1702	14713512.aa	57	452
12ap10324orf2	1262	1713	10353192.aa	2	386
06cp20302orf10	1149	1600	203192.aa	92	497
09ap20802orf5	1220	1671	32704686.aa	255	712
11gel0309orf14	1240	1691	24222885.aa	164	591
11gel0309orf14	1240	1691	2548562.aa	201	638
06gp10409orf7	1164	1615	34666680.aa	278	740
06gp10409orf8	1165	1616	3203142.aa	245	697

-36-

hp3el1168orf29	1404	1855	23853165.aa	921	569
06cp11118orf6	1144	1595	16412593.aa	896	470
06cp11118orf6	1144	1595	32236462.aa	248	700
07ee20513orf28	1182	1633	24132293.aa	159	586
07ee20513orf28	1182	1633	486075.aa	979	823
06ep10306orf12	1157	1608	24651083.aa	194	627
06ep10306orf3	1160	1611	24651083.aa	194	627
06ep10306orf3	1160	1611	30089217.aa	946	684
13ep12003orf20	1300	1751	23493756.aa	916	551
14ge10705orf11	1321	1772	17086587.aa	76	478
14ge10705orf11	1321	1772	21486677.aa	905	508
14ge10705orf11	1321	1772	23468781.aa	914	545
14ge10705orf11	1321	1772	24708129.aa	931	628
14gp11820orf13	1323	1774	14494077.aa	50	443
14gp11820orf13	1323	1774	3242337.aa	250	702
14gp11820orf13	1323	1774	3962777.aa	969	776
14gp12015orf12	1329	1780	15824052.aa	66	461
14gp12015orf12	1329	1780	34489543.aa	275	737
14gp12015orf16	1332	1783	4698838.aa	330	809
27ze10351orf17	1345	1796	25605166.aa	204	642
29zp10241orf14	1358	1809	9776562.aa	383	879
hplp13947orf2	1375	1826	3953143.aa	303	773
hp4p11352orf4	1417	1868	16406265.aa	70	468
13ap11517orf20	1283	1734	5267037.aa	983	842
16ae10113orf1	1335	1786	423131.aa	972	788
hplp13922orf22	1368	1819	24611590.aa	929	624
07ee11620orf2	1179	1630	423131.aa	972	788
12ae10622orf9	1255	1706	259665.aa	936	644
12ae10622orf9	1255	1706	34097707.aa	267	727
12ae11404orf15	1258	1709	24806290.aa	197	631
02ce10213orf14	1044	1495	14645905.aa	55	450
12ge10305orf15	1273	1724	14642202.aa	54	448
01xe21717orf18	1024	1475	26261040.aa	210	653
A.3. Transporters					
09ap20802orf27	1219	1670	20032561.aa	90	495
12ge10305orf16	1274	1725	11132778.aa	15	400
09ae11601orf14	1210	1661	23439633.aa	913	541
09ae11601orf14	1210	1661	29302003.aa	227	673
hp5el1726orf7	1422	1873	179677.aa	79	482
14cel1113orf1	1302	1753	24609593.aa	191	622
14cp10119orf12	1308	1759	30662792.aa	238	689
14cp10119orf15	1310	1761	34427317.aa	274	736
14gp12015orf14	1331	1782	12617677.aa	27	417
hp5el5440orf16	1432	1883	33203192.aa	258	716
hp5el5440orf16	1432	1883	36573502.aa	295	762
02cel1022orf7	1052	1503	1071890.aa	10	395
04ep10811orf4	1091	1542	24215.aa	160	587

-37-

04ep10811orf4	1091	1542	289711.aa	225	669
hp5e11726orf4	1421	1872	36203402.aa	964	758
02ge20116orf28	1069	1520	24238762.aa	166	593
01ce11513orf21	1005	1456	1464715.aa	56	451
01ce11513orf21	1005	1456	4882763.aa	980	827
01ce11618orf10	1007	1458	207817.aa	903	502
06gp11202orf7	1166	1617	33399142.aa	261	719
07cp21714orf13	1177	1628	16406581.aa	71	469
07gp11807orf25	1193	1644	3319687.aa	955	715
07gp11807orf8	1206	1657	5875152.aa	361	847
07gp11807orf9	1207	1658	14714687.aa	58	453
14ce20219orf1	1304	1755	22441050.aa	114	527
14ce20219orf2	1305	1756	26258562.aa	940	652
27ze10351orf18	1346	1797	35345228.aa	960	745
27ze10351orf24	1348	1799	23728388.aa	144	567
27ze10351orf29	1350	1801	5878208.aa	362	848
02ae11611orf11	1032	1483	13726562.aa	40	430
02ae11611orf11	1032	1483	35428912.aa	285	748
02ce11022orf8	1053	1504	10723412.aa	11	396
02ce11022orf8	1053	1504	24218968.aa	161	588
02ce11022orf8	1053	1504	4455467.aa	974	795
03ee11215orf29	1081	1532	22265691.aa	111	523
05cp11911orf41	1124	1575	4338438.aa	316	791
hp2p10625orf28	1382	1833	32952.aa	257	714
hp5p15641orf12	1437	1888	17787558.aa	78	481
12ap10324orf3	1263	1714	3906712.aa	966	765
A.4. Outer membrane proteins					
07ap80601orf8	1173	1624	5083193.aa	352	837
hp3e11168orf30	1405	1856	4960952.aa	981	833
hp3p10156orf12	1406	1857	24104558.aa	158	585
hp4e13394orf2	1410	1861	7116626.aa	989	865
04ce11617orf2	1086	1537	36126938.aa	963	764
14ge10705orf5	1322	1773	1431462.aa	48	440
14ge10705orf5	1322	1773	16225006.aa	68	465
12ap10324orf7	1266	1717	23531562.aa	135	555
13ae10712orf9	1282	1733	22379952.aa	910	526
12ge10305orf1	1271	1722	30478562.aa	236	687
12ge10305orf1	1271	1722	31250333.aa	241	692
07gp31516orf4	1208	1659	31262.aa	949	693
05cp20518orf33	1126	1577	29479681.aa	945	677
12ap11614orf8	1270	1721	26054702.aa	207	649
12ge20305orf2	1278	1729	4721061.aa	977	812
A.5. Other cell envelope proteins					
hp4p11352orf9	1419	1870	4821082.aa	978	820
05cp20518orf3	1125	1576	978477.aa	994	880
07ee20513orf14	1181	1632	24220627.aa	163	590
hp4p11352orf2	1416	1867	32705252.aa	256	713

-38-

hp4p11352orf2	1416	1867	35445843.aa	287	750
04ge11713orf11	1096	1547	24427340.aa	184	613
03ee11215orf30	1082	1533	1416312.aa	45	437
06cp11722orf15	1146	1597	23535937.aa	136	556
06cp11722orf15	1146	1597	26366312.aa	214	657
06cp11722orf12	1145	1596	114505.aa	16	402
05ae20220orf32	1108	1559	2461062.aa	192	623
06cp11722orf21	1148	1599	6828218.aa	373	862
16ae10508orf13	1337	1788	14642217.aa	892	449
16ae10508orf14	1338	1789	30703183.aa	239	690
hp5e12982orf14	1424	1875	1365943.aa	34	424
01ae22001orf2	1000	1451	4826401.aa	340	821
01xe21717orf5	1027	1478	1385937.aa	41	432
01xe21717orf5	1027	1478	4714375.aa	332	811
07ce10203orf22	1175	1626	23526667.aa	134	554
14gp12015orf13	1330	1781	4698838.aa	330	809
B. CYTOPLASMIC PROTEINS					
B.1. Proteins involved in energy conversion					
06cp11722orf16	1147	1598	10553192.aa	882	390
13ee10216orf55	1288	1739	914087.aa	382	876
14gp11820orf20	1324	1775	23475342.aa	130	547
hp1p11244orf7	1363	1814	29500075.aa	230	678
B.2. Proteins involved in amino acid metabolism					
01ae12021orf1	997	1448	34109763.aa	269	729
01ee11621orf6	1015	1466	4177212.aa	312	786
03ge31106orf1	1084	1535	26301059.aa	211	654
04ep71403orf15	1094	1545	34194093.aa	959	734
04ge11713orf37	1099	1550	25992137.aa	938	646
09gp10903orf3	1229	1680	21976637.aa	110	522
11gp10904orf27	1250	1701	31681556.aa	244	696
12ap11614orf4	1268	1719	45914063.aa	328	807
13ee12016orf10	1293	1744	30082267.aa	235	683
16ae10508orf21	1339	1790	429192.aa	315	790
hp3p10349orf16	1408	1859	36594167.aa	296	763
hp5e15211orf22	1429	1880	4578469.aa	976	806
hp5e15440orf19	1434	1885	4492217.aa	321	799
09cp10713orf29	1228	1679	1408.aa	43	434
02ae11611orf1	1031	1482	35269000.aa	281	743
02ae11612orf13	1034	1485	4570262.aa	326	804
01ce11618orf18	1008	1459	34189716.aa	272	733
B.3. Proteins involved in nucleotide metabolism					
02cp20821orf10	1061	1512	4882652.aa	344	826
02ep30607orf10	1064	1515	23598962.aa	139	562
07ge20415orf6	1191	1642	12897656.aa	30	420
09ap20802orf1	1217	1668	2738378.aa	220	664
hp1p13852orf5	1365	1816	598933.aa	364	850
hp3e11024orf24	1394	1845	6517040.aa	369	857

-39-

hp4e14535orf3	1414	1865	677088.aa	372	861
hp4e14535orf4	1415	1866	867183.aa	991	872
hp5e15440orf21	1435	1886	23442642.aa	128	544
02cp11822orf22	1058	1509	4895327.aa	347	830
02cp11822orf26	1059	1510	14574201.aa	52	446
B.4. Proteins involved in carbohydrate metabolism					
03ee11215orf26	1080	1531	10737627.aa	12	397
05cp20518orf5	1128	1579	32144532.aa	247	699
05cp20518orf64	1133	1584	15807794.aa	64	459
09ae11601orf3	1211	1662	2149041.aa	101	509
11gp11422orf1	1252	1703	4787562.aa	338	818
11gp11422orf2	1253	1704	19541302.aa	83	488
13ee10216orf43	1286	1737	14257751.aa	46	438
13ee10216orf56	1289	1740	4897177.aa	348	831
13ee10216orf9	1291	1742	2855006.aa	223	667
14ce11519orf2	1303	1754	13723593.aa	39	429
hp3e11060orf11	1396	1847	29557266.aa	232	680
01ae11421orf1	996	1447	24300682.aa	168	597
B.5. Proteins involved in cofactor metabolism					
04ge10816orf2	1095	1546	1581937.aa	65	460
06ee10709orf5	1156	1607	3261306.aa	952	709
06ep10306orf13	1158	1609	485375.aa	341	822
06ep10306orf14	1159	1610	16251627.aa	69	466
12ge20305orf14	1277	1728	24089437.aa	924	584
02ae11612orf26	1038	1489	10407625.aa	4	388
B.6. Proteins involved in lipid metabolism					
12ae11404orf14	1257	1708	24806290.aa	197	631
29zp10241orf11	1357	1808	422937.aa	313	787
hp5e15440orf22	1436	1887	22667967.aa	119	532
B.7. Proteins involved in mRNA translation and ribosome biogenesis					
02ce10213orf2	1047	1498	24500088.aa	188	619
02cp11404orf11	1055	1506	33601578.aa	956	723
06ce10515orf4	1141	1592	25595387.aa	935	641
09cp10713orf28	1227	1678	32036462.aa	246	698
14gp11820orf5	1327	1778	24803280.aa	196	630
hp4e14522orf11	1412	1863	785437.aa	376	869
B.8. Proteins involved in genome replication, transcription, recombination& repair					
01ce11016orf14	1003	1454	24396937.aa	172	601
04ce11617orf27	1087	1538	12520952.aa	25	415
05ap11505orf1	1116	1567	23440814.aa	126	542
05cp20518orf56	1130	1581	32431687.aa	951	704
05cp20518orf63	1132	1583	23880087.aa	147	572
07ge11504orf4	1185	1636	16305252.aa	895	467
07ge20415orf30	1188	1639	10745275.aa	14	399
07gp11807orf35	1198	1649	24036302.aa	154	579

-40-

09ap20802orf22	1218	1669	34574062.aa	277	739
09ap20802orf22	1218	1669	5879160.aa	363	849
11ge10309orf51	1244	1695	487750.aa	342	824
14ce21516orf1	1306	1757	85786.aa	378	871
14gpl1820orf27	1325	1776	23475342.aa	130	547
hp3e11060orf2	1397	1848	24818802.aa	198	633
hp3e11060orf9	1398	1849	3166040.aa	243	695
hp3p10156orf8	1407	1858	11719687.aa	19	405
hp5e15440orf18	1433	1884	10677187.aa	9	394
hp5e15440orf18	1433	1884	36523442.aa		761
B.9. Proteins involved in outer membrane or cell wall biosynthesis					
09apl1406orf8	1216	1667	23912807.aa	149	574
09apl1406orf8	1216	1667	24298127.aa	167	596
11ep12011orf9	1239	1690	495312.aa	349	832
29zpl0241orf7	1362	1813	26197187.aa	209	651
01ep30520orf16	1017	1468	7225666.aa	990	867
01ep30520orf27	1019	1470	24441412.aa	185	614
01ep30520orf27	1019	1470	11253.aa	883	401
29zpl0241orf4	1360	1811	10675632.aa	8	393
B.10. Chaperones					
hp5e12982orf13	1423	1874	12343763.aa	887	413
hp5e15211orf10	1425	1876	50253.aa	350	835
hplp13947orf1	1374	1825	6845425.aa	987	863
B.11 Other cytoplasmic proteins					
01xe21717orf9	1028	1479	156587.aa	63	458
02ae11612orf25	1037	1488	32422343.aa	249	701
03ee11215orf10	1077	1528	22542803.aa	118	531
05ae20220orf99	1115	1566	23492181.aa	132	550
11ce10917orf14	1232	1683	14313885.aa	47	439
11ge10309orf15	1241	1692	21647676.aa	106	516
12apl1614orf2	1267	1718	4562712.aa	324	802
06ge10115orf15	1163	1614	24070250.aa	155	581
02ge20116orf22	1068	1519	22704567.aa	121	535
02ge20116orf22	1068	1519	24003758.aa	153	578
02ge20116orf22	1068	1519	19626250.aa	87	492
02cpl1404orf9	1056	1507	6517192.aa	986	858
03ae10516orf11	1072	1523	33476715.aa	262	720
03ae10516orf11	1072	1523	4726503.aa	333	813
03ap21820orf10	1073	1524	13673328.aa	36	426
04ep71403orf10	1092	1543	50062.aa	982	834
04gpl1213orf36	1102	1553	24414687.aa	180	609
04gpl1213orf60	1103	1554	19556290.aa	84	489
05ae10307orf1	1104	1555	17497107.aa	900	480
05ae20220orf54	1111	1562	1179838.aa	20	406
05cpl1911orf11	1119	1570	10664078.aa	7	392
05gpl1901orf20	1136	1587	15039062.aa	61	456

-41-

05gp11901orf24	1137	1588	32600912.aa	253	707
06ael1405orf10	1140	1591	22687687.aa	120	533
06cel1002orf2	1142	1593	34099062.aa	268	728
11cel10917orf9	1233	1684	391313.aa	299	769
11cp12006orf17	1238	1689	291700.aa	942	671
11ge10309orf25	1243	1694	24406401.aa	173	602
11ge10309orf56	1245	1696	24495312.aa	187	618
11ge10309orf66	1247	1698	24495312.aa	187	618
11gp10904orf12	1249	1700	29844512.aa	234	682
12ael1404orf9	1261	1712	22303918.aa	112	524
12ap11614orf6	1269	1720	4562712.aa	324	802
12ge20305orf30	1279	1730	4095342.aa	971	785
13ap11517orf31	1284	1735	15126875.aa	62	457
13eel10216orf82	1290	1741	4035262.aa	308	781
13eel2016orf24	1297	1748	16459375.aa	74	473
14gp12015orf1	1328	1779	10009666.aa	1	384
hp1p13922orf30	1370	1821	34089087.aa	266	726
hp1p13939orf13	1372	1823	4766691.aa	337	817
hp2e10911orf25	1377	1828	2035936.aa	93	498
hp2p10625orf30	1383	1834	1411681.aa	44	436
hp2p10625orf7	1384	1835	4740887.aa	335	815
hp2p10625orf8	1385	1836	6495137.aa	368	856
hp3e10349orf18	1388	1839	260941.aa	208	650
hp3e11168orf14	1401	1852	5325005.aa	358	844
hp3e11168orf15	1402	1853	24039587.aa	923	580
hp4p11352orf8	1418	1869	4040928.aa	310	783
hp4p13402orf1	1420	1871	1256885.aa	26	416
hp5e15211orf15	1427	1878	35156938.aa	279	741
02ge20116orf33	1070	1521	14480927.aa	890	442
06cp20302orf8	1151	1602	4569693.aa	325	803
07cel1409orf4	1176	1627	21742157.aa	109	520
01ael2021orf8	999	1450	23646885.aa	143	566
01cel1513orf24	1006	1457	23539006.aa	918	557
01cp11710orf27	1012	1463	32595137.aa	252	706
01ep30520orf20	1018	1469	32627125.aa	953	710
02ael1211orf19	1030	1481	19537968.aa	902	487
02ael1611orf5	1033	1484	24407533.aa	174	603
02cel10114orf1	1041	1492	16440842.aa	73	472
02cel10213orf32	1049	1500	16839562.aa	898	476
02cel1220orf2	1054	1505	3930468.aa	300	770
02cp11721orf13	1057	1508	5265957.aa	356	841
04ep10811orf1	1090	1541	3907042.aa	298	768
04ge11713orf27	1097	1548	5111308.aa	354	839
05cp20518orf50	1129	1580	23573294.aa	138	560
06ael1020orf2	1139	1590	4486092.aa	319	796
06cel1002orf8	1143	1594	194415.aa	80	483
06cp30603orf11	1152	1603	24824087.aa	933	634

-42-

06ee10207orf2	1153	1604	14572133.aa	891	445
06ee10709orf17	1155	1606	6136430.aa	366	853
06ep11108orf20	1161	1612	22370182.aa	113	525
06ge10115orf12	1162	1613	4491093.aa	320	798
07ap11111orf3	1169	1620	23490686.aa	915	549
07ap80601orf10	1170	1621	5078593.aa	351	836
07ap80601orf12	1171	1622	24219012.aa	162	589
07ee20513orf1	1180	1631	36520792.aa	965	760
07gp11807orf28	1194	1645	16100038.aa	67	462
07gp11807orf29	1195	1646	42683.aa	314	789
07gp11807orf38	1199	1650	214812.aa	904	507
07gp11807orf41	1200	1651	4882842.aa	345	828
07gp11807orf42	1201	1652	719606.aa	374	866
07gp11807orf44	1202	1653	35949212.aa	962	754
07gp11807orf54	1205	1656	34161500.aa	270	730
14cp10923orf1	1312	1763	24492192.aa	186	617
16ae10508orf10	1336	1787	14864452.aa	60	455
27ze10351orf25	1349	1800	875042.aa	379	873
29gp10119orf6	1355	1806	14094816.aa	889	435
29zp10241orf18	1359	1810	3906937.aa	967	766
hp4e14535orf2	1413	1864	43490713.aa	973	793
hp5e15211orf13	1426	1877	35163962.aa	280	742
hp5e15211orf29	1430	1881	24329712.aa	170	599
			625277.aa	985	854
			24816915.aa	932	632
C. SECRETED OR PERIPLASMIC PROTEINS					
C.1. Secreted or periplasmic proteins					
01cel1016orf19	1004	1455	22460468.aa	117	530
05gp11901orf25	1138	1589	32609403.aa	254	708
02ge20116orf20	1067	1518	12505125.aa	24	414
03eel1215orf15	1078	1529	3157067.aa	242	694
14cp10923orf3	1314	1765	3242952.aa	950	703
14eel1217orf1	1319	1770	33595708.aa	263	721
14eel1217orf1	1319	1770	35442513.aa	286	749
hp2e10911orf30	1378	1829	30100332.aa	947	685
05ae20220orf124	1105	1556	14570443.aa	51	444
05ae20220orf92	1114	1565	24410643.aa	177	606
05ap21216orf7	1118	1569	24078837.aa	156	582
05cp11911orf12	1120	1571	24609431.aa	190	621
05cp11911orf27	1123	1574	783432.aa	375	868
05cp20518orf41	1127	1578	2843912.aa	222	666
09ael1601orf4	1212	1663	11876471.aa	21	408
09cp10502orf17	1223	1674	23438887.aa	912	538
09cp10713orf25	1225	1676	23912707.aa	148	573
11gel0309orf63	1246	1697	25501501.aa	202	639
11gel0309orf9	1248	1699	289077.aa	224	668
12ael1404orf3	1259	1710	22303918.aa	112	524

-43-

12ap10324orf4	1264	1715	13178562.aa	32	422
12ap10324orf5	1265	1716	4805318.aa	339	819
13ae10712orf4	1281	1732	24416083.aa	182	611
13ap11517orf7	1285	1736	29386577.aa	228	674
13ee12016orf15	1294	1745	23958179.aa	152	577
13ee12016orf5	1298	1749	272058.aa	219	663
13ee12016orf8	1299	1750	23564012.aa	137	558
14cp10923orf8	1315	1766	4414000.aa	318	794
14cp11121orf6	1316	1767	23631292.aa	141	564
14ee10308orf8	1317	1768	24230058.aa	165	592
14ee10308orf9	1318	1769	4728193.aa	334	814
16ep10117orf8	1344	1795	10742963.aa	13	398
27ze10351orf5	1351	1802	3906963.aa	297	767
29ge10111orf1	1353	1804	1367157.aa	35	425
hp1p13939orf9	1373	1824	26423583.aa	216	659
hp2e11858orf5	1380	1831	21687842.aa	908	517
hp3e10349orf17	1387	1838	23439055.aa	124	539
hp3e10349orf24	1389	1840	16603418.aa	75	475
hp3e11024orf22	1393	1844	2445812.aa	927	615
hp3e11024orf22	1393	1844	2774062.aa	221	665
hp4e13394orf5	1411	1862	24411011.aa	178	607
hp5e15211orf21	1428	1879	24328910.aa	169	598
hp5e15276orf14	1431	1882	36335436.aa	293	759
hp5p15641orf8	1439	1890	35837767.aa	289	752
02ce10213orf11	1043	1494	24276587.aa	926	595
07ge11504orf2	1183	1634	30283516.aa	948	686
07ge11504orf3	1184	1635	22447252.aa	115	528
07gp11807orf32	1196	1647	32462543.aa	251	705
07gp11807orf33	1197	1648	4882842.aa	345	828
07gp11807orf48	1203	1654	116018.aa	17	403
01ae11403orf1	995	1446	23594838.aa	920	561
01ae12021orf7	998	1449	20415937.aa	95	500
01ce10516orf2	1001	1452	1962590.aa	86	491
01gp11016orf14	1022	1473	5869090.aa	360	846
01xe21717orf12	1023	1474	34179577.aa	271	732
02ae11211orf10	1029	1480	3987580.aa	970	778
02ae11612orf4	1040	1491	35704718.aa	288	751
02ce10216orf1	1051	1502	35336707.aa	282	744
02cp20821orf12	1062	1513	20836042.aa	98	504
02cp20821orf12	1062	1513	12698442.aa	29	419
06ee10709orf16	1154	1605	4339708.aa	317	792
14ep11115orf1	1320	1771	4882318.aa	343	825
C.2. Proteins likely to be secreted or periplasmic					
03ap21820orf5	1075	1526	36131282.aa	291	756
05ae20220orf24	1106	1557	21720017.aa	108	519
05ae20220orf50	1109	1560	80257.aa	377	870
05cp20518orf9	1134	1585	3964593.aa	305	777

-44-

05cp20518orf9	1134	1585	4687507.aa	305	808
09cp10502orf14	1221	1672	2111040.aa	100	506
09cp10713orf26	1226	1677	7031343.aa	988	864
11cel1603orf22	1235	1686	26306340.aa	212	655
14cel0720orf2	1301	1752	1181418.aa	884	407
14cp10119orf7	1311	1762	1370202.aa	37	427
14gpl1820orf4	1326	1777	3953952.aa	968	774
16cp30109orf6	1341	1792	4490717.aa	975	797
29gp10119orf5	1354	1805	30603402.aa	237	688
hplp11256orf7	1364	1815	4740887.aa	335	815
hplp13868orf24	1366	1817	33397538.aa	260	718
hplp14013orf4	1376	1827	663530.aa	370	859
hp3el1024orf16	1391	1842	20173437.aa	91	496
hp3el1024orf16	1391	1842	34573431.aa	276	738
hp3el1024orf6	1395	1846	4062813.aa	311	784
hp6pl0723orf7	1445	1896	24406401.aa	173	602
03eel1215orf20	1079	1530	2150290.aa	102	510
07ge20415orf22	1186	1637	3958537.aa	304	775
01cel1618orf20	1010	1461	882827.aa	380	874
01ep10216orf6	1016	1467	23441078.aa	127	543
07ap80601orf5	1172	1623	917200.aa	993	878
04gel1713orf35	1098	1549	24256572.aa	925	594
03ap21820orf9	1076	1527	24415917.aa	181	610
07cel0203orf14	1174	1625	24395801.aa	171	600
D. OTHER SURFACE AND MEMBRANE PROTEINS					
D.1. Proteins likely to contain a single membrane					
spanning region					
02cp11822orf8	1060	1511	907827.aa	381	875
05ae20220orf51	1110	1561	29458178.aa	229	676
05ae20220orf6	1112	1563	4548792.aa	323	801
11ael0305orf4	1230	1681	6696887.aa	371	860
12ael11404orf8	1260	1711	35417942.aa	284	747
12ge20305orf35	1280	1731	22453166.aa	116	529
13eel11718orf2	1292	1743	1038312.aa	3	387
13eel2016orf19	1296	1747	10580417.aa	6	391
13eel2016orf19	1296	1747	21618785.aa	907	515
14ce21516orf3	1307	1758	24634750.aa	193	625
hp6pl0723orf20	1442	1893	23831562.aa	145	568
hp6pl0723orf5	1444	1895	14726542.aa	59	454
02cel0213orf1	1042	1493	4531568.aa	322	800
02ael1612orf36	1039	1490	2040717.aa	94	499
04gel1713orf41	1100	1551	3991067.aa	306	779
			10037799.aa	881	385
D.2. Proteins likely to contain two membrane spans					
05cp11911orf15	1122	1573	26052137.aa	939	648
12ael0622orf16	1254	1705	25925.aa	205	643
12ael11404orf12	1256	1707	23438840.aa	123	537

-45-

12ge10305orf10	1272	1723	21503772.aa	906	511
12ge10305orf10	1272	1723	24488537.aa	928	616
12ge10305orf21	1275	1726	489057.aa	346	829
14cp10119orf14	1309	1760	23473437.aa	129	546
14cp10119orf14	1309	1760	40339452.aa	307	780
14cp10923orf14	1313	1764	23515833.aa	133	553
27ze10351orf22	1347	1798	23486342.aa	131	548
27ze10351orf7	1352	1803	11924177.aa	886	410
29gp10119orf7	1356	1807	24413512.aa	179	608
hp5p15641orf5	1438	1889	21563752.aa	104	513
hp6p10723orf13	1441	1892	26351567.aa	213	656
01ce11618orf19	1009	1460	55843.aa	359	845
01xe21717orf40	1026	1477	23610905.aa	140	563
02ce10213orf23	1048	1499	23867207.aa	146	570
02cp20821orf8	1063	1514	4572168.aa	327	805
07ge20415orf39	1190	1641	5993958.aa	365	851
D.3. Proteins likely to contain 3 membrane spanning regions					
03ge10505orf14	1083	1534	1364378.aa	33	423
05ae20220orf88	1113	1564	4708337.aa	331	810
09cp10502orf16	1222	1673	24409577.aa	175	604
13ee12016orf18	1295	1746	25398250.aa	200	636
16ep10117orf7	1343	1794	36134661.aa	292	757
hp3e11024orf17	1392	1843	1206675.aa	23	412
hp6p10723orf43	1443	1894	4744128.aa	336	816
D.4. Proteins likely to contain 4 membrane spanning regions					
03xe11215orf5	1085	1536	3933437.aa	301	771
04ep71403orf12	1093	1544	12694087.aa	28	418
05ap11505orf10	1117	1568	26758437.aa	941	662
05cp11911orf13	1121	1572	21511555.aa	103	512
05cp11911orf13	1121	1572	29531590.aa	231	679
05cp20518orf61	1131	1582	24409641.aa	176	605
13ee10216orf5	1287	1738	12969218.aa	31	421
13ee10216orf5	1287	1738	23494043.aa	917	552
hp5p15641orf9	1440	1891	23945317.aa	151	576
09ae11601orf11	1209	1660	23867687.aa	922	571
D.5. Proteins likely to contain 5 membrane spanning regions					
16ep10117orf6	1342	1793			
hp2p10625orf14	1381	1832	33986087.aa	265	725
hp3e10349orf25	1390	1841	23631317.aa	142	565
hp3p10349orf32	1409	1860	33218912.aa	259	717
02ae11612orf14	1035	1486	23437502.aa	122	536
			25995917.aa	206	647
			11878127.aa	885	409
D.6. Proteins likely to contain 6 membrane spanning regions					
01cp11710orf34	1014	1465	2042312.aa	96	501
01cp11710orf34	1014	1465	5083577.aa	353	838
04ep10206orf22	1088	1539	13704718.aa	38	428

04ep10206orf22	1088	1539	20023400.aa	89	494
11ge10309orf18	1242	1693	17089217.aa	77	479
07cp21714orf14	1178	1629	32663212.aa	954	711
07cp21714orf14	1178	1629	3360130.aa	264	722
D.7. Proteins likely to contain 7 or more membrane spanning regions					
04ep10206orf23	1089	1540	25976418.aa	937	645
04ep10206orf23	1089	1540	2915903.aa	226	670
16ae10508orf3	1340	1791	35360843.aa	283	746
03ap21820orf13	1074	1525	197166.aa	88	493
03ap21820orf13	1074	1525	234391.aa	125	540
03ap21820orf13	1074	1525	24417212.aa	183	612
05ae20220orf31	1107	1558	24798427.aa	195	629
07gp11807orf49	1204	1655	19531291.aa	81	484
07gp11807orf49	1204	1655	19536375.aa	901	485
02ep30607orf31	1066	1517	19536458.aa	82	486
02ep30607orf31	1066	1517	13865928.aa	42	433

[In Table 1, "nt" represents nucleotide Seq. ID number and "aa" represents amino Seq. ID number]

Definitions

- 5 A purified or isolated polypeptide or a substantially pure preparation of a polypeptide are used interchangeably herein and, as used herein, mean a polypeptide that has been separated from other proteins, lipids, and nucleic acids with which it naturally occurs. Preferably, the polypeptide is also separated from substances, e.g., antibodies or gel matrix, e.g., polyacrylamide, which are used to purify it. Preferably, the polypeptide
- 10 constitutes at least 10, 20, 50 70, 80 or 95% dry weight of the purified preparation. Preferably, the preparation contains: sufficient polypeptide to allow protein sequencing; at least 1, 10, or 100 µg of the polypeptide; at least 1, 10, or 100 mg of the polypeptide.

- A purified preparation of cells refers to, in the case of plant or animal cells, an *in vitro* preparation of cells and not an entire intact plant or animal. In the case of cultured
- 15 cells or microbial cells, it consists of a preparation of at least 10% and more preferably 50% of the subject cells.

- A purified or isolated or a substantially pure nucleic acid, e.g., a substantially pure DNA, (are terms used interchangeably herein) is a nucleic acid which is one or both of the following: not immediately contiguous with both of the coding sequences with which it is
- 20 immediately contiguous (i.e., one at the 5' end and one at the 3' end) in the naturally-occurring genome of the organism from which the nucleic acid is derived; or which is substantially free of a nucleic acid with which it occurs in the organism from which the nucleic acid is derived. The term includes, for example, a recombinant DNA which is incorporated into a vector, e.g., into an autonomously replicating plasmid or virus, or into
- 25 the genomic DNA of a prokaryote or eukaryote, or which exists as a separate molecule (e.g., a cDNA or a genomic DNA fragment produced by PCR or restriction endonuclease treatment) independent of other DNA sequences. Substantially pure DNA also includes a

recombinant DNA which is part of a hybrid gene encoding additional *H. pylori* DNA sequence.

A "contig" as used herein is a nucleic acid representing a continuous stretch of genomic sequence of an organism.

- 5 An "open reading frame", also referred to herein as ORF, is a region of nucleic acid which encodes a polypeptide. This region may represent a portion of a coding sequence or a total sequence and can be determined from a stop to stop codon or from a start to stop codon.

- 10 As used herein, a "coding sequence" is a nucleic acid which is transcribed into messenger RNA and/or translated into a polypeptide when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a translation start codon at the five prime terminus and a translation stop code at the three prime terminus. A coding sequence can include but is not limited to messenger RNA, synthetic DNA, and recombinant nucleic acid sequences.

- 15 A "complement" of a nucleic acid as used herein refers to an anti-parallel or antisense sequence that participates in Watson-Crick base-pairing with the original sequence.

A "gene product" is a protein or structural RNA which is specifically encoded by a gene.

- 20 As used herein, the term "probe" refers to a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest. Probes are often associated with or capable of associating with a label. A label is a chemical moiety capable of detection. Typical labels comprise dyes, radioisotopes, luminescent and chemiluminescent moieties, fluorophores, enzymes, precipitating agents, amplification sequences, and the like.
- 25 Similarly, a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest and immobilizes such molecule is referred herein as a "capture ligand". Capture ligands are typically associated with or capable of associating with a support such as nitro-cellulose, glass, nylon membranes, beads, particles and the like. The specificity of hybridization is dependent on conditions such as the base pair composition of the
- 30 nucleotides, and the temperature and salt concentration of the reaction. These conditions are readily discernable to one of ordinary skill in the art using routine experimentation.

- Homologous refers to the sequence similarity or sequence identity between two polypeptides or between two nucleic acid molecules. When a position in both of the two compared sequences is occupied by the same base or amino acid monomer subunit, e.g., if
- 35 a position in each of two DNA molecules is occupied by adenine, then the molecules are homologous at that position. The percent of homology between two sequences is a function of the number of matching or homologous positions shared by the two sequences divided by the number of positions compared x 100. For example, if 6 of 10 of the positions in two sequences are matched or homologous then the two sequences are 60%

homologous. By way of example, the DNA sequences ATTGCC and TATGGC share 50% homology. Generally, a comparison is made when two sequences are aligned to give maximum homology.

5 Nucleic acids are hybridizable to each other when at least one strand of a nucleic acid can anneal to the other nucleic acid under defined stringency conditions. Stringency of hybridization is determined by: (a) the temperature at which hybridization and/or washing is performed; and (b) the ionic strength and polarity of the hybridization and washing solutions. Hybridization requires that the two nucleic acids contain complementary sequences; depending on the stringency of hybridization, however, mismatches may be
10 tolerated. Typically, hybridization of two sequences at high stringency (such as, for example, in a solution of 0.5X SSC, at 65° C) requires that the sequences be essentially completely homologous. Conditions of intermediate stringency (such as, for example, 2X SSC at 65 ° C) and low stringency (such as, for example 2X SSC at 55° C), require correspondingly less overall complementarity between the hybridizing sequences. (1X
15 SSC is 0.15 M NaCl, 0.015 M Na citrate).

The terms peptides, proteins, and polypeptides are used interchangeably herein.

As used herein, the term "surface protein" refers to all surface accessible proteins, e.g. inner and outer membrane proteins, proteins adhering to the cell wall, and secreted proteins.

20 A polypeptide has *H. pylori* biological activity if it has one, two and preferably more of the following properties: (1) if when expressed in the course of an *H. pylori* infection, it can promote, or mediate the attachment of *H. pylori* to a cell; (2) it has an enzymatic activity, structural or regulatory function characteristic of an *H. pylori* protein; (3) or the gene which encodes it can rescue a lethal mutation in an *H. pylori* gene. A
25 polypeptide has biological activity if it is an antagonist, agonist, or super-agonist of a polypeptide having one of the above-listed properties.

A biologically active fragment or analog is one having an *in vivo* or *in vitro* activity which is characteristic of the *H. pylori* polypeptides of the invention contained in the Sequence Listing, or of other naturally occurring *H. pylori* polypeptides, e.g., one or more
30 of the biological activities described herein. Especially preferred are fragments which exist *in vivo*, e.g., fragments which arise from post transcriptional processing or which arise from translation of alternatively spliced RNA's. Fragments include those expressed in native or endogenous cells as well as those made in expression systems, e.g., in CHO cells. Because peptides such as *H. pylori* polypeptides often exhibit a range of physiological properties
35 and because such properties may be attributable to different portions of the molecule, a useful *H. pylori* fragment or *H. pylori* analog is one which exhibits a biological activity in any biological assay for *H. pylori* activity. Most preferably the fragment or analog possesses 10%, preferably 40%, more preferably 60%, 70%, 80% or 90% or greater of the activity of *H. pylori*, in any *in vivo* or *in vitro* assay.

5 Analogues can differ from naturally occurring *H. pylori* polypeptides in amino acid sequence or in ways that do not involve sequence, or both. Non-sequence modifications include changes in acetylation, methylation, phosphorylation, carboxylation, or glycosylation. Preferred analogues include *H. pylori* polypeptides (or biologically active fragments thereof) whose sequences differ from the wild-type sequence by one or more conservative amino acid substitutions or by one or more non-conservative amino acid substitutions, deletions, or insertions which do not substantially diminish the biological activity of the *H. pylori* polypeptide. Conservative substitutions typically include the substitution of one amino acid for another with similar characteristics, e.g., substitutions within the following groups: valine, glycine; glycine, alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid; asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine. Other conservative substitutions can be made in view of the table below.

15

TABLE 2
CONSERVATIVE AMINO ACID REPLACEMENTS

For Amino Acid	Code	Replace with any of
Alanine	A	D-Ala, Gly, beta-Ala, L-Cys, D-Cys
Arginine	R	D-Arg, Lys, D-Lys, homo-Arg, D-homo-Arg, Met, Ile, D-Met, D-Ile, Orn, D-Orn
Asparagine	N	D-Asn, Asp, D-Asp, Glu, D-Glu, Gln, D-Gln
Aspartic Acid	D	D-Asp, D-Asn, Asn, Glu, D-Glu, Gln, D-Gln
Cysteine	C	D-Cys, S-Me-Cys, Met, D-Met, Thr, D-Thr
Glutamine	Q	D-Gln, Asn, D-Asn, Glu, D-Glu, Asp, D-Asp
Glutamic Acid	E	D-Glu, D-Asp, Asp, Asn, D-Asn, Gln, D-Gln
Glycine	G	Ala, D-Ala, Pro, D-Pro, β -Ala, Acp
Isoleucine	I	D-Ile, Val, D-Val, Leu, D-Leu, Met, D-Met
Leucine	L	D-Leu, Val, D-Val, Leu, D-Leu, Met, D-Met
Lysine	K	D-Lys, Arg, D-Arg, homo-Arg, D-homo-Arg, Met, D-Met, Ile, D-Ile, Orn, D-Orn
Methionine	M	D-Met, S-Me-Cys, Ile, D-Ile, Leu, D-Leu, Val, D-Val
Phenylalanine	F	D-Phe, Tyr, D-Thr, L-Dopa, His, D-His, Trp, D-Trp, Trans-3,4, or 5-phenylproline, cis-3,4, or 5-phenylproline

-50-

Proline	P	D-Pro, L-I-thioazolidine-4-carboxylic acid, D-or L-1-oxazolidine-4-carboxylic acid
Serine	S	D-Ser, Thr, D-Thr, allo-Thr, Met, D-Met, Met(O), D-Met(O), L-Cys, D-Cys
Threonine	T	D-Thr, Ser, D-Ser, allo-Thr, Met, D-Met, Met(O), D-Met(O), Val, D-Val
Tyrosine	Y	D-Tyr, Phe, D-Phe, L-Dopa, His, D-His
Valine	V	D-Val, Leu, D-Leu, Ile, D-Ile, Met, D-Met

Other analogs within the invention are those with modifications which increase peptide stability; such analogs may contain, for example, one or more non-peptide bonds (which replace the peptide bonds) in the peptide sequence. Also included are: analogs that
5 include residues other than naturally occurring L-amino acids, e.g., D-amino acids or non-naturally occurring or synthetic amino acids, e.g., β or γ amino acids; and cyclic analogs.

As used herein, the term "fragment", as applied to an *H. pylori* analog, will ordinarily be at least about 20 residues, more typically at least about 40 residues, preferably at least about 60 residues in length. Fragments of *H. pylori* polypeptides can be generated
10 by methods known to those skilled in the art. The ability of a candidate fragment to exhibit a biological activity of *H. pylori* polypeptide can be assessed by methods known to those skilled in the art as described herein. Also included are *H. pylori* polypeptides containing residues that are not required for biological activity of the peptide or that result from alternative mRNA splicing or alternative protein processing events.

15 An "immunogenic component" as used herein is a moiety, such as an *H. pylori* polypeptide, analog or fragment thereof, that is capable of eliciting a humoral and/or cellular immune response in a host animal.

An "antigenic component" as used herein is a moiety, such as an *H. pylori* polypeptide, analog or fragment thereof, that is capable of binding to a specific antibody
20 with sufficiently high affinity to form a detectable antigen-antibody complex.

As used herein, the term "transgene" means a nucleic acid (encoding, e.g., one or more polypeptides), which is partly or entirely heterologous, i.e., foreign, to the transgenic animal or cell into which it is introduced, or, is homologous to an endogenous gene of the transgenic animal or cell into which it is introduced, but which is designed to be inserted, or
25 is inserted, into the cell's genome in such a way as to alter the genome of the cell into which it is inserted (e.g., it is inserted at a location which differs from that of the natural gene or its insertion results in a knockout). A transgene can include one or more transcriptional regulatory sequences and any other nucleic acid, such as introns, that may be necessary for optimal expression of the selected nucleic acid, all operably linked to the selected nucleic acid, and may include an enhancer sequence.
30

-51-

As used herein, the term "transgenic cell" refers to a cell containing a transgene.

As used herein, a "transgenic animal" is any animal in which one or more, and preferably essentially all, of the cells of the animal includes a transgene. The transgene can be introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by a process of transformation of competent cells or by microinjection or by infection with a recombinant virus. This molecule may be integrated within a chromosome, or it may be extrachromosomally replicating DNA.

The term "antibody" as used herein is intended to include fragments thereof which are specifically reactive with *H. pylori* polypeptides.

As used herein, the term "cell-specific promoter" means a DNA sequence that serves as a promoter, i.e., regulates expression of a selected DNA sequence operably linked to the promoter, and which effects expression of the selected DNA sequence in specific cells of a tissue. The term also covers so-called "leaky" promoters, which regulate expression of a selected DNA primarily in one tissue, but cause expression in other tissues as well.

Misexpression, as used herein, refers to a non-wild type pattern of gene expression. It includes: expression at non-wild type levels, i.e., over or under expression; a pattern of expression that differs from wild type in terms of the time or stage at which the gene is expressed, e.g., increased or decreased expression (as compared with wild type) at a predetermined developmental period or stage; a pattern of expression that differs from wild type in terms of decreased expression (as compared with wild type) in a predetermined cell type or tissue type; a pattern of expression that differs from wild type in terms of the splicing size, amino acid sequence, post-translational modification, or biological activity of the expressed polypeptide; a pattern of expression that differs from wild type in terms of the effect of an environmental stimulus or extracellular stimulus on expression of the gene, e.g., a pattern of increased or decreased expression (as compared with wild type) in the presence of an increase or decrease in the strength of the stimulus.

As used herein, "host cells" and other such terms denoting microorganisms or higher eukaryotic cell lines cultured as unicellular entities refers to cells which can become or have been used as recipients for a recombinant vector or other transfer DNA, and include the progeny of the original cell which has been transfected. It is understood by individuals skilled in the art that the progeny of a single parental cell may not necessarily be completely identical in genomic or total DNA complement to the original parent, due to accident or deliberate mutation.

As used herein, the term "control sequence" refers to a nucleic acid having a base sequence which is recognized by the host organism to effect the expression of encoded sequences to which they are ligated. The nature of such control sequences differs depending upon the host organism; in prokaryotes, such control sequences generally include a

-52-

promoter, ribosomal binding site, terminators, and in some cases operators; in eukaryotes, generally such control sequences include promoters, terminators and in some instances, enhancers. The term control sequence is intended to include at a minimum, all components whose presence is necessary for expression, and may also include additional components whose presence is advantageous, for example, leader sequences.

As used herein, the term "operably linked" refers to sequences joined or ligated to function in their intended manner. For example, a control sequence is operably linked to coding sequence by ligation in such a way that expression of the coding sequence is achieved under conditions compatible with the control sequence and host cell.

The metabolism of a substance, as used herein, means any aspect of the, expression, function, action, or regulation of the substance. The metabolism of a substance includes modifications, e.g., covalent or non-covalent modifications of the substance. The metabolism of a substance includes modifications, e.g., covalent or non-covalent modification, the substance induces in other substances. The metabolism of a substance also includes changes in the distribution of the substance. The metabolism of a substance includes changes the substance induces in the distribution of other substances.

A "sample" as used herein refers to a biological sample, such as, for example, tissue or fluid isolated from an individual (including without limitation plasma, serum, cerebrospinal fluid, lymph, tears, saliva and tissue sections) or from *in vitro* cell culture constituents, as well as samples from the environment.

The practice of the invention will employ, unless otherwise indicated, conventional techniques of chemistry, molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See e.g., Sambrook, Fritsch, and Maniatis, *Molecular Cloning; Laboratory Manual* 2nd ed. (1989); *DNA Cloning*, Volumes I and II (D.N Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed, 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); the series, *Methods in Enzymology* (Academic Press, Inc.), particularly Vol. 154 and Vol. 155 (Wu and Grossman, eds.) and *PCR-A Practical Approach* (McPherson, Quirke, and Taylor, eds., 1991).

I. Isolation of Nucleic Acids of *H. pylori* and Uses Therefor

H. pylori Genomic Sequence

This invention provides nucleotide sequences of the genome of *H. pylori* which thus comprises a DNA sequence library of *H. pylori* genomic DNA. The detailed description that follows provides nucleotide sequences of *H. pylori*, and also describes how the sequences were obtained and how ORFs and protein-coding sequences were identified. Also described are methods of using the disclosed *H. pylori* sequences in methods including diagnostic and therapeutic applications. Furthermore, the library can be used as a

-53-

database for identification and comparison of medically important sequences in this and other strains of *H. pylori*.

To determine the genomic sequence of *H. pylori*, DNA was isolated from a strain of *H. pylori* (ATCC # 55679) and mechanically sheared by nebulization to a median size of 2 kb. Following size fractionation by gel electrophoresis, the fragments were blunt-ended, ligated to adapter oligonucleotides, and cloned into each of 20 different pMPX vectors (Rice et al., abstracts of Meeting of Genome Mapping and Sequencing, Cold Spring Harbor, NY, 5/11-5/15, 1994, p. 225) to construct a series of "shotgun" subclone libraries.

DNA sequencing was achieved using multiplex sequencing procedures essentially as disclosed in Church et al., 1988, *Science* 240:185; U.S. Patents No. 4,942,124 and 5,149,625). DNA was extracted from pooled cultures and subjected to chemical or enzymatic sequencing. Sequencing reactions were resolved by electrophoresis, and the products were transferred and covalently bound to nylon membranes. Finally, the membranes were sequentially hybridized with a series of labelled oligonucleotides complimentary to "tag" sequences present in the different shotgun cloning vectors. In this manner, a large number of sequences could be obtained from a single set of sequencing reactions. The cloning and sequencing procedures are described in more detail in the Exemplification.

Individual sequence reads obtained in this manner were assembled using the FALCON™ program (Church et al., 1994, *Automated DNA Sequencing and Analysis*, J.C. Venter, ed., Academic Press) and PHRAP (P. Green, Abstracts of DOE Human Genome Program Contractor-Grantee Workshop V, Jan. 1996, p.157). The average contig length was about 3-4 kb.

A variety of approaches are used to order the contigs so as to obtain a continuous sequence representing the entire *H. pylori* genome. Synthetic oligonucleotides are designed that are complementary to sequences at the end of each contig. These oligonucleotides may be hybridized to libraries of *H. pylori* genomic DNA in, for example, lambda phage vectors or plasmid vectors to identify clones that contain sequences corresponding to the junctional regions between individual contigs. Such clones are then used to isolate template DNA and the same oligonucleotides are used as primers in polymerase chain reaction (PCR) to amplify junctional fragments, the nucleotide sequence of which is then determined.

The *H. pylori* sequences were analyzed for the presence of open reading frames (ORFs) comprising at least 180 nucleotides. As a result of the analysis of ORFs based on stop-to-stop codon reads, it should be understood that these ORFs may not correspond to the ORF of a naturally-occurring *H. pylori* polypeptide. These ORFs may contain start codons which indicate the initiation of protein synthesis of a naturally-occurring *H. pylori* polypeptide. Such start codons within the ORFs provided herein can be identified by those of ordinary skill in the relevant art, and the resulting ORF and the encoded *H. pylori* polypeptide is within the scope of this invention. For example, within the ORFs a codon

such as AUG or GUG (encoding methionine or valine) which is part of the initiation signal for protein synthesis can be identified and the ORF modified to correspond to a naturally-occurring *H. pylori* polypeptide. The predicted coding regions were defined by evaluating the coding potential of such sequences with the program GENEMARK™ (Borodovsky and
5 McIninch, 1993, *Comp. Chem.* 17:123).

Other *H. pylori* Nucleic Acids

The nucleic acids of this invention may be obtained directly from the DNA of the above referenced *H. pylori* strain by using the polymerase chain reaction (PCR). See "PCR,
10 *A Practical Approach*" (McPherson, Quirke, and Taylor, eds., IRL Press, Oxford, UK, 1991) for details about the PCR. High fidelity PCR can be used to ensure a faithful DNA copy prior to expression. In addition, the authenticity of amplified products can be checked by conventional sequencing methods. Clones carrying the desired sequences described in this invention may also be obtained by screening the libraries by means of the PCR or by
15 hybridization of synthetic oligonucleotide probes to filter lifts of the library colonies or plaques as known in the art (see, e.g., Sambrook et al., *Molecular Cloning, A Laboratory Manual* 2nd edition, 1989, Cold Spring Harbor Press, NY).

It is also possible to obtain nucleic acids encoding *H. pylori* polypeptides from a cDNA library in accordance with protocols herein described. A cDNA encoding an *H.*
20 *pylori* polypeptide can be obtained by isolating total mRNA from an appropriate strain. Double stranded cDNAs can then be prepared from the total mRNA. Subsequently, the cDNAs can be inserted into a suitable plasmid or viral (e.g., bacteriophage) vector using any one of a number of known techniques. Genes encoding *H. pylori* polypeptides can also be cloned using established polymerase chain reaction techniques in accordance with the
25 nucleotide sequence information provided by the invention. The nucleic acids of the invention can be DNA or RNA. Preferred nucleic acids of the invention are contained in the Sequence Listing.

The nucleic acids of the invention can also be chemically synthesized using standard techniques. Various methods of chemically synthesizing polydeoxynucleotides
30 are known, including solid-phase synthesis which, like peptide synthesis, has been fully automated in commercially available DNA synthesizers (See e.g., Itakura *et al.* U.S. Patent No. 4,598,049; Caruthers *et al.* U.S. Patent No. 4,458,066; and Itakura U.S. Patent Nos. 4,401,796 and 4,373,071, incorporated by reference herein).

Nucleic acids isolated or synthesized in accordance with features of the present
35 invention are useful, by way of example, without limitation, as probes, primers, capture ligands, antisense genes and for developing expression systems for the synthesis of proteins and peptides corresponding to such sequences. As probes, primers, capture ligands and antisense agents, the nucleic acid normally consists of all or part (approximately twenty or more nucleotides for specificity as well as the ability to form stable hybridization products)

of the nucleic acids of the invention contained in the Sequence Listing. These uses are described in further detail below.

Probes

5 A nucleic acid isolated or synthesized in accordance with the sequence of the invention contained in the Sequence Listing can be used as a probe to specifically detect *H. pylori*. With the sequence information set forth in the present application, sequences of twenty or more nucleotides are identified which provide the desired inclusivity and exclusivity with respect to *H. pylori*, and extraneous nucleic acids likely to be encountered
10 during hybridization conditions. More preferably, the sequence will comprise at least twenty to thirty nucleotides to convey stability to the hybridization product formed between the probe and the intended target molecules.

Sequences larger than 1000 nucleotides in length are difficult to synthesize but can be generated by recombinant DNA techniques. Individuals skilled in the art will readily
15 recognize that the nucleic acids, for use as probes, can be provided with a label to facilitate detection of a hybridization product.

Nucleic acid isolated and synthesized in accordance with the sequence of the invention contained in the Sequence Listing can also be useful as probes to detect homologous regions (especially homologous genes) of other *Helicobacter* species using
20 appropriate stringency hybridization conditions as described herein.

Capture Ligand

For use as a capture ligand, the nucleic acid selected in the manner described above with respect to probes, can be readily associated with a support. The manner in which nucleic acid is associated with supports is well known. Nucleic acid having twenty or more
25 nucleotides in a sequence of the invention contained in the Sequence Listing have utility to separate *H. pylori* nucleic acid from the nucleic acid of each other and other organisms. Nucleic acid having twenty or more nucleotides in a sequence of the invention contained in the Sequence Listing can also have utility to separate other *Helicobacter* species from each other and from other organisms. Preferably, the sequence will comprise at least twenty
30 nucleotides to convey stability to the hybridization product formed between the probe and the intended target molecules. Sequences larger than 1000 nucleotides in length are difficult to synthesize but can be generated by recombinant DNA techniques.

Primers

Nucleic acid isolated or synthesized in accordance with the sequences described
35 herein have utility as primers for the amplification of *H. pylori* nucleic acid. These nucleic acids may also have utility as primers for the amplification of nucleic acids in other *Helicobacter* species. With respect to polymerase chain reaction (PCR) techniques, nucleic acid sequences of ≥ 10 -15 nucleotides of the invention contained in the Sequence Listing have utility in conjunction with suitable enzymes and reagents to create copies of *H. pylori*

-56-

nucleic acid. More preferably, the sequence will comprise twenty or more nucleotides to convey stability to the hybridization product formed between the primer and the intended target molecules. Binding conditions of primers greater than 100 nucleotides are more difficult to control to obtain specificity. High fidelity PCR can be used to ensure a faithful DNA copy prior to expression. In addition, amplified products can be checked by conventional sequencing methods.

The copies can be used in diagnostic assays to detect specific sequences, including genes from *H. pylori* and/or other *Helicobacter* species. The copies can also be incorporated into cloning and expression vectors to generate polypeptides corresponding to the nucleic acid synthesized by PCR, as is described in greater detail herein.

Antisense

Nucleic acid or nucleic acid-hybridizing derivatives isolated or synthesized in accordance with the sequences described herein have utility as antisense agents to prevent the expression of *H. pylori* genes. These sequences also have utility as antisense agents to prevent expression of genes of other *Helicobacter* species.

In one embodiment, nucleic acid or derivatives corresponding to *H. pylori* nucleic acids is loaded into a suitable carrier such as a liposome or bacteriophage for introduction into bacterial cells. For example, a nucleic acid having twenty or more nucleotides is capable of binding to bacteria nucleic acid or bacteria messenger RNA. Preferably, the antisense nucleic acid is comprised of 20 or more nucleotides to provide necessary stability of a hybridization product of non-naturally occurring nucleic acid and bacterial nucleic acid and/or bacterial messenger RNA. Nucleic acid having a sequence greater than 1000 nucleotides in length is difficult to synthesize but can be generated by recombinant DNA techniques. Methods for loading antisense nucleic acid in liposomes is known in the art as exemplified by U.S. Patent 4,241,046 issued December 23, 1980 to Papahadjopoulos et al.

II. Expression of *H. pylori* Nucleic Acids

Nucleic acid isolated or synthesized in accordance with the sequences described herein have utility to generate polypeptides. The nucleic acid of the invention exemplified in the Sequence Listing or fragments of said nucleic acid encoding active portions of *H. pylori* polypeptides can be cloned into suitable vectors or used to isolate nucleic acid. The isolated nucleic acid is combined with suitable DNA linkers and cloned into a suitable vector.

The function of a specific gene or operon can be ascertained by expression in a bacterial strain under conditions where the activity of the gene product(s) specified by the gene or operon in question can be specifically measured. Alternatively, a gene product may be produced in large quantities in an expressing strain for use as an antigen, an industrial reagent, for structural studies, etc. This expression can be accomplished in a mutant strain which lacks the activity of the gene to be tested, or in a strain that does not produce the

same gene product(s). This includes, but is not limited to other *Helicobacter* strains, or other bacterial strains such as *E. coli*, *Nocardia*, *Corynebacterium*, *Campylobacter*, and *Streptomyces* species. In some cases the expression host will utilize the natural *Helicobacter* promoter whereas in others, it will be necessary to drive the gene with a promoter sequence derived from the expressing organism (e.g., an *E. coli* beta-galactosidase promoter for expression in *E. coli*).

To express a gene product using the natural *H. pylori* promoter, a procedure such as the following can be used. A restriction fragment containing the gene of interest, together with its associated natural promoter element and regulatory sequences (identified using the DNA sequence data) is cloned into an appropriate recombinant plasmid containing an origin of replication that functions in the host organism and an appropriate selectable marker. This can be accomplished by a number of procedures known to those skilled in the art. It is most preferably done by cutting the plasmid and the fragment to be cloned with the same restriction enzyme to produce compatible ends that can be ligated to join the two pieces together. The recombinant plasmid is introduced into the host organism by, for example, electroporation and cells containing the recombinant plasmid are identified by selection for the marker on the plasmid. Expression of the desired gene product is detected using an assay specific for that gene product.

In the case of a gene that requires a different promoter, the body of the gene (coding sequence) is specifically excised and cloned into an appropriate expression plasmid. This subcloning can be done by several methods, but is most easily accomplished by PCR amplification of a specific fragment and ligation into an expression plasmid after treating the PCR product with a restriction enzyme or exonuclease to create suitable ends for cloning.

A suitable host cell for expression of a gene can be any procaryotic or eucaryotic cell. For example, an *H. pylori* polypeptide can be expressed in bacterial cells such as *E. coli*, insect cells (baculovirus), yeast, or mammalian cells such as Chinese hamster ovary cell (CHO). Other suitable host cells are known to those skilled in the art.

Expression in eucaryotic cells such as mammalian, yeast, or insect cells can lead to partial or complete glycosylation and/or formation of relevant inter- or intra-chain disulfide bonds of a recombinant peptide product. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, et al., (1987) *Embo J.* 6:229-234), pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz et al., (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Baculovirus vectors available for expression of proteins in cultured insect cells (SF 9 cells) include the pAc series (Smith et al., (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow, V.A., and Summers, M.D., (1989) *Virology* 170:31-39). Generally, COS cells (Gluzman, Y., (1981) *Cell* 23:175-182) are used in conjunction with such vectors as pCDM 8 (Aruffo, A. and Seed, B., (1987) *Proc. Natl. Acad. Sci. USA* 84:8573-8577) for transient

-58-

amplification/expression in mammalian cells, while CHO (dhfr⁻ Chinese Hamster Ovary) cells are used with vectors such as pMT2PC (Kaufman et al. (1987), *EMBO J.* 6:187-195) for stable amplification/expression in mammalian cells. Vector DNA can be introduced into mammalian cells via conventional techniques such as calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, or electroporation. Suitable methods for transforming host cells can be found in Sambrook et al. (Molecular Cloning: A Laboratory Manual, 2nd Edition, Cold Spring Harbor Laboratory press (1989)), and other laboratory textbooks.

Expression in procaryotes is most often carried out in *E. coli* with either fusion or non-fusion inducible expression vectors. Fusion vectors usually add a number of NH₂ terminal amino acids to the expressed target gene. These NH₂ terminal amino acids often are referred to as a reporter group. Such reporter groups usually serve two purposes: 1) to increase the solubility of the target recombinant protein; and 2) to aid in the purification of the target recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the reporter group and the target recombinant protein to enable separation of the target recombinant protein from the reporter group subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Amrad Corp., Melbourne, Australia), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase, maltose E binding protein, or protein A, respectively, to the target recombinant protein. A preferred reporter group is poly(His), which may be fused to the amino or carboxy terminus of the protein and which renders the recombinant fusion protein easily purifiable by metal chelate chromatography.

Inducible non-fusion expression vectors include pTrc (Amann et al., (1988) *Gene* 69:301-315) and pET11d (Studier et al., Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, California (1990) 60-89). While target gene expression relies on host RNA polymerase transcription from the hybrid trp-lac fusion promoter in pTrc, expression of target genes inserted into pET11d relies on transcription from the T7 gn10-lac 0 fusion promoter mediated by coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 under the transcriptional control of the lacUV 5 promoter.

For example, a host cell transfected with a nucleic acid vector directing expression of a nucleotide sequence encoding an *H. pylori* polypeptide can be cultured under appropriate conditions to allow expression of the polypeptide to occur. The polypeptide may be secreted and isolated from a mixture of cells and medium containing the peptide. Alternatively, the polypeptide may be retained cytoplasmically and the cells harvested, lysed and the protein isolated. A cell culture includes host cells, media and other

byproducts. Suitable media for cell culture are well known in the art. Polypeptides of the invention can be isolated from cell culture medium, host cells, or both using techniques known in the art for purifying proteins including ion-exchange chromatography, gel filtration chromatography, ultrafiltration, electrophoresis, and immunoaffinity purification with antibodies specific for such polypeptides. Additionally, in many situations, polypeptides can be produced by chemical cleavage of a native protein (e.g., tryptic digestion) and the cleavage products can then be purified by standard techniques.

In the case of membrane bound proteins, these can be isolated from a host cell by contacting a membrane-associated protein fraction with a detergent forming a solubilized complex, where the membrane-associated protein is no longer entirely embedded in the membrane fraction and is solubilized at least to an extent which allows it to be chromatographically isolated from the membrane fraction. Several different criteria are used for choosing a detergent suitable for solubilizing these complexes. For example, one property considered is the ability of the detergent to solubilize the *H. pylori* protein within the membrane fraction at minimal denaturation of the membrane-associated protein allowing for the activity or functionality of the membrane-associated protein to return upon reconstitution of the protein. Another property considered when selecting the detergent is the critical micelle concentration (CMC) of the detergent in that the detergent of choice preferably has a high CMC value allowing for ease of removal after reconstitution. A third property considered when selecting a detergent is the hydrophobicity of the detergent. Typically, membrane-associated proteins are very hydrophobic and therefore detergents which are also hydrophobic, e.g., the triton series, would be useful for solubilizing the hydrophobic proteins. Another property important to a detergent can be the capability of the detergent to remove the *H. pylori* protein with minimal protein-protein interaction facilitating further purification. A fifth property of the detergent which should be considered is the charge of the detergent. For example, if it is desired to use ion exchange resins in the purification process then preferably detergent should be an uncharged detergent. Chromatographic techniques which can be used in the final purification step are known in the art and include hydrophobic interaction, lectin affinity, ion exchange, dye affinity and immunoaffinity.

One strategy to maximize recombinant *H. pylori* peptide expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, California (1990) 119-128). Another strategy would be to alter the nucleic acid encoding an *H. pylori* peptide to be inserted into an expression vector so that the individual codons for each amino acid would be those preferentially utilized in highly expressed *E. coli* proteins (Wada et al., (1992) *Nuc. Acids Res.* 20:2111-2118). Such alteration of nucleic acids of the invention can be carried out by standard DNA synthesis techniques.

-60-

The nucleic acids of the invention can also be chemically synthesized using standard techniques. Various methods of chemically synthesizing polydeoxynucleotides are known, including solid-phase synthesis which, like peptide synthesis, has been fully automated in commercially available DNA synthesizers (See, e.g., Itakura et al. U.S. Patent No. 4,598,049; Caruthers et al. U.S. Patent No. 4,458,066; and Itakura U.S. Patent Nos. 4,401,796 and 4,373,071, incorporated by reference herein).

III. *H. pylori* Polypeptides

This invention encompasses isolated *H. pylori* polypeptides encoded by the disclosed *H. pylori* genomic sequences, including the polypeptides of the invention contained in the Sequence Listing. Polypeptides of the invention are preferably at least 5 amino acid residues in length. Using the DNA sequence information provided herein, the amino acid sequences of the polypeptides encompassed by the invention can be deduced using methods well-known in the art. It will be understood that the sequence of an entire nucleic acid encoding an *H. pylori* polypeptide can be isolated and identified based on an ORF that encodes only a fragment of the cognate protein-coding region. This can be achieved, for example, by using the isolated nucleic acid encoding the ORF, or fragments thereof, to prime a polymerase chain reaction with genomic *H. pylori* DNA as template; this is followed by sequencing the amplified product.

The polypeptides of the invention can be isolated from wild-type or mutant *H. pylori* cells or from heterologous organisms or cells (including, but not limited to, bacteria, yeast, insect, plant and mammalian cells) into which an *H. pylori* nucleic acid has been introduced and expressed. In addition, the polypeptides can be part of recombinant fusion proteins.

H. pylori polypeptides of the invention can be chemically synthesized using commercially automated procedures such as those referenced herein.

Many of the polypeptides of the invention are related to one another. Some of these relationships are described in Table 3 below. Most polypeptides described in Table 3 are over 90% identical to one another as noted in the last two columns; some are between 70% and 90% identical to one another; and very few share between 60% and 70% identity with each other. The polypeptides represented by the sequence identification numbers in the third column of Table 3 result from translations carried out from stop codon to stop codon in the genomic nucleotide sequence of the invention, while those in the first column result from translations carried out from the first methionine or valine codon following the prior stop codon and proceeding to the final stop codon in the nucleotide sequence. In some cases, the nucleotide sequence encoding the related polypeptides is slightly different, resulting in some differences in amino acid residues of the related polypeptides. In many cases, the related polypeptides differ significantly in length, with one polypeptide containing amino acid residues in addition to those in common between the two

polypeptides. In all cases, the relationships described in Table 3 are highly significant, and the nucleotide sequences encoding these related polypeptides are also very similar to one another. For example, the nucleotide probes derived from the coding sequence of the polypeptides in column one can be used in PCR or hybridization experiments to identify clones carrying the nucleotide sequence encoding the polypeptides of column three.

The relationships between the polypeptides shown in Table 3 can be classified in five broad categories as follows. First, for many polypeptides (designated "A" in the last column of the Table 3), the polypeptide denoted in column one is identical to the polypeptide denoted in column three except for an occasional addition of a few putative amino acid residues at the N-terminus which result from the fact that the polypeptides of column three were derived by translating from stop codon to stop codon instead of from a predicted start codon (i.e., Met or Val) to a stop codon as was done for the polypeptides in column one.

Second, for most polypeptides (designated "B" in the last column of the Table 3), the polypeptide of column one is at least 95% identical to the polypeptide of column three except that the polypeptide in column three is longer (at either or both ends) by one or more amino acid residues which do not result from the difference between reading from stop to stop instead of from start to stop.

Third, for some polypeptides (designated "C" in the last column of Table 3), the converse is true, the polypeptide of column one is at least 95% identical to the polypeptide of column three except that the polypeptide in column three is shorter (at either or both ends).

Fourth, for some polypeptides (designated "D" in the last column of Table 3), the polypeptide of column one shares a high level of amino acid identity (i.e., at least 95%) with the polypeptide of column three in the region in which they overlap, but shares little or no identity (i.e., less than 95%) at one or both ends. The level of identity of the polypeptides in columns one and three in categories "B", "C" and "D" is highly significant. For example, a typical *H. pylori* gene product will exhibit amino acid sequence identities of between 92% to 100% among strains of *H. pylori* isolated from human patients (see Table 10 below).

Finally, a fifth class of polypeptides in column one (designated "E" in the last column of Table 3) are closely related but differ significantly (i.e., less than 95% identical) from the polypeptide of column three. These polypeptides are likely "paralogs," members of related gene families in *H. pylori*.

TABLE 3

TABLE 3					
SeqID #	Length (aa)	SeqID #	Length (aa)	% Identity: Overlap Length	Category
384	509	1779	593	100.0 : 504 aa	B
386	133	1713	205	99.2 : 127 aa	B
387	158	1743	340	98.7 : 155 aa	B
388	112	1489	330	100.0 : 105 aa	B
389	650	1643	369	95.4 : 65 aa	D
390	62	1598	327	90.2 : 61 aa	E
391	619	1747	991	99.3 : 608 aa	B
392	110	1570	183	93.1 : 101 aa	E
393	68	1811	85	97.1 : 68 aa	B
394	446	1884	594	99.5 : 433 aa	B
395	84	1503	347	100.0 : 84 aa	B
396	40	1504	519	88.2 : 34 aa	E
397	300	1531	273	98.9 : 267 aa	C
398	214	1795	197	99.0 : 192 aa	C
399	137	1639	199	96.4 : 137 aa	B
400	272	1725	285	99.3 : 271 aa	B
401	287	1470	455	98.9 : 277 aa	D
402	106	1596	302	99.1 : 106 aa	B
403	157	1654	197	99.3 : 150 aa	B
404	278	1552	362	100.0 : 277 aa	B
405	120	1858	529	100.0 : 116 aa	B
406	226	1562	297	100.0 : 216 aa	B
407	62	1752	157	77.6 : 58 aa	E
408	50	1663	74	97.9 : 47 aa	B
410	188	1803	351	87.1 : 155 aa	E
411	130	1685	497	100.0 : 129 aa	B
412	183	1843	185	100.0 : 183 aa	A
413	194	1874	508	97.6 : 169 aa	D
414	235	1518	246	100.0 : 235 aa	B
415	88	1538	676	97.5 : 80 aa	B
416	109	1871	335	99.1 : 109 aa	B
417	107	1782	593	94.4 : 90 aa	E
418	136	1544	441	100.0 : 135 aa	B
419	54	1513	175	97.0 : 33 aa	E
420	125	1642	539	96.7 : 122 aa	B
421	249	1738	346	99.6 : 249 aa	B
422	86	1715	128	97.5 : 79 aa	B
423	128	1534	149	100.0 : 128 aa	B
424	93	1875	178	100.0 : 93 aa	B
425	88	1804	105	97.7 : 88 aa	B
426	128	1524	116	62.4 : 117 aa	E
427	108	1762	109	100.0 : 108 aa	A
428	118	1539	276	100.0 : 118 aa	B
429	54	1754	113	89.6 : 48 aa	E
430	288	1483	377	95.5 : 286 aa	B
431	303	1785	248	98.2 : 170 aa	D
431	303	1784	148	96.4 : 138 aa	D
432	192	1478	408	99.5 : 192 aa	B
433	168	1517	426	99.3 : 151 aa	D

-63-

434	153	1679	403	100.0 : 153 aa	B
435	162	1806	173	98.1 : 161 aa	B
436	59	1834	80	37.5 : 24 aa	E
437	222	1533	288	100.0 : 221 aa	B
438	53	1737	260	93.5 : 31 aa	E
439	109	1683	121	100.0 : 109 aa	B
440	73	1773	280	100.0 : 73 aa	B
441	237	1685	497	96.0 : 198 aa	D
442	92	1521	646	100.0 : 84 aa	D
443	97	1774	327	100.0 : 96 aa	B
444	280	1556	284	100.0 : 280 aa	A
445	187	1604	253	95.5 : 155 aa	D
446	58	1510	198	96.4 : 55 aa	B
447	85	1496	155	100.0 : 85 aa	B
448	90	1724	90	100.0 : 90 aa	A
449	105	1788	141	98.0 : 100 aa	D
450	172	1495	239	100.0 : 172 aa	B
451	212	1456	139	81.7 : 126 aa	E
452	182	1702	192	97.0 : 166 aa	D
453	224	1658	228	100.0 : 224 aa	A
454	131	1895	159	100.0 : 131 aa	B
455	73	1787	370	100.0 : 54 aa	D
456	92	1587	295	96.6 : 87 aa	B
457	205	1735	310	100.0 : 195 aa	B
458	41	1479	144	97.6 : 41 aa	B
459	219	1584	297	100.0 : 219 aa	B
460	188	1546	375	89.3 : 187 aa	E
461	231	1780	438	97.3 : 225 aa	B
462	63	1645	71	100.0 : 63 aa	B
463	183	1664	242	97.8 : 182 aa	B
464	117	1586	234	99.1 : 113 aa	B
465	153	1773	280	98.0 : 153 aa	B
466	43	1610	308	100.0 : 43 aa	B
467	240	1636	255	97.0 : 237 aa	B
468	209	1868	240	96.6 : 206 aa	B
469	95	1628	321	98.5 : 65 aa	D
470	229	1595	375	96.5 : 228 aa	B
471	92	1713	205	90.1 : 71 aa	E
472	96	1492	352	95.4 : 87 aa	B
473	1178	1748	1183	100.0 : 1178 aa	A
474	163	1822	113	92.7 : 109 aa	E
474	163	1820	88	93.1 : 58 aa	E
475	466	1840	467	100.0 : 466 aa	A
476	60	1500	90	97.0 : 33 aa	D
477	249	1854	254	100.0 : 248 aa	B
478	44	1772	528	100.0 : 44 aa	B
479	421	1693	421	99.8 : 421 aa	A
480	167	1555	340	98.1 : 162 aa	B
481	89	1888	236	100.0 : 89 aa	B
482	237	1873	461	97.5 : 236 aa	B
483	471	1594	428	99.3 : 301 aa	C
484	123	1655	366	87.9 : 107 aa	E
485	127	1655	366	99.2 : 127 aa	B
486	259	1517	259	100.0 : 259 aa	A
487	17	1481	101	93.3 : 15 aa	E
488	77	1704	246	100.0 : 77 aa	B

-64-

489	180	1554	180	100.0 : 180 aa	A
490	213	1638	577	92.3 : 209 aa	E
491	148	1452	157	100.0 : 148 aa	B
492	281	1519	849	99.6 : 281 aa	B
493	144	1525	377	94.9 : 118 aa	D
494	73	1539	276	95.8 : 71 aa	B
495	311	1670	446	99.0 : 311 aa	B
496	115	1842	384	99.1 : 114 aa	B
497	200	1600	459	100.0 : 200 aa	B
498	264	1828	458	100.0 : 264 aa	B
499	339	1490	362	99.7 : 339 aa	B
500	146	1449	430	94.4 : 142 aa	E
501	60	1465	240	98.3 : 58 aa	B
502	351	1458	532	98.6 : 346 aa	B
503	233	1666	296	94.3 : 230 aa	E
504	32	1513	175	100.0 : 32 aa	B
505	171	1462	452	91.8 : 171 aa	B
506	33	1672	121	100.0 : 24 aa	D
507	100	1650	192	80.0 : 90 aa	E
508	79	1772	528	80.8 : 78 aa	E
509	70	1662	88	96.2 : 53 aa	D
510	130	1530	131	100.0 : 130 aa	A
511	53	1723	163	91.8 : 49 aa	E
512	79	1572	189	98.5 : 65 aa	D
513	102	1889	114	99.0 : 100 aa	B
514	15	1516	407	100.0 : 12 aa	B
515	378	1747	991	97.9 : 377 aa	B
516	1027	1692	2440	100.0 : 1027 aa	B
517	155	1831	182	89.6 : 154 aa	E
518	62	1552	362	74.5 : 47 aa	E
519	237	1557	241	100.0 : 237 aa	A
520	83	1627	424	100.0 : 83 aa	B
522	64	1680	227	98.4 : 63 aa	B
523	228	1532	241	100.0 : 228 aa	B
524	273	1710	189	97.2 : 180 aa	C
524	273	1712	115	100.0 : 99 aa	C
525	15	1612	65	100.0 : 15 aa	B
526	115	1733	112	94.6 : 111 aa	C
527	67	1755	156	100.0 : 62 aa	D
528	323	1635	336	100.0 : 322 aa	B
529	10	1731	101	50.0 : 10 aa	B
530	12	1455	284	100.0 : 12 aa	B
531	79	1528	101	94.9 : 79 aa	B
532	95	1887	279	100.0 : 95 aa	B
533	154	1591	168	100.0 : 152 aa	B
534	68	1501	283	100.0 : 67 aa	B
535	313	1519	849	95.5 : 313 aa	B
536	319	1486	325	100.0 : 319 aa	A
537	118	1707	154	90.9 : 110 aa	E
538	89	1674	161	88.2 : 76 aa	E
539	92	1838	100	100.0 : 92 aa	A
540	138	1525	377	86.9 : 137 aa	B
541	277	1661	394	96.0 : 273 aa	D
542	254	1567	392	98.0 : 254 aa	B
543	185	1467	594	99.5 : 185 aa	B
544	37	1886	326	100.0 : 37 aa	B

-65-

545	94	1772	528	89.1 : 92 aa	E
546	182	1760	366	100.0 : 182 aa	B
547	247	1776	150	100.0 : 146 aa	C
547	247	1775	88	100.0 : 87 aa	C
548	422	1798	426	100.0 : 422 aa	A
549	61	1620	78	96.7 : 60 aa	B
550	54	1566	309	37.8 : 45 aa	E
551	298	1751	518	98.0 : 297 aa	B
552	91	1738	346	95.5 : 88 aa	D
553	111	1764	130	100.0 : 111 aa	B
554	137	1626	93	100.0 : 84 aa	D
555	124	1717	114	89.2 : 111 aa	E
556	86	1597	432	89.7 : 78 aa	E
557	87	1457	97	100.0 : 86 aa	B
558	108	1750	154	99.1 : 108 aa	B
559	142	1619	211	97.9 : 141 aa	B
560	231	1580	315	99.6 : 231 aa	B
561	186	1446	275	88.3 : 180 aa	E
562	183	1515	198	100.0 : 183 aa	B
563	154	1477	188	100.0 : 154 aa	B
564	288	1767	303	100.0 : 288 aa	B
565	420	1841	424	100.0 : 420 aa	A
566	72	1450	486	98.5 : 67 aa	D
567	205	1799	270	99.5 : 199 aa	D
568	328	1893	338	100.0 : 328 aa	B
569	140	1855	614	84.8 : 125 aa	E
570	76	1499	184	98.1 : 53 aa	D
571	194	1660	201	100.0 : 193 aa	B
572	140	1583	163	96.9 : 130 aa	D
573	308	1676	316	100.0 : 308 aa	B
574	339	1667	468	99.1 : 335 aa	B
575	207	1688	208	98.1 : 207 aa	A
576	251	1891	267	100.0 : 251 aa	B
577	69	1745	109	96.7 : 61 aa	D
578	112	1519	849	99.1 : 112 aa	B
579	152	1649	543	98.7 : 152 aa	B
580	130	1853	220	98.3 : 120 aa	D
581	113	1614	134	100.0 : 113 aa	B
582	174	1569	209	100.0 : 174 aa	B
583	35	1752	157	34.4 : 32 aa	E
584	308	1728	316	100.0 : 307 aa	B
585	702	1857	797	99.9 : 702 aa	B
586	293	1633	664	96.2 : 293 aa	B
587	52	1542	429	100.0 : 52 aa	B
588	182	1504	519	100.0 : 182 aa	B
589	251	1622	262	99.6 : 251 aa	B
590	40	1632	61	97.5 : 40 aa	B
591	122	1691	717	99.1 : 113 aa	D
592	113	1768	121	100.0 : 113 aa	B
593	437	1520	448	100.0 : 437 aa	A
594	146	1549	200	93.2 : 146 aa	E
595	128	1494	131	99.2 : 127 aa	B
596	95	1667	468	100.0 : 93 aa	B
597	102	1447	149	100.0 : 91 aa	D
598	127	1879	138	100.0 : 127 aa	B
599	502	1881	928	99.2 : 500 aa	B

-66-

600	42	1625	91	100.0 : 42 aa	B
601	341	1454	381	99.7 : 341 aa	B
602	465	1694	442	98.2 : 433 aa	D
602	465	1896	259	99.6 : 238 aa	D
603	193	1484	229	99.4 : 170 aa	D
604	141	1673	130	97.6 : 126 aa	D
605	159	1582	358	83.3 : 156 aa	E
606	376	1565	382	100.0 : 376 aa	B
607	352	1862	363	99.1 : 352 aa	B
608	88	1807	144	98.7 : 77 aa	D
609	86	1553	181	72.0 : 82 aa	E
610	76	1527	77	100.0 : 76 aa	A
611	98	1732	118	98.9 : 95 aa	B
612	162	1525	377	91.3 : 161 aa	E
613	58	1547	152	98.3 : 58 aa	B
614	66	1470	455	85.2 : 61 aa	E
615	117	1844	982	95.5 : 111 aa	D
616	83	1723	163	96.3 : 82 aa	B
617	77	1763	275	89.6 : 77 aa	E
618	176	1696	149	93.6 : 125 aa	E
618	176	1698	231	92.3 : 65 aa	E
619	144	1498	577	96.0 : 124 aa	D
620	90	1516	407	98.9 : 90 aa	B
621	268	1571	275	100.0 : 268 aa	B
622	171	1753	206	99.4 : 171 aa	B
623	102	1559	256	100.0 : 84 aa	D
624	117	1819	640	94.2 : 104 aa	E
625	237	1758	842	99.6 : 233 aa	B
626	199	1464	200	100.0 : 198 aa	C
627	225	1611	347	97.7 : 221 aa	B
627	225	1608	97	97.8 : 91 aa	C
628	86	1772	528	90.4 : 83 aa	E
629	496	1558	539	100.0 : 496 aa	B
630	142	1778	332	99.1 : 116 aa	D
631	153	1709	111	76.9 : 108 aa	E
631	153	1708	76	60.9 : 46 aa	E
633	93	1848	106	100.0 : 93 aa	B
634	177	1603	531	98.9 : 175 aa	B
635	88	1812	93	100.0 : 88 aa	A
636	115	1746	122	100.0 : 115 aa	B
637	261	1850	304	98.5 : 260 aa	B
638	191	1691	717	99.5 : 185 aa	B
639	351	1697	373	99.7 : 351 aa	B
640	351	1601	355	100.0 : 342 aa	D
641	146	1592	320	96.6 : 145 aa	B
642	190	1796	376	100.0 : 190 aa	B
643	489	1705	957	99.4 : 468 aa	D
644	249	1706	249	100.0 : 248 aa	A
645	120	1540	269	100.0 : 104 aa	D
646	109	1550	350	100.0 : 108 aa	B
648	158	1573	237	95.5 : 155 aa	D
649	312	1721	312	100.0 : 312 aa	A
650	56	1839	242	98.1 : 52 aa	D
651	199	1813	261	99.5 : 196 aa	B
652	82	1756	99	96.3 : 81 aa	D
653	89	1475	227	100.0 : 89 aa	B

-67-

654	111	1535	119	98.2 : 111 aa	B
655	65	1686	276	98.3 : 59 aa	D
656	268	1892	272	100.0 : 268 aa	A
657	100	1597	432	100.0 : 84 aa	D
658	80	1640	276	97.2 : 72 aa	D
659	205	1824	217	100.0 : 205 aa	B
660	124	1471	67	98.4 : 64 aa	D
660	124	1472	186	96.7 : 60 aa	D
661	93	1618	95	98.9 : 93 aa	B
662	80	1568	170	98.7 : 79 aa	B
663	214	1749	224	100.0 : 214 aa	B
664	78	1668	214	97.3 : 75 aa	D
665	177	1844	982	78.6 : 173 aa	E
666	258	1578	275	94.1 : 254 aa	E
667	75	1742	360	100.0 : 75 aa	B
668	421	1699	421	99.5 : 421 aa	A
669	81	1542	429	100.0 : 81 aa	B
670	112	1540	269	76.1 : 113 aa	E
671	326	1689	246	92.8 : 208 aa	E
672	272	1727	279	100.0 : 271 aa	A
673	78	1661	394	100.0 : 78 aa	B
674	400	1736	419	100.0 : 400 aa	B
675	91	1522	273	95.5 : 88 aa	D
676	126	1561	131	100.0 : 126 aa	A
677	195	1577	301	76.5 : 196 aa	E
678	72	1814	90	98.6 : 72 aa	B
679	111	1572	189	100.0 : 111 aa	B
680	142	1847	207	92.6 : 135 aa	E
681	63	1516	407	96.4 : 56 aa	D
682	310	1700	446	99.3 : 301 aa	B
683	169	1744	219	100.0 : 169 aa	B
684	85	1611	347	88.1 : 84 aa	E
685	77	1829	251	97.3 : 75 aa	D
686	197	1634	425	99.0 : 194 aa	D
687	142	1722	197	100.0 : 136 aa	D
688	86	1805	87	100.0 : 86 aa	A
689	121	1759	356	97.5 : 118 aa	B
690	59	1789	77	84.6 : 52 aa	E
691	142	1675	420	97.1 : 140 aa	B
692	80	1722	197	83.3 : 60 aa	E
693	180	1659	187	100.0 : 179 aa	B
694	75	1529	159	100.0 : 75 aa	B
695	99	1849	119	100.0 : 99 aa	B
696	209	1701	430	99.5 : 205 aa	B
697	75	1616	196	100.0 : 75 aa	B
698	121	1678	460	100.0 : 121 aa	B
699	102	1579	139	99.0 : 100 aa	B
700	131	1595	375	99.2 : 131 aa	B
701	441	1488	444	96.9 : 426 aa	D
702	127	1774	327	99.1 : 116 aa	D
703	287	1765	327	93.9 : 279 aa	E
704	46	1581	111	95.2 : 21 aa	D
705	115	1647	117	100.0 : 115 aa	A
706	86	1463	111	100.0 : 86 aa	B
707	44	1588	68	100.0 : 44 aa	B
708	560	1589	1413	98.8 : 560 aa	B

-68-

709	125	1607	443	95.8 : 118 aa	D
710	96	1469	540	100.0 : 73 aa	D
711	81	1629	244	96.3 : 80 aa	D
712	141	1671	375	100.0 : 125 aa	D

713	51	1867	193	96.1 : 51 aa	B
714	233	1833	240	99.5 : 218 aa	D
715	266	1644	271	100.0 : 265 aa	B
716	158	1883	226	94.7 : 150 aa	E
717	191	1860	240	100.0 : 189 aa	B
718	243	1817	256	99.6 : 243 aa	B
719	236	1617	667	98.3 : 236 aa	B
720	175	1523	592	97.1 : 172 aa	B
721	226	1770	340	92.7 : 218 aa	E
722	79	1629	244	100.0 : 74 aa	D
723	65	1506	229	100.0 : 49 aa	D
724	138	1675	426	93.2 : 132 aa	E
725	210	1832	215	100.0 : 210 aa	A
726	296	1821	223	100.0 : 190 aa	D
726	296	1819	640	99.1 : 106 aa	D
727	94	1706	249	97.8 : 91 aa	D
728	83	1593	171	100.0 : 83 aa	B
729	203	1448	268	100.0 : 202 aa	B
730	220	1656	242	100.0 : 220 aa	B
731	116	1818	196	100.0 : 115 aa	B
732	248	1474	248	100.0 : 248 aa	A
733	150	1459	347	100.0 : 118 aa	D
734	228	1545	302	96.9 : 227 aa	B
735	187	1597	432	100.0 : 172 aa	D
736	198	1761	354	100.0 : 198 aa	B
737	208	1780	438	93.8 : 208 aa	E
738	201	1842	384	100.0 : 193 aa	D
739	127	1669	405	21.6 : 74 aa	E
740	79	1615	280	97.3 : 75 aa	D
741	49	1878	443	91.3 : 46 aa	E
742	412	1877	425	97.8 : 412 aa	B
743	89	1482	111	100.0 : 89 aa	B
744	192	1502	222	98.4 : 189 aa	B
745	109	1797	304	96.3 : 109 aa	B
746	116	1791	359	94.8 : 116 aa	B
747	163	1711	321	100.0 : 163 aa	B
748	40	1483	377	100.0 : 40 aa	B
749	45	1770	340	95.2 : 42 aa	D
750	118	1867	193	92.2 : 116 aa	E
751	200	1491	211	100.0 : 200 aa	B
752	79	1890	80	100.0 : 79 aa	A
753	98	1837	268	98.7 : 79 aa	D
754	146	1653	413	100.0 : 141 aa	B
755	206	1638	577	93.7 : 206 aa	B
756	97	1526	89	100.0 : 66 aa	D
757	197	1794	198	100.0 : 197 aa	A
758	149	1872	94	97.5 : 80 aa	D
759	68	1882	291	100.0 : 68 aa	B
760	135	1631	162	99.3 : 134 aa	B
761	93	1884	594	100.0 : 69 aa	D
762	73	1883	226	100.0 : 73 aa	B
763	268	1859	430	95.4 : 263 aa	B

-69-

764	274	1537	277	100.0 : 273 aa	B
765	134	1714	136	99.2 : 133 aa	A
766	72	1810	74	95.8 : 71 aa	A
767	147	1802	285	100.0 : 147 aa	B
768	144	1541	241	100.0 : 144 aa	B
769	47	1684	75	100.0 : 47 aa	B
770	129	1505	183	90.2 : 122 aa	E
771	242	1536	235	99.1 : 232 aa	C
772	97	1851	129	99.0 : 97 aa	B
773	143	1826	259	96.5 : 143 aa	B
774	218	1777	383	99.5 : 217 aa	B
775	84	1637	143	100.0 : 84 aa	B
776	76	1774	327	95.9 : 73 aa	D
777	155	1585	263	79.7 : 133 aa	E
778	192	1480	299	91.5 : 189 aa	E
779	171	1551	186	99.4 : 171 aa	B
780	141	1760	366	99.2 : 129 aa	D
781	70	1741	95	100.0 : 70 aa	B
782	153	1687	223	98.0 : 153 aa	B
783	183	1869	184	100.0 : 183 aa	A
784	67	1846	231	100.0 : 67 aa	B
785	254	1730	256	100.0 : 253 aa	B
786	173	1466	251	100.0 : 166 aa	D
787	259	1808	322	100.0 : 238 aa	D
788	294	1786	131	93.7 : 126 aa	E
788	294	1630	163	94.0 : 116 aa	E
789	194	1655	366	99.2 : 122 aa	D
789	194	1646	75	100.0 : 72 aa	C
790	132	1790	273	100.0 : 132 aa	B
791	213	1575	216	98.1 : 213 aa	A
792	47	1605	86	100.0 : 47 aa	B
793	143	1864	342	93.0 : 143 aa	E
794	69	1766	93	100.0 : 69 aa	B
795	144	1504	519	95.7 : 138 aa	D
796	190	1590	193	100.0 : 190 aa	A
797	84	1792	215	83.5 : 79 aa	E
798	135	1613	138	100.0 : 135 aa	A
799	255	1885	424	99.6 : 253 aa	B
800	243	1493	205	87.1 : 140 aa	E
800	243	1497	131	100.0 : 126 aa	C
801	252	1563	255	100.0 : 252 aa	A
802	165	1720	91	100.0 : 88 aa	C
802	165	1718	99	92.7 : 82 aa	E
803	171	1602	297	85.5 : 159 aa	E
804	62	1485	165	100.0 : 61 aa	B
805	199	1514	219	100.0 : 199 aa	B
806	131	1880	391	86.2 : 130 aa	E
807	101	1719	257	95.0 : 100 aa	B
808	80	1585	263	98.8 : 80 aa	B
809	447	1781	344	99.7 : 331 aa	D
809	447	1783	118	98.3 : 117 aa	C
810	218	1564	250	100.0 : 218 aa	B
811	192	1478	408	99.5 : 192 aa	B
812	341	1729	354	100.0 : 340 aa	B
813	201	1523	592	100.0 : 158 aa	D
814	130	1769	306	92.3 : 130 aa	E

-70-

815	144	1835	548	78.4 : 116 aa	E
815	144	1815	377	84.3 : 121 aa	E
816	309	1894	310	100.0 : 309 aa	A
817	164	1823	156	96.7 : 153 aa	D
818	54	1703	87	100.0 : 53 aa	B
819	202	1716	215	99.5 : 202 aa	B
820	169	1870	115	100.0 : 110 aa	D
821	186	1451	254	100.0 : 186 aa	B
822	72	1609	180	96.6 : 58 aa	D
823	122	1633	664	94.9 : 118 aa	D
824	13	1695	70	100.0 : 13 aa	B
824	13	1567	392	100.0 : 13 aa	B
825	99	1771	144	100.0 : 86 aa	D
826	71	1512	154	98.6 : 71 aa	B
827	150	1456	139	93.7 : 127 aa	E
828	255	1651	155	100.0 : 155 aa	C
828	255	1648	109	98.0 : 102 aa	D
829	106	1726	147	99.1 : 106 aa	B
830	527	1509	567	99.8 : 524 aa	B
831	124	1740	214	99.2 : 123 aa	B
832	110	1690	400	98.2 : 110 aa	B
833	326	1856	325	100.0 : 325 aa	C
834	253	1543	191	96.7 : 184 aa	D
835	597	1876	638	100.0 : 594 aa	B
836	156	1621	345	99.4 : 154 aa	B
837	157	1624	253	97.4 : 155 aa	B
838	191	1465	241	96.8 : 190 aa	B
839	90	1548	231	92.9 : 85 aa	E
840	277	1682	298	99.6 : 277 aa	B
841	58	1508	270	98.1 : 54 aa	D
842	139	1734	139	88.4 : 129 aa	E
843	279	1476	276	100.0 : 269 aa	C
844	36	1852	83	94.4 : 36 aa	B
845	129	1460	196	100.0 : 129 aa	B
846	127	1473	172	100.0 : 105 aa	D
847	276	1657	319	100.0 : 276 aa	B
848	126	1801	187	98.4 : 126 aa	B
849	242	1669	405	97.0 : 236 aa	D
850	151	1816	217	100.0 : 151 aa	B
851	154	1641	194	100.0 : 154 aa	B
852	496	1665	327	97.5 : 314 aa	C
853	179	1606	272	97.2 : 179 aa	B
855	160	1487	198	96.9 : 160 aa	B
856	94	1836	420	100.0 : 93 aa	B
857	146	1845	371	99.3 : 146 aa	B
858	205	1507	366	98.5 : 202 aa	B
859	173	1827	198	100.0 : 149 aa	D
860	193	1681	294	100.0 : 175 aa	D
861	104	1865	253	100.0 : 104 aa	B
862	355	1599	358	100.0 : 355 aa	B
863	93	1825	236	97.8 : 92 aa	B
864	82	1677	315	97.5 : 81 aa	B
865	234	1861	249	99.1 : 233 aa	B
866	239	1652	405	99.2 : 238 aa	B
867	86	1468	201	77.4 : 84 aa	E
868	289	1574	395	94.4 : 284 aa	E

-71-

869	436	1863	662	100.0 : 436 aa	B
870	114	1560	121	100.0 : 114 aa	B
871	173	1757	362	98.8 : 173 aa	B
872	116	1866	145	98.1 : 105 aa	D
873	127	1797	304	63.9 : 83 aa	E
873	127	1799	270	89.7 : 58 aa	E
873	127	1800	62	97.4 : 38 aa	D
873	127	1801	187	82.0 : 50 aa	E
874	150	1461	179	100.0 : 150 aa	B
875	209	1511	339	98.9 : 188 aa	D
876	234	1739	615	99.6 : 230 aa	B
877	395	1830	879	99.7 : 379 aa	D
878	103	1623	413	97.0 : 99 aa	D
879	265	1809	566	89.8 : 265 aa	B
880	364	1576	442	98.6 : 346 aa	D

IV. Identification of Nucleic Acids Encoding Vaccine Components and Targets for Agents Effective Against *H. pylori*

The disclosed *H. pylori* genome sequence includes segments that direct the synthesis of ribonucleic acids and polypeptides, as well as origins of replication, promoters, other types of regulatory sequences, and intergenic nucleic acids. The invention encompasses nucleic acids encoding immunogenic components of vaccines and targets for agents effective against *H. pylori*. Identification of said immunogenic components involved in the determination of the function of the disclosed sequences, which can be achieved using a variety of approaches. Non-limiting examples of these approaches are described briefly below.

Homology to known sequences: Computer-assisted comparison of the disclosed *H. pylori* sequences with previously reported sequences present in publicly available databases is useful for identifying functional *H. pylori* nucleic acid and polypeptide sequences. It will be understood that protein-coding sequences, for example, may be compared as a whole, and that a high degree of sequence homology between two proteins (such as, for example, >80-90%) at the amino acid level indicates that the two proteins also possess some degree of functional homology, such as, for example, among enzymes involved in metabolism, DNA synthesis, or cell wall synthesis, and proteins involved in transport, cell division, etc. In addition, many structural features of particular protein classes have been identified and correlate with specific consensus sequences, such as, for example, binding domains for nucleotides, DNA, metal ions, and other small molecules; sites for covalent modifications such as phosphorylation, acylation, and the like; sites of protein:protein interactions, etc. These consensus sequences may be quite short and thus may represent only a fraction of the entire protein-coding sequence. Identification of such a feature in an *H. pylori* sequence is therefore useful in determining the function of the encoded protein and identifying useful targets of antibacterial drugs.

Of particular relevance to the present invention are structural features that are common to secretory, transmembrane, and surface proteins, including secretion signal

-72-

peptides and hydrophobic transmembrane domains. *H. pylori* proteins identified as containing putative signal sequences and/or transmembrane domains are useful as immunogenic components of vaccines.

5 Identification of essential genes: Nucleic acids that encode proteins essential for growth or viability of *H. pylori* are preferred drug targets. *H. pylori* genes can be tested for their biological relevance to the organism by examining the effect of deleting and/or disrupting the genes, i.e., by so-called gene "knockout", using techniques known to those skilled in the relevant art. In this manner, essential genes may be identified.

10 Strain-specific sequences: Because of the evolutionary relationship between different *H. pylori* strains, it is believed that the presently disclosed *H. pylori* sequences are useful for identifying, and/or discriminating between, previously known and new *H. pylori* strains. It is believed that other *H. pylori* strains will exhibit at least 70% sequence homology with the presently disclosed sequence. Systematic and routine analyses of DNA sequences derived from samples containing *H. pylori* strains, and comparison with the
15 present sequence allows for the identification of sequences that can be used to discriminate between strains, as well as those that are common to all *H. pylori* strains. In one embodiment, the invention provides nucleic acids, including probes, and peptide and polypeptide sequences that discriminate between different strains of *H. pylori*. Strain-specific components can also be identified functionally by their ability to elicit or react with
20 antibodies that selectively recognize one or more *H. pylori* strains.

In another embodiment, the invention provides nucleic acids, including probes, and peptide and polypeptide sequences that are common to all *H. pylori* strains but are *not* found in other bacterial species.

25 Specific Example: Determination Of Candidate Protein Antigens For Antibody And Vaccine Development

The selection of candidate protein antigens for vaccine development can be derived from the nucleic acids encoding *H. pylori* polypeptides. First, the ORF's can be analyzed for homology to other known exported or membrane proteins and analyzed using the
30 discriminant analysis described by Klein, et al. (Klein, P., Kanehsia, M., and DeLisi, C. (1985) *Biochimica et Biophysica Acta* 815, 468-476) for predicting exported and membrane proteins.

Homology searches can be performed using the BLAST algorithm contained in the Wisconsin Sequence Analysis Package (Genetics Computer Group, University Research
35 Park, 575 Science Drive, Madison, WI 53711) to compare each predicted ORF amino acid sequence with all sequences found in the current GenBank, SWISS-PROT and PIR databases. BLAST searches for local alignments between the ORF and the databank sequences and reports a probability score which indicates the probability of finding this sequence by chance in the database. ORF's with significant homology (e.g. probabilities

-73-

lower than 1×10^{-6} that the homology is only due to random chance) to membrane or exported proteins represent protein antigens for vaccine development. Possible functions can be provided to *H. pylori* genes based on sequence homology to genes cloned in other organisms.

- 5 Discriminant analysis (Klein, et al. supra) can be used to examine the ORF amino acid sequences. This algorithm uses the intrinsic information contained in the ORF amino acid sequence and compares it to information derived from the properties of known membrane and exported proteins. This comparison predicts which proteins will be exported, membrane associated or cytoplasmic. ORF amino acid sequences identified as
10 exported or membrane associated by this algorithm are likely protein antigens for vaccine development.

Infrequently it is not possible to distinguish between multiple possible nucleotides at a given position in the nucleic acid sequence. In those cases the ambiguities are denoted by an extended alphabet as follows:

- 15 These are the official IUPAC-IUB single-letter base codes

Code	Base Description	
G	Guanine	
A	Adenine	
T	Thymine	
C	Cytosine	
R	Purine	(A or G)
Y	Pyrimidine	(C or T or U)
M	Amino	(A or C)
K	Ketone	(G or T)
S	Strong interaction	(C or G)
W	Weak interaction	(A or T)
H	Not-G	(A or C or T)
B	Not-A	(C or G or T)
V	Not-T (not-U)	(A or C or G)
D	Not-C	(A or G or T)
N	Any	(A or C or G or T)

- The amino acid translations of this invention account for the ambiguity in the nucleic acid sequence by translating the ambiguous codon as the letter "X". In all cases, the
20 permissible amino acid residues at a position are clear from an examination of the nucleic acid sequence based on the standard genetic code.

V. Production of Fragments and Analogs of *H. pylori* Nucleic Acids and Polypeptides

Based on the discovery of the *H. pylori* gene products of the invention provided in the Sequence Listing, one skilled in the art can alter the disclosed structure (of *H. pylori* genes), e.g., by producing fragments or analogs, and test the newly produced structures for activity. Examples of techniques known to those skilled in the relevant art which allow the production and testing of fragments and analogs are discussed below. These, or analogous methods can be used to make and screen libraries of polypeptides, e.g., libraries of random peptides or libraries of fragments or analogs of cellular proteins for the ability to bind *H. pylori* polypeptides. Such screens are useful for the identification of inhibitors of *H. pylori*.

Generation of Fragments

Fragments of a protein can be produced in several ways, e.g., recombinantly, by proteolytic digestion, or by chemical synthesis. Internal or terminal fragments of a polypeptide can be generated by removing one or more nucleotides from one end (for a terminal fragment) or both ends (for an internal fragment) of a nucleic acid which encodes the polypeptide. Expression of the mutagenized DNA produces polypeptide fragments. Digestion with "end-nibbling" endonucleases can thus generate DNA's which encode an array of fragments. DNA's which encode fragments of a protein can also be generated by random shearing, restriction digestion or a combination of the above-discussed methods.

Fragments can also be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry. For example, peptides of the present invention may be arbitrarily divided into fragments of desired length with no overlap of the fragments, or divided into overlapping fragments of a desired length.

Alteration of Nucleic Acids and Polypeptides: Random Methods

Amino acid sequence variants of a protein can be prepared by random mutagenesis of DNA which encodes a protein or a particular domain or region of a protein. Useful methods include PCR mutagenesis and saturation mutagenesis. A library of random amino acid sequence variants can also be generated by the synthesis of a set of degenerate oligonucleotide sequences. (Methods for screening proteins in a library of variants are elsewhere herein).

(A) PCR Mutagenesis

In PCR mutagenesis, reduced Taq polymerase fidelity is used to introduce random mutations into a cloned fragment of DNA (Leung et al., 1989, *Technique* 1:11-15). The DNA region to be mutagenized is amplified using the polymerase chain reaction (PCR) under conditions that reduce the fidelity of DNA synthesis by Taq DNA polymerase, e.g., by using a dGTP/dATP ratio of five and adding Mn^{2+} to the PCR reaction. The pool of amplified DNA fragments are inserted into appropriate cloning vectors to provide random mutant libraries.

-75-

(B) Saturation Mutagenesis

Saturation mutagenesis allows for the rapid introduction of a large number of single base substitutions into cloned DNA fragments (Mayers et al., 1985, *Science* 229:242). This technique includes generation of mutations, e.g., by chemical treatment or irradiation of single-stranded DNA *in vitro*, and synthesis of a complimentary DNA strand. The mutation frequency can be modulated by modulating the severity of the treatment, and essentially all possible base substitutions can be obtained. Because this procedure does not involve a genetic selection for mutant fragments both neutral substitutions, as well as those that alter function, are obtained. The distribution of point mutations is not biased toward conserved sequence elements.

(C) Degenerate Oligonucleotides

A library of homologs can also be generated from a set of degenerate oligonucleotide sequences. Chemical synthesis of a degenerate sequences can be carried out in an automatic DNA synthesizer, and the synthetic genes then ligated into an appropriate expression vector. The synthesis of degenerate oligonucleotides is known in the art (see for example, Narang, SA (1983) *Tetrahedron* 39:3; Itakura et al. (1981) *Recombinant DNA, Proc 3rd Cleveland Sympos. Macromolecules*, ed. AG Walton, Amsterdam: Elsevier pp273-289; Itakura et al. (1984) *Annu. Rev. Biochem.* 53:323; Itakura et al. (1984) *Science* 198:1056; Ike et al. (1983) *Nucleic Acid Res.* 11:477. Such techniques have been employed in the directed evolution of other proteins (see, for example, Scott et al. (1990) *Science* 249:386-390; Roberts et al. (1992) *PNAS* 89:2429-2433; Devlin et al. (1990) *Science* 249: 404-406; Cwirla et al. (1990) *PNAS* 87: 6378-6382; as well as U.S. Patents Nos. 5,223,409, 5,198,346, and 5,096,815).

25 Alteration of Nucleic Acids and Polypeptides: Methods for Directed Mutagenesis

Non-random or directed, mutagenesis techniques can be used to provide specific sequences or mutations in specific regions. These techniques can be used to create variants which include, e.g., deletions, insertions, or substitutions, of residues of the known amino acid sequence of a protein. The sites for mutation can be modified individually or in series, e.g., by (1) substituting first with conserved amino acids and then with more radical choices depending upon results achieved, (2) deleting the target residue, or (3) inserting residues of the same or a different class adjacent to the located site, or combinations of options 1-3.

(A) Alanine Scanning Mutagenesis

Alanine scanning mutagenesis is a useful method for identification of certain residues or regions of the desired protein that are preferred locations or domains for mutagenesis, Cunningham and Wells (*Science* 244:1081-1085, 1989). In alanine scanning, a residue or group of target residues are identified (e.g., charged residues such as Arg, Asp, His, Lys, and Glu) and replaced by a neutral or negatively charged amino acid (most preferably alanine or polyalanine). Replacement of an amino acid can affect the interaction

of the amino acids with the surrounding aqueous environment in or outside the cell. Those domains demonstrating functional sensitivity to the substitutions are then refined by introducing further or other variants at or for the sites of substitution. Thus, while the site for introducing an amino acid sequence variation is predetermined, the nature of the mutation per se need not be predetermined. For example, to optimize the performance of a mutation at a given site, alanine scanning or random mutagenesis may be conducted at the target codon or region and the expressed desired protein subunit variants are screened for the optimal combination of desired activity.

(B) Oligonucleotide-Mediated Mutagenesis

Oligonucleotide-mediated mutagenesis is a useful method for preparing substitution, deletion, and insertion variants of DNA, see, e.g., Adelman et al., (*DNA* 2:183, 1983). Briefly, the desired DNA is altered by hybridizing an oligonucleotide encoding a mutation to a DNA template, where the template is the single-stranded form of a plasmid or bacteriophage containing the unaltered or native DNA sequence of the desired protein. After hybridization, a DNA polymerase is used to synthesize an entire second complementary strand of the template that will thus incorporate the oligonucleotide primer, and will code for the selected alteration in the desired protein DNA. Generally, oligonucleotides of at least 25 nucleotides in length are used. An optimal oligonucleotide will have 12 to 15 nucleotides that are completely complementary to the template on either side of the nucleotide(s) coding for the mutation. This ensures that the oligonucleotide will hybridize properly to the single-stranded DNA template molecule. The oligonucleotides are readily synthesized using techniques known in the art such as that described by Crea et al. (*Proc. Natl. Acad. Sci. USA*, 75: 5765[1978]).

(C) Cassette Mutagenesis

Another method for preparing variants, cassette mutagenesis, is based on the technique described by Wells et al. (*Gene*, 34:315[1985]). The starting material is a plasmid (or other vector) which includes the protein subunit DNA to be mutated. The codon(s) in the protein subunit DNA to be mutated are identified. There must be a unique restriction endonuclease site on each side of the identified mutation site(s). If no such restriction sites exist, they may be generated using the above-described oligonucleotide-mediated mutagenesis method to introduce them at appropriate locations in the desired protein subunit DNA. After the restriction sites have been introduced into the plasmid, the plasmid is cut at these sites to linearize it. A double-stranded oligonucleotide encoding the sequence of the DNA between the restriction sites but containing the desired mutation(s) is synthesized using standard procedures. The two strands are synthesized separately and then hybridized together using standard techniques. This double-stranded oligonucleotide is referred to as the cassette. This cassette is designed to have 3' and 5' ends that are comparable with the ends of the linearized plasmid, such that it can be directly ligated to

-77-

the plasmid. This plasmid now contains the mutated desired protein subunit DNA sequence.

(D) Combinatorial Mutagenesis

Combinatorial mutagenesis can also be used to generate mutants (Ladner et al., WO 88/06630). In this method, the amino acid sequences for a group of homologs or other related proteins are aligned, preferably to promote the highest homology possible. All of the amino acids which appear at a given position of the aligned sequences can be selected to create a degenerate set of combinatorial sequences. The variegated library of variants is generated by combinatorial mutagenesis at the nucleic acid level, and is encoded by a variegated gene library. For example, a mixture of synthetic oligonucleotides can be enzymatically ligated into gene sequences such that the degenerate set of potential sequences are expressible as individual peptides, or alternatively, as a set of larger fusion proteins containing the set of degenerate sequences.

15 Other Modifications of *H. pylori* Nucleic Acids and Polypeptides

It is possible to modify the structure of an *H. pylori* polypeptide for such purposes as increasing solubility, enhancing stability (e.g., shelf life *ex vivo* and resistance to proteolytic degradation *in vivo*). A modified *H. pylori* protein or peptide can be produced in which the amino acid sequence has been altered, such as by amino acid substitution, deletion, or addition as described herein.

An *H. pylori* peptide can also be modified by substitution of cysteine residues preferably with alanine, serine, threonine, leucine or glutamic acid residues to minimize dimerization via disulfide linkages. In addition, amino acid side chains of fragments of the protein of the invention can be chemically modified. Another modification is cyclization of the peptide.

In order to enhance stability and/or reactivity, an *H. pylori* polypeptide can be modified to incorporate one or more polymorphisms in the amino acid sequence of the protein resulting from any natural allelic variation. Additionally, D-amino acids, non-natural amino acids, or non-amino acid analogs can be substituted or added to produce a modified protein within the scope of this invention. Furthermore, an *H. pylori* polypeptide can be modified using polyethylene glycol (PEG) according to the method of A. Schon and co-workers (Wie et al., *supra*) to produce a protein conjugated with PEG. In addition, PEG can be added during chemical synthesis of the protein. Other modifications of *H. pylori* proteins include reduction/alkylation (Tarr, *Methods of Protein Microcharacterization*, J. E. Silver ed., Humana Press, Clifton NJ 155-194 (1986)); acylation (Tarr, *supra*); chemical coupling to an appropriate carrier (Mishell and Shiigi, eds, *Selected Methods in Cellular Immunology*, WH Freeman, San Francisco, CA (1980), U.S. Patent 4,939,239; or mild formalin treatment (Marsh, (1971) *Int. Arch. of Allergy and Appl. Immunol.*, 41: 199 - 215).

-78-

To facilitate purification and potentially increase solubility of an *H. pylori* protein or peptide, it is possible to add an amino acid fusion moiety to the peptide backbone. For example, hexa-histidine can be added to the protein for purification by immobilized metal ion affinity chromatography (Hochuli, E. et al., (1988) *Bio/Technology*, 6: 1321 - 1325). In addition, to facilitate isolation of peptides free of irrelevant sequences, specific endoprotease cleavage sites can be introduced between the sequences of the fusion moiety and the peptide.

To potentially aid proper antigen processing of epitopes within an *H. pylori* polypeptide, canonical protease sensitive sites can be engineered between regions, each comprising at least one epitope via recombinant or synthetic methods. For example, charged amino acid pairs, such as KK or RR, can be introduced between regions within a protein or fragment during recombinant construction thereof. The resulting peptide can be rendered sensitive to cleavage by cathepsin and/or other trypsin-like enzymes which would generate portions of the protein containing one or more epitopes. In addition, such charged amino acid residues can result in an increase in the solubility of the peptide.

Primary Methods for Screening Polypeptides and Analogs

Various techniques are known in the art for screening generated mutant gene products. Techniques for screening large gene libraries often include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the genes under conditions in which detection of a desired activity, e.g., in this case, binding to *H. pylori* polypeptide or an interacting protein, facilitates relatively easy isolation of the vector encoding the gene whose product was detected. Each of the techniques described below is amenable to high through-put analysis for screening large numbers of sequences created, e.g., by random mutagenesis techniques.

(A) Two Hybrid Systems

Two hybrid assays such as the system described above (as with the other screening methods described herein), can be used to identify polypeptides, e.g., fragments or analogs of a naturally-occurring *H. pylori* polypeptide, e.g., of cellular proteins, or of randomly generated polypeptides which bind to an *H. pylori* protein. (The *H. pylori* domain is used as the bait protein and the library of variants are expressed as fish fusion proteins.) In an analogous fashion, a two hybrid assay (as with the other screening methods described herein), can be used to find polypeptides which bind a *H. pylori* polypeptide.

(B) Display Libraries

In one approach to screening assays, the candidate peptides are displayed on the surface of a cell or viral particle, and the ability of particular cells or viral particles to bind an appropriate receptor protein via the displayed product is detected in a "panning assay". For example, the gene library can be cloned into the gene for a surface membrane protein of a bacterial cell, and the resulting fusion protein detected by panning (Ladner et al., WO

88/06630; Fuchs et al. (1991) *Bio/Technology* 9:1370-1371; and Goward et al. (1992) *TIBS* 18:136-140). In a similar fashion, a detectably labeled ligand can be used to score for potentially functional peptide homologs. Fluorescently labeled ligands, e.g., receptors, can be used to detect homologs which retain ligand-binding activity. The use of fluorescently
5 labeled ligands, allows cells to be visually inspected and separated under a fluorescence microscope, or, where the morphology of the cell permits, to be separated by a fluorescence-activated cell sorter.

A gene library can be expressed as a fusion protein on the surface of a viral particle. For instance, in the filamentous phage system, foreign peptide sequences can be expressed
10 on the surface of infectious phage, thereby conferring two significant benefits. First, since these phage can be applied to affinity matrices at concentrations well over 10^{13} phage per milliliter, a large number of phage can be screened at one time. Second, since each infectious phage displays a gene product on its surface, if a particular phage is recovered from an affinity matrix in low yield, the phage can be amplified by another round of
15 infection. The group of almost identical *E. coli* filamentous phages M13, fd., and f1 are most often used in phage display libraries. Either of the phage gIII or gVIII coat proteins can be used to generate fusion proteins without disrupting the ultimate packaging of the viral particle. Foreign epitopes can be expressed at the NH₂-terminal end of pIII and phage bearing such epitopes recovered from a large excess of phage lacking this epitope (Ladner
20 et al. PCT publication WO 90/02909; Garrard et al., PCT publication WO 92/09690; Marks et al. (1992) *J. Biol. Chem.* 267:16007-16010; Griffiths et al. (1993) *EMBO J* 12:725-734; Clackson et al. (1991) *Nature* 352:624-628; and Barbas et al. (1992) *PNAS* 89:4457-4461).

A common approach uses the maltose receptor of *E. coli* (the outer membrane protein, LamB) as a peptide fusion partner (Charbit et al. (1986) *EMBO* 5, 3029-3037).
25 Oligonucleotides have been inserted into plasmids encoding the LamB gene to produce peptides fused into one of the extracellular loops of the protein. These peptides are available for binding to ligands, e.g., to antibodies, and can elicit an immune response when the cells are administered to animals. Other cell surface proteins, e.g., OmpA (Schorr et al. (1991) *Vaccines* 9, pp. 387-392), PhoE (Agterberg, et al. (1990) *Gene* 88, 37-45), and
30 PAL (Fuchs et al. (1991) *Bio/Tech* 9, 1369-1372), as well as large bacterial surface structures have served as vehicles for peptide display. Peptides can be fused to pilin, a protein which polymerizes to form the pilus-a conduit for interbacterial exchange of genetic information (Thiry et al. (1989) *Appl. Environ. Microbiol.* 55, 984-993). Because of its
35 role in interacting with other cells, the pilus provides a useful support for the presentation of peptides to the extracellular environment. Another large surface structure used for peptide display is the bacterial motive organ, the flagellum. Fusion of peptides to the subunit protein flagellin offers a dense array of many peptide copies on the host cells (Kuwajima et al. (1988) *Bio/Tech.* 6, 1080-1083). Surface proteins of other bacterial species have also served as peptide fusion partners. Examples include the *Staphylococcus*

protein A and the outer membrane IgA protease of *Neisseria* (Hansson et al. (1992) *J. Bacteriol.* 174, 4239-4245 and Klauser et al. (1990) *EMBO J.* 9, 1991-1999).

In the filamentous phage systems and the LamB system described above, the physical link between the peptide and its encoding DNA occurs by the containment of the DNA within a particle (cell or phage) that carries the peptide on its surface. Capturing the peptide captures the particle and the DNA within. An alternative scheme uses the DNA-binding protein LacI to form a link between peptide and DNA (Cull *et al.* (1992) *PNAS USA* 89:1865-1869). This system uses a plasmid containing the LacI gene with an oligonucleotide cloning site at its 3'-end. Under the controlled induction by arabinose, a LacI-peptide fusion protein is produced. This fusion retains the natural ability of LacI to bind to a short DNA sequence known as LacO operator (LacO). By installing two copies of LacO on the expression plasmid, the LacI-peptide fusion binds tightly to the plasmid that encoded it. Because the plasmids in each cell contain only a single oligonucleotide sequence and each cell expresses only a single peptide sequence, the peptides become specifically and stably associated with the DNA sequence that directed its synthesis. The cells of the library are gently lysed and the peptide-DNA complexes are exposed to a matrix of immobilized receptor to recover the complexes containing active peptides. The associated plasmid DNA is then reintroduced into cells for amplification and DNA sequencing to determine the identity of the peptide ligands. As a demonstration of the practical utility of the method, a large random library of dodecapeptides was made and selected on a monoclonal antibody raised against the opioid peptide dynorphin B. A cohort of peptides was recovered, all related by a consensus sequence corresponding to a six-residue portion of dynorphin B. (Cull et al. (1992) *Proc. Natl. Acad. Sci. U.S.A.* 89-1869)

This scheme, sometimes referred to as peptides-on-plasmids, differs in two important ways from the phage display methods. First, the peptides are attached to the C-terminus of the fusion protein, resulting in the display of the library members as peptides having free carboxy termini. Both of the filamentous phage coat proteins, pIII and pVIII, are anchored to the phage through their C-termini, and the guest peptides are placed into the outward-extending N-terminal domains. In some designs, the phage-displayed peptides are presented right at the amino terminus of the fusion protein. (Cwirla, et al. (1990) *Proc. Natl. Acad. Sci. U.S.A.* 87, 6378-6382) A second difference is the set of biological biases affecting the population of peptides actually present in the libraries. The LacI fusion molecules are confined to the cytoplasm of the host cells. The phage coat fusions are exposed briefly to the cytoplasm during translation but are rapidly secreted through the inner membrane into the periplasmic compartment, remaining anchored in the membrane by their C-terminal hydrophobic domains, with the N-termini, containing the peptides, protruding into the periplasm while awaiting assembly into phage particles. The peptides in the LacI and phage libraries may differ significantly as a result of their exposure to different proteolytic activities. The phage coat proteins require transport across the inner

membrane and signal peptidase processing as a prelude to incorporation into phage. Certain peptides exert a deleterious effect on these processes and are underrepresented in the libraries (Gallop et al. (1994) *J. Med. Chem.* 37(9):1233-1251). These particular biases are not a factor in the LacI display system.

- 5 The number of small peptides available in recombinant random libraries is enormous. Libraries of 10^7 - 10^9 independent clones are routinely prepared. Libraries as large as 10^{11} recombinants have been created, but this size approaches the practical limit for clone libraries. This limitation in library size occurs at the step of transforming the DNA containing randomized segments into the host bacterial cells. To circumvent this
- 10 limitation, an *in vitro* system based on the display of nascent peptides in polysome complexes has recently been developed. This display library method has the potential of producing libraries 3-6 orders of magnitude larger than the currently available phage/phagemid or plasmid libraries. Furthermore, the construction of the libraries, expression of the peptides, and screening, is done in an entirely cell-free format.
- 15 In one application of this method (Gallop et al. (1994) *J. Med. Chem.* 37(9):1233-1251), a molecular DNA library encoding 10^{12} decapeptides was constructed and the library expressed in an *E. coli* S30 *in vitro* coupled transcription/translation system. Conditions were chosen to stall the ribosomes on the mRNA, causing the accumulation of a substantial proportion of the RNA in polysomes and yielding complexes containing nascent
- 20 peptides still linked to their encoding RNA. The polysomes are sufficiently robust to be affinity purified on immobilized receptors in much the same way as the more conventional recombinant peptide display libraries are screened. RNA from the bound complexes is recovered, converted to cDNA, and amplified by PCR to produce a template for the next round of synthesis and screening. The polysome display method can be coupled to the
- 25 phage display system. Following several rounds of screening, cDNA from the enriched pool of polysomes was cloned into a phagemid vector. This vector serves as both a peptide expression vector, displaying peptides fused to the coat proteins, and as a DNA sequencing vector for peptide identification. By expressing the polysome-derived peptides on phage, one can either continue the affinity selection procedure in this format or assay the peptides
- 30 on individual clones for binding activity in a phage ELISA, or for binding specificity in a completion phage ELISA (Barret, et al. (1992) *Anal. Biochem* 204,357-364). To identify the sequences of the active peptides one sequences the DNA produced by the phagemid host.

35 Secondary Screening of Polypeptides and Analogs

The high through-put assays described above can be followed by secondary screens in order to identify further biological activities which will, e.g., allow one skilled in the art to differentiate agonists from antagonists. The type of a secondary screen used will depend on the desired activity that needs to be tested. For example, an assay can be developed in

which the ability to inhibit an interaction between a protein of interest and its respective ligand can be used to identify antagonists from a group of peptide fragments isolated though one of the primary screens described above.

Therefore, methods for generating fragments and analogs and testing them for activity are known in the art. Once the core sequence of interest is identified, it is routine for one skilled in the art to obtain analogs and fragments.

Peptide Mimetics of *H. pylori* Polypeptides

The invention also provides for reduction of the protein binding domains of the subject *H. pylori* polypeptides to generate mimetics, e.g. peptide or non-peptide agents. The peptide mimetics are able to disrupt binding of a polypeptide to its counter ligand, e.g., in the case of an *H. pylori* polypeptide binding to a naturally occurring ligand. The critical residues of a subject *H. pylori* polypeptide which are involved in molecular recognition of a polypeptide can be determined and used to generate *H. pylori*-derived peptidomimetics which competitively or noncompetitively inhibit binding of the *H. pylori* polypeptide with an interacting polypeptide (see, for example, European patent applications EP-412,762A and EP-B31,080A).

For example, scanning mutagenesis can be used to map the amino acid residues of a particular *H. pylori* polypeptide involved in binding an interacting polypeptide, peptidomimetic compounds (e.g. diazepine or isoquinoline derivatives) can be generated which mimic those residues in binding to an interacting polypeptide, and which therefore can inhibit binding of an *H. pylori* polypeptide to an interacting polypeptide and thereby interfere with the function of *H. pylori* polypeptide. For instance, non-hydrolyzable peptide analogs of such residues can be generated using benzodiazepine (e.g., see Freidinger et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), azepine (e.g., see Huffman et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), substituted gamma lactam rings (Garvey et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), keto-methylene pseudopeptides (Ewenson et al. (1986) *J Med Chem* 29:295; and Ewenson et al. in *Peptides: Structure and Function* (Proceedings of the 9th American Peptide Symposium) Pierce Chemical Co. Rockland, IL, 1985), β -turn dipeptide cores (Nagai et al. (1985) *Tetrahedron Lett* 26:647; and Sato et al. (1986) *J Chem Soc Perkin Trans* 1:1231), and β -aminoalcohols (Gordon et al. (1985) *Biochem Biophys Res Commun* 126:419; and Dann et al. (1986) *Biochem Biophys Res Commun* 134:71).

VI. Vaccine Formulations for *H. pylori* Nucleic Acids and Polypeptides

This invention also features vaccine compositions for protection against infection by *H. pylori* or for treatment of *H. pylori* infection, a gram-negative spiral microaerophilic bacterium. In one embodiment, the vaccine compositions contain one or more
5 immunogenic components such as a surface protein from *H. pylori*, or portion thereof, and a pharmaceutically acceptable carrier. Nucleic acids within the scope of the invention are exemplified by the nucleic acids of the invention contained in the Sequence Listing which encode *H. pylori* surface proteins. For example, the preferred nucleic acid for a vaccine composition of the invention is isolated from the group of nucleic acids which encode cell
10 envelope proteins as outlined in Table 1. More specifically, the amino acids of SEQ ID NO:812, SEQ ID NO:820, SEQ ID NO:880, SEQ ID NO:658, SEQ ID NO:865, SEQ ID NO:1729, SEQ ID NO:1861, or fragments thereof, can be used alone or in combination for the formulation of vaccine compositions of the invention, as well as, their corresponding nucleic acids of SEQ ID NO:977, SEQ ID NO:978, SEQ ID NO:994, SEQ ID NO:215,
15 SEQ ID NO:989, SEQ ID NO:1278, and SEQ ID NO:1410. However, any nucleic acid encoding an immunogenic *H. pylori* protein, or portion thereof, which is capable of expression in a cell, can be used in the present invention. These vaccines have therapeutic and prophylactic utilities.

One aspect of the invention provides a vaccine composition for protection against
20 infection by *H. pylori* which contains at least one immunogenic fragment of an *H. pylori* protein and a pharmaceutically acceptable carrier. Preferred fragments include peptides of at least about 10 amino acid residues in length, preferably about 10-20 amino acid residues in length, and more preferably about 12-16 amino acid residues in length.

Immunogenic components of the invention can be obtained, for example, by
25 screening polypeptides recombinantly produced from the corresponding fragment of the nucleic acid encoding the full-length *H. pylori* protein. In addition, fragments can be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry.

In one embodiment, immunogenic components are identified by the ability of the
30 peptide to stimulate T cells. Peptides which stimulate T cells, as determined by, for example, T cell proliferation or cytokine secretion are defined herein as comprising at least one T cell epitope. T cell epitopes are believed to be involved in initiation and perpetuation of the immune response to the protein allergen which is responsible for the clinical symptoms of allergy. These T cell epitopes are thought to trigger early events at the level
35 of the T helper cell by binding to an appropriate HLA molecule on the surface of an antigen presenting cell, thereby stimulating the T cell subpopulation with the relevant T cell receptor for the epitope. These events lead to T cell proliferation, lymphokine secretion, local inflammatory reactions, recruitment of additional immune cells to the site of antigen/T cell interaction, and activation of the B cell cascade, leading to the production of

antibodies. A T cell epitope is the basic element, or smallest unit of recognition by a T cell receptor, where the epitope comprises amino acids essential to receptor recognition (e.g., approximately 6 or 7 amino acid residues). Amino acid sequences which mimic those of the T cell epitopes are within the scope of this invention.

5 Screening immunogenic components can be accomplished using one or more of several different assays. For example, *in vitro*, peptide T cell stimulatory activity is assayed by contacting a peptide known or suspected of being immunogenic with an antigen presenting cell which presents appropriate MHC molecules in a T cell culture. Presentation of an immunogenic *H. pylori* peptide in association with appropriate MHC molecules to T
10 cells in conjunction with the necessary costimulation has the effect of transmitting a signal to the T cell that induces the production of increased levels of cytokines, particularly of interleukin-2 and interleukin-4. The culture supernatant can be obtained and assayed for interleukin-2 or other known cytokines. For example, any one of several conventional assays for interleukin-2 can be employed, such as the assay described in *Proc. Natl. Acad.*
15 *Sci USA*, 86: 1333 (1989) the pertinent portions of which are incorporated herein by reference. A kit for an assay for the production of interferon is also available from Genzyme Corporation (Cambridge, MA).

 Alternatively, a common assay for T cell proliferation entails measuring tritiated thymidine incorporation. The proliferation of T cells can be measured *in vitro* by
20 determining the amount of ³H-labeled thymidine incorporated into the replicating DNA of cultured cells. Therefore, the rate of DNA synthesis and, in turn, the rate of cell division can be quantified.

 Vaccine compositions of the invention containing immunogenic components (e.g., *H. pylori* polypeptide or fragment thereof or nucleic acid encoding an *H. pylori* polypeptide
25 or fragment thereof) preferably include a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier that does not cause an allergic reaction or other untoward effect in patients to whom it is administered. Suitable pharmaceutically acceptable carriers include, for example, one or more of water, saline, phosphate buffered saline, dextrose, glycerol, ethanol and the like, as well as combinations
30 thereof. Pharmaceutically acceptable carriers may further comprise minor amounts of auxiliary substances such as wetting or emulsifying agents, preservatives or buffers, which enhance the shelf life or effectiveness of the antibody. For vaccines of the invention containing *H. pylori* polypeptides, the polypeptide is coadministered with a suitable adjuvant.

35 It will be apparent to those of skill in the art that the therapeutically effective amount of DNA or protein of this invention will depend, *inter alia*, upon the administration schedule, the unit dose of antibody administered, whether the protein or DNA is administered in combination with other therapeutic agents, the immune status and health of the patient, and the therapeutic activity of the particular protein or DNA.

Vaccine compositions are conventionally administered parenterally, e.g., by injection, either subcutaneously or intramuscularly. Methods for intramuscular immunization are described by Wolff et al. (1990) *Science* 247: 1465-1468 and by Sedegah et al. (1994) *Immunology* 91: 9866-9870. Other modes of administration include oral and pulmonary formulations, suppositories, and transdermal applications. Oral immunization is preferred over parenteral methods for inducing protection against infection by *H. pylori*. Czinn et. al. (1993) *Vaccine* 11: 637-642. Oral formulations include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, and the like.

The vaccine compositions of the invention can include an adjuvant, including, but not limited to aluminum hydroxide; N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP); N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine (CGP 11637, referred to as nor-MDP); N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (CGP 19835A, referred to as MTP-PE); RIBI, which contains three components from bacteria; monophosphoryl lipid A; trehalose dimycolate; cell wall skeleton (MPL + TDM + CWS) in a 2% squalene/Tween 80 emulsion; and cholera toxin. Others which may be used are non-toxic derivatives of cholera toxin, including its B subunit, and/or conjugates or genetically engineered fusions of the *H. pylori* polypeptide with cholera toxin or its B subunit, procholeraenoid, fungal polysaccharides, including schizophyllan, muramyl dipeptide, muramyl dipeptide derivatives, phorbol esters, labile toxin of *E. coli*, non-*H. pylori* bacterial lysates, block polymers or saponins.

Other suitable delivery methods include biodegradable microcapsules or immunostimulating complexes (ISCOMs), cochleates, or liposomes, genetically engineered attenuated live vectors such as viruses or bacteria, and recombinant (chimeric) virus-like particles, e.g., bluetongue. The amount of adjuvant employed will depend on the type of adjuvant used. For example, when the mucosal adjuvant is cholera toxin, it is suitably used in an amount of 5 µg to 50 µg, for example 10 µg to 35 µg. When used in the form of microcapsules, the amount used will depend on the amount employed in the matrix of the microcapsule to achieve the desired dosage. The determination of this amount is within the skill of a person of ordinary skill in the art.

Carrier systems in humans may include enteric release capsules protecting the antigen from the acidic environment of the stomach, and including *H. pylori* polypeptide in an insoluble form as fusion proteins. Suitable carriers for the vaccines of the invention are enteric coated capsules and polylactide-glycolide microspheres. Suitable diluents are 0.2 N NaHCO₃ and/or saline.

Vaccines of the invention can be administered as a primary prophylactic agent in adults or in children, as a secondary prevention, after successful eradication of *H. pylori* in an infected host, or as a therapeutic agent in the aim to induce an immune response in a

susceptible host to prevent infection by *H. pylori*. The vaccines of the invention are administered in amounts readily determined by persons of ordinary skill in the art. Thus, for adults a suitable dosage will be in the range of 10 µg to 10 g, preferably 10 µg to 100 mg, for example 50 µg to 50 mg. A suitable dosage for adults will also be in the range of 5 µg to 500 mg. Similar dosage ranges will be applicable for children. Those skilled in the art will recognize that the optimal dose may be more or less depending upon the patient's body weight, disease, the route of administration, and other factors. Those skilled in the art will also recognize that appropriate dosage levels can be obtained based on results with known oral vaccines such as, for example, a vaccine based on an *E. coli* lysate (6 mg dose daily up to total of 540 mg) and with an enterotoxigenic *E. coli* purified antigen (4 doses of 1 mg) (Schulman et al., *J. Urol.* 150:917-921 (1993); Boedecker et al., *American Gastroenterological Assoc.* 999:A-222 (1993)). The number of doses will depend upon the disease, the formulation, and efficacy data from clinical trials. Without intending any limitation as to the course of treatment, the treatment can be administered over 3 to 8 doses for a primary immunization schedule over 1 month (Boedecker, *American Gastroenterological Assoc.* 888:A-222 (1993)).

In a preferred embodiment, a vaccine composition of the invention can be based on a killed whole *E. coli* preparation with an immunogenic fragment of an *H. pylori* protein of the invention expressed on its surface or it can be based on an *E. coli* lysate, wherein the killed *E. coli* acts as a carrier or an adjuvant.

It will be apparent to those skilled in the art that some of the vaccine compositions of the invention are useful only for preventing *H. pylori* infection, some are useful only for treating *H. pylori* infection, and some are useful for both preventing and treating *H. pylori* infection. In a preferred embodiment, the vaccine composition of the invention provides protection against *H. pylori* infection by stimulating humoral and/or cell-mediated immunity against *H. pylori*. It should be understood that amelioration of any of the symptoms of *H. pylori* infection is a desirable clinical goal, including a lessening of the dosage of medication used to treat *H. pylori*-caused disease, or an increase in the production of antibodies in the serum or mucous of patients.

VII. Antibodies Reactive With *H. pylori* Polypeptides

The invention also includes antibodies specifically reactive with the subject *H. pylori* polypeptide. Anti-protein/anti-peptide antisera or monoclonal antibodies can be made by standard protocols (See, for example, *Antibodies: A Laboratory Manual* ed. by Harlow and Lane (Cold Spring Harbor Press: 1988)). A mammal such as a mouse, a hamster or rabbit can be immunized with an immunogenic form of the peptide. Techniques for conferring immunogenicity on a protein or peptide include conjugation to carriers or other techniques well known in the art. An immunogenic portion of the subject *H. pylori* polypeptide can be administered in the presence of adjuvant. The progress of immunization

can be monitored by detection of antibody titers in plasma or serum. Standard ELISA or other immunoassays can be used with the immunogen as antigen to assess the levels of antibodies.

5 In a preferred embodiment, the subject antibodies are immunospecific for antigenic determinants of the *H. pylori* polypeptides of the invention, e.g. antigenic determinants of a polypeptide of the invention contained in the Sequence Listing, or a closely related human or non-human mammalian homolog (e.g., 90% homologous, more preferably at least 95% homologous). In yet a further preferred embodiment of the invention, the anti-*H. pylori* antibodies do not substantially cross react (i.e., react specifically) with a protein which is
10 for example, less than 80% percent homologous to a sequence of the invention contained in the Sequence Listing. By "not substantially cross react", it is meant that the antibody has a binding affinity for a non-homologous protein which is less than 10 percent, more preferably less than 5 percent, and even more preferably less than 1 percent, of the binding affinity for a protein of the invention contained in the Sequence Listing. In a most
15 preferred embodiment, there is no crossreactivity between bacterial and mammalian antigens.

The term antibody as used herein is intended to include fragments thereof which are also specifically reactive with *H. pylori* polypeptides. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as
20 described above for whole antibodies. For example, F(ab')₂ fragments can be generated by treating antibody with pepsin. The resulting F(ab')₂ fragment can be treated to reduce disulfide bridges to produce Fab' fragments. The antibody of the invention is further intended to include bispecific and chimeric molecules having an anti-*H. pylori* portion.

Both monoclonal and polyclonal antibodies (Ab) directed against *H. pylori*
25 polypeptides or *H. pylori* polypeptide variants, and antibody fragments such as Fab' and F(ab')₂, can be used to block the action of *H. pylori* polypeptide and allow the study of the role of a particular *H. pylori* polypeptide of the invention in aberrant or unwanted intracellular signaling, as well as the normal cellular function of the *H. pylori* and by microinjection of anti-*H. pylori* polypeptide antibodies of the present invention.

30 Antibodies which specifically bind *H. pylori* epitopes can also be used in immunohistochemical staining of tissue samples in order to evaluate the abundance and pattern of expression of *H. pylori* antigens. Anti *H. pylori* polypeptide antibodies can be used diagnostically in immuno-precipitation and immuno-blotting to detect and evaluate *H. pylori* levels in tissue or bodily fluid as part of a clinical testing procedure. Likewise, the
35 ability to monitor *H. pylori* polypeptide levels in an individual can allow determination of the efficacy of a given treatment regimen for an individual afflicted with such a disorder. The level of an *H. pylori* polypeptide can be measured in cells found in bodily fluid, such as in urine samples or can be measured in tissue, such as produced by gastric biopsy. Diagnostic assays using anti-*H. pylori* antibodies can include, for example, immunoassays

-88-

designed to aid in early diagnosis of *H. pylori* infections. The present invention can also be used as a method of detecting antibodies contained in samples from individuals infected by this bacterium using specific *H. pylori* antigens.

Another application of anti-*H. pylori* polypeptide antibodies of the invention is in the immunological screening of cDNA libraries constructed in expression vectors such as λ gt11, λ gt18-23, λ ZAP, and λ ORF8. Messenger libraries of this type, having coding sequences inserted in the correct reading frame and orientation, can produce fusion proteins. For instance, λ gt11 will produce fusion proteins whose amino termini consist of β -galactosidase amino acid sequences and whose carboxy termini consist of a foreign polypeptide. Antigenic epitopes of a subject *H. pylori* polypeptide can then be detected with antibodies, as, for example, reacting nitrocellulose filters lifted from infected plates with anti-*H. pylori* polypeptide antibodies. Phage, scored by this assay, can then be isolated from the infected plate. Thus, the presence of *H. pylori* gene homologs can be detected and cloned from other species, and alternate isoforms (including splicing variants) can be detected and cloned.

VIII. Kits Containing Nucleic Acids, Polypeptides or Antibodies of the Invention

The nucleic acid, polypeptides and antibodies of the invention can be combined with other reagents and articles to form kits. Kits for diagnostic purposes typically comprise the nucleic acid, polypeptides or antibodies in vials or other suitable vessels. Kits typically comprise other reagents for performing hybridization reactions, polymerase chain reactions (PCR), or for reconstitution of lyophilized components, such as aqueous media, salts, buffers, and the like. Kits may also comprise reagents for sample processing such as detergents, chaotropic salts and the like. Kits may also comprise immobilization means such as particles, supports, wells, dipsticks and the like. Kits may also comprise labeling means such as dyes, developing reagents, radioisotopes, fluorescent agents, luminescent or chemiluminescent agents, enzymes, intercalating agents and the like. With the nucleic acid and amino acid sequence information provided herein, individuals skilled in art can readily assemble kits to serve their particular purpose. Kits further can include instructions for use.

IX. Drug Screening Assays Using *H. pylori* Polypeptides

By making available purified and recombinant *H. pylori* polypeptides, the present invention provides assays which can be used to screen for drugs which are either agonists or antagonists of the normal cellular function, in this case, of the subject *H. pylori* polypeptides, or of their role in intracellular signaling. Such inhibitors or potentiators may be useful as new therapeutic agents to combat *H. pylori* infections in humans. A variety of assay formats will suffice and, in light of the present inventions, will be comprehended by the skilled artisan.

In many drug screening programs which test libraries of compounds and natural extracts, high throughput assays are desirable in order to maximize the number of compounds surveyed in a given period of time. Assays which are performed in cell-free systems, such as may be derived with purified or semi-purified proteins, are often preferred
5 as "primary" screens in that they can be generated to permit rapid development and relatively easy detection of an alteration in a molecular target which is mediated by a test compound. Moreover, the effects of cellular toxicity and/or bioavailability of the test compound can be generally ignored in the *in vitro* system, the assay instead being focused primarily on the effect of the drug on the molecular target as may be manifest in an
10 alteration of binding affinity with other proteins or change in enzymatic properties of the molecular target. Accordingly, in an exemplary screening assay of the present invention, the compound of interest is contacted with an isolated and purified *H. pylori* polypeptide.

Screening assays can be constructed *in vitro* with a purified *H. pylori* polypeptide or fragment thereof, such as an *H. pylori* polypeptide having enzymatic activity, such that the
15 activity of the polypeptide produces a detectable reaction product. The efficacy of the compound can be assessed by generating dose response curves from data obtained using various concentrations of the test compound. Moreover, a control assay can also be performed to provide a baseline for comparison. Suitable products include those with distinctive absorption, fluorescence, or chemi-luminescence properties, for example,
20 because detection may be easily automated. A variety of synthetic or naturally occurring compounds can be tested in the assay to identify those which inhibit or potentiate the activity of the *H. pylori* polypeptide. Some of these active compounds may directly, or with chemical alterations to promote membrane permeability or solubility, also inhibit or potentiate the same activity (e.g., enzymatic activity) in whole, live *H. pylori* cells.

25

EXEMPLIFICATION

I. Cloning and Sequencing of *H. pylori* DNA

H. pylori chromosomal DNA was isolated according to a basic DNA protocol
30 outlined in Schleif R.F. and Wensink P.C., *Practical Methods in Molecular Biology*, p.98, Springer-Verlag, NY., 1981, with minor modifications. Briefly, cells were pelleted, resuspended in TE (10 mM Tris, 1 mM EDTA, pH 7.6) and GES lysis buffer (5.1 M guanidium thiocyanate, 0.1 M EDTA, pH 8.0, 0.5% N-laurylsarcosine) was added. Suspension was chilled and ammonium acetate (NH₄Ac) was added to final concentration
35 of 2.0 M. DNA was extracted, first with chloroform, then with phenol-chloroform, and reextracted with chloroform. DNA was precipitated with isopropanol, washed twice with 70% EtOH, dried and resuspended in TE.

Following isolation whole genomic *H. pylori* DNA was nebulized (Bodenteich et al., *Automated DNA Sequencing and Analysis* (J.C. Venter, ed.), Academic Press, 1994) to

-90-

a median size of 2000 bp. After nebulization, the DNA was concentrated and separated on a standard 1% agarose gel. Several fractions, corresponding to approximate sizes 900-1300 bp, 1300-1700 bp, 1700-2200 bp, 2200-2700 bp, were excised from the gel and purified by the GeneClean procedure (Bio101, Inc.).

5 The purified DNA fragments were then blunt-ended using T4 DNA polymerase. The healed DNA was then ligated to unique BstXI-linker adapters (5' TCTAGACCACCTGC and 5' GTGGTCTAGA in 100-1000 fold molar excess). These linkers are complimentary to the BstXI-cut pMPX vectors, while the overhang is not self-complimentary. Therefore, the linkers will not concatemerize nor will the cut-vector
10 religate itself easily. The linker-adopted inserts were separated from the unincorporated linkers on a 1% agarose gel and purified using GeneClean. The linker-adopted inserts were then ligated to each of the 20 pMPX vectors to construct a series of "shotgun" subclone libraries. The vectors contain an out-of-frame lacZ gene at the cloning site which becomes in-frame in the event that an adapter-dimer is cloned, allowing these to be avoided by their
15 blue-color.

 All subsequent steps were based on the multiplex DNA sequencing protocols outlined in Church G.M. and Kieffer-Higgins S., *Science* 240:185-188, 1988. Only major modifications to the protocols are highlighted. Briefly, each of the 20 vectors was then transformed into DH5 α competent cells (Gibco/BRL, DH5 α transformation protocol). The
20 libraries were assessed by plating onto antibiotic plates containing ampicillin, methicillin and IPTG/Xgal. The plates were incubated overnight at 37°C. Successful transformants were then used for plating of clones and pooling into the multiplex pools. The clones were picked and pooled into 40 ml growth medium cultures. The cultures were grown overnight at 37°C. DNA was purified using the Qiagen Midi-prep kits and Tip-100 columns
25 (Qiagen, Inc.). In this manner, 100 μ g of DNA was obtained per pool. Fifteen 96-well plates of DNA were generated to obtain a 5-10 fold sequence redundancy assuming 250-300 base average read-lengths.

 These purified DNA samples were then sequenced using the multiplex DNA sequencing based on chemical degradation methods (Church G.M. and Kieffer-Higgins S.,
30 *Science* 240:185-188, 1988) or by Sequithrem (Epicenter Technologies) dideoxy sequencing protocols. The sequencing reactions were electrophoresed and transferred onto nylon membranes by direct transfer electrophoresis from 40 cm gels (Richterich P. and Church G.M., *Methods in Enzymology* 218:187-222, 1993) or by electroblotting (Church, *supra*). 24 samples were run per gel. 45 successful membranes were produced by chemical
35 sequencing and 8 were produced by dideoxy sequencing. The DNA was covalently bound to the membranes by exposure to ultraviolet light, and hybridized with labeled oligonucleotides complimentary to tag sequences on the vectors (Church, *supra*). The membranes were washed to rinse off non-specifically bound probe, and exposed to X-ray film to visualize individual sequence ladders. After autoradiography, the hybridized probe

-91-

was removed by incubation at 65° C, and the hybridization cycle repeated with another tag sequence until the membrane had been probed 38 times for chemical sequencing membranes and 10 times for the dideoxy sequencing membranes. Thus, each gel produced a large number of films, each containing new sequencing information. Whenever a new
5 blot was processed, it was initially probed for an internal standard sequence added to each of the pools.

Digital images of the films were generated using a laser-scanning densitometer (Molecular Dynamics, Sunnyvale, CA). The digitized images were processed on computer workstations (VaxStation 4000's) using the program REPLICA™ (Church et al.,
10 *Automated DNA Sequencing and Analysis* (J.C. Venter, ed.), Academic Press, 1994). Image processing included lane straightening, contrast adjustment to smooth out intensity differences, and resolution enhancement by iterative gaussian deconvolution. The sequences were then automatically picked in REPLICA™ and displayed for interactive proofreading before being stored in a project database. The proofreading was accomplished
15 by a quick visual scan of the film image followed by mouse clicks on the bands of the displayed image to modify the base calls. Many of the sequence errors could be detected and corrected because multiple sequence reads covering the same portion of the genomic DNA provide adequate sequence redundancy for editing. Each sequence automatically received an identification number (corresponding to microtiter plate, probe information,
20 and lane set number). This number serves as a permanent identifier of the sequence so it is always possible to identify the original of any particular sequence without recourse to a specialized database.

Routine assembly of *H. pylori* sequences was done using the program FALCON (Church, Church et al., *Automated DNA Sequencing and Analysis* (J.C. Venter, ed.),
25 Academic Press, 1994). This program has proven to be fast and reliable for most sequences. The assembled contigs were displayed using a modified version of GelAssemble, developed by the Genetics Computer Group (GCG) (Devereux et al., *Nucleic Acid Res.* 12:387-95, 1984) that interacts with REPLICA™. This provided for an integrated editor that allows multiple sequence gel images to be instantaneously called up
30 from the REPLICA™ database and displayed to allow rapid scanning of contigs and proofreading of gel traces where discrepancies occurred between different sequence reads in the assembly.

II. Identification, cloning and expression of recombinant *H. pylori* DNA sequences

35 To facilitate the cloning, expression and purification of membrane and secreted proteins from *H. pylori* a powerful gene expression system, the pET System (Novagen), for cloning and expression of recombinant proteins in *E. coli*, was selected. Also, a DNA sequence encoding a peptide tag, the His-Tag, was fused to the 3' end of DNA sequences of interest in order to facilitate purification of the recombinant protein products. The 3' end

was selected for fusion in order to avoid alteration of any 5' terminal signal sequence. The exception to the above was ppiB, a gene cloned for use as a control in the expression studies. In this study, the sequence for *H. pylori* ppiB contains a DNA sequence encoding a His-Tag fused to the 5' end of the full length gene, because the protein product of this gene
5 does not contain a signal sequence and is expressed as a cytosolic protein.

PCR Amplification and cloning of DNA sequences containing ORF's for membrane and secreted proteins from the J99 Strain of Helicobacter pylori.

Sequences chosen (from the list of the DNA sequences of the invention) for cloning
10 from the J99 strain of *H. pylori* were prepared for amplification cloning by polymerase chain reaction (PCR). Synthetic oligonucleotide primers (Table 4) specific for the 5' and 3' ends of open reading frames (ORFs) were designed and purchased (GibcoBRL Life Technologies, Gaithersburg, MD, USA). All forward primers (specific for the 5' end of the sequence) were designed to include an NcoI cloning site at the extreme 5' terminus, except
15 for HpSeq. 4821082 (SEQ ID NO: 820) where NdeI was used. These primers were designed to permit initiation of protein translation at a methionine residue followed by a valine residue and the coding sequence for the remainder of the native *H. pylori* DNA sequence. An exception is *H. pylori* sequence 4821082 (SEQ ID NO: 820) where the initiator methionine is immediately followed by the remainder of the native *H. pylori* DNA
20 sequence. All reverse primers (specific for the 3' end of any *H. pylori* ORF) included a EcoRI site at the extreme 5' terminus to permit cloning of each *H. pylori* sequence into the reading frame of the pET-28b. The pET-28b vector provides sequence encoding an additional 20 carboxy-terminal amino acids (only 19 amino acids in HpSeq. 26380318 (SEQ ID NO: 658) and HpSeq. 14640637 (SEQ ID NO: 447)) including six histidine
25 residues (at the extreme C-terminus), which comprise the His-Tag. An exception to the above, as noted earlier, is the vector construction for the ppiB gene. A synthetic oligonucleotide primer specific for the 5' end of ppiB gene encoded a BamHI site at its extreme 5' terminus and the primer for the 3' end of the ppiB gene encoded a XhoI site at its extreme 5' terminus.

30

TABLE 4

Oligonucleotide primers used for PCR amplification of *H. pylori* DNA sequences

Outer membrane Proteins	Forward primer 5' to 3'	Reverse Primer 5' to 3'
16225006 (SEQ ID NO: 465)	5'-TATACCATGGTGGG CGCTAA-3' (SEQ ID NO:1897)	5'-ATGAATTCGAGTAAG GATTTTGTG-3' (SEQ ID NO:1898)
26054702 (SEQ ID NO: 649)	5'-TTAACCATGGTGAAA AGCGATA-3' (SEQ ID NO:1899)	5'-TAGAATTCGCATAAC GATCAATC-3' (SEQ ID NO:1900)
7116626 (SEQ ID NO: 865)	5'-ATATCCATGGTGAGT TTGATGA-3' (SEQ ID NO:1901)	5'-ATGAATTCAATTTT TATTTTGCCA-3' (SEQ ID NO:1902)
29479681 (SEQ ID NO: 677)	5'-AATTCCATGGTGGGG GCTATG-3' (SEQ ID NO:1903)	5'-ATGAATTCTCGATAG CCAAAATC-3' (SEQ ID NO:1904)
14640637 (SEQ ID NO: 447)	5'-AATTCCATGGTGCA AACTTCCATT-3' (SEQ ID NO:1905)	5'-AAGAATTCTCTAGCA TCCAAATGGA-3' (SEQ ID NO:1906)
Periplasmic/ Secreted Proteins		
30100332 (SEQ ID NO: 685)	5'-ATTTCATGGTCATG TCTCATATT-3' (SEQ ID NO:1907)	5'-ATGAATTCCATCTTT TATTCCAC-3' (SEQ ID NO:1908)
4721061 (SEQ ID NO: 812)	5'-AACCATGGTGATTT TAAGCATTGAAAG-3' (SEQ ID NO:1909)	5'-AAGAATTCCACTCA AAATTTTTTAACAG-3' (SEQ ID NO:1910)
Other Surface Proteins		
4821082 (SEQ ID NO: 820)	5'-GATCATCCATATGTT ATCTTCTAAT-3' (SEQ ID NO:1911)	5'-TGAATTCAACCATT TAACCCTG-3' (SEQ ID NO:1912)
978477 (SEQ ID NO: 880)	5'-TATACCATGGTGAA ATTTTTCTTTTA-3' (SEQ ID NO:1913)	5'-AGAATTCAATTGCG TCTTGTAAG-3' (SEQ ID NO:1914)
Inner Membrane Protein		
26380318 (SEQ ID NO: 658)	5'-TATACCATGGTGAT GGACAACTC-3' (SEQ ID NO:1915)	5'-ATGAATTCCCACTT GGGCGATA-3' (SEQ ID NO:1916)
Cytoplasmic Protein		
ppi	5'-TTATGGATCCAAAC CAATTAAG-3' (SEQ ID NO:1917)	5'-TATCTCGAGTTATA GAGAAGGGC-3' (SEQ ID NO:1918)

-94-

Genomic DNA prepared from the J99 strain of *H. pylori* (ATCC #55679) was used as the source of template DNA for PCR amplification reactions (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). To amplify a DNA sequence containing an *H. pylori* ORF, genomic DNA (50 nanograms) was introduced into a reaction vial containing 2 mM MgCl₂, 1 micromolar synthetic oligonucleotide primers (forward and reverse primers) complementary to and flanking a defined *H. pylori* ORF, 0.2 mM of each deoxynucleotide triphosphate; dATP, dGTP, dCTP, dTTP and 2.5 units of heat stable DNA polymerase (Amplitaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA) in a final volume of 100 microliters. The following thermal cycling conditions were used to obtain amplified DNA products for each ORF using a Perkin Elmer Cetus/ GeneAmp PCR System 9600 thermal cycler:

Sequences 26054702 (SEQ ID NO: 649), 7116626 (SEQ ID NO: 865), 29479681 (SEQ ID NO: 677), 30100332 (SEQ ID NO: 685), 4821082 (SEQ ID NO: 820) and 978477 (SEQ ID NO: 880);

Denaturation at 94°C for 2 min,

2 cycles at 94°C for 15 sec, 30°C for 15 sec and 72°C for 1.5 min

23 cycles at 94°C for 15 sec, 55°C for 15 sec and 72°C for 1.5 min

Reactions were concluded at 72°C for 6 minutes.

Sequence 16225006 (SEQ ID NO: 465);

Denaturation at 94°C for 2 min,

25 cycles at 95°C for 15 sec, 55°C for 15 sec and 72°C for 1.5 min

Reaction was concluded at 72°C for 6 minutes.

Sequence 4721061 (SEQ ID NO: 812);

Denaturation at 94°C for 2 min.

2 cycles at 94°C for 15 sec, 36°C for 15 sec and 72°C for 1.5 min

23 cycles at 94°C for 15 sec, 60°C for 15 sec and 72°C for 1.5 min

Reactions were concluded at 72°C for 6 minutes.

Sequence 26380318 (SEQ ID NO: 658);

Denaturation at 94°C for 2 min.

2 cycles at 94°C for 15 sec, 38°C for 15 sec and 72°C for 1.5 min

23 cycles at 94°C for 15 sec, 62°C for 15 sec and 72°C for 1.5 min

Reactions were concluded at 72°C for 6 minutes.

-95-

Sequence 14640637 (SEQ ID NO: 447);

Denaturation at 94°C for 2 min,

2 cycles at 94°C for 15 sec, 33°C for 15 sec and 72°C for 1.5 min

30 cycles at 94°C for 15 sec, 55°C for 15 sec and 72°C for 1.5 min

5 Reactions were concluded at 72°C for 6 minutes.

Conditions for amplification of *H. pylori* ppiB;

Denaturation at 94°C for 2 min,

2 cycles at 94°C for 15 sec, 32°C for 15 sec and 72°C for 1.5 min

10 25 cycles at 94°C for 15 sec, 56°C for 15 sec and 72°C for 1.5 min

Reactions were concluded at 72°C for 6 minutes

Upon completion of thermal cycling reactions, each sample of amplified DNA was washed and purified using the Qiaquick Spin PCR purification kit (Qiagen, Gaithersburg, MD, USA). All amplified DNA samples were subjected to digestion with the restriction endonucleases, NcoI and EcoRI (New England BioLabs, Beverly, MA, USA), or in the case of HpSeq. 4821082 (SEQ ID NO: 820), with NdeI and EcoRI (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). DNA samples were then subjected to electrophoresis on 1.0 % NuSeive (FMC BioProducts, Rockland, ME USA) agarose gels. DNA was visualized by exposure to ethidium bromide and long wave uv irradiation. DNA contained in slices isolated from the agarose gel was purified using the Bio 101 GeneClean Kit protocol (Bio 101 Vista, CA, USA)

Cloning of *H. pylori* DNA sequences into the pET-28b prokaryotic expression vector.

The pET-28b vector was prepared for cloning by digestion with NcoI and EcoRI, or in the case of *H. pylori* sequence 4821082 (SEQ ID NO: 820) with NdeI and EcoRI (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). In the case of cloning ppiB, the pET-28a vector, which encodes a His-Tag that can be fused to the 5' end of an inserted gene, was used and the cloning site prepared for cloning with the ppiB gene by digestion with BamHI and XhoI restriction endonucleases.

Following digestion, DNA inserts were cloned (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994) into the previously digested pET-28b expression vector, except for the amplified insert for ppiB, which was cloned into the pET-28a expression vector. Products of the ligation reaction were then used to transform the BL21 strain of *E. coli* (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994) as described below.

Transformation of competent bacteria with recombinant plasmids

Competent bacteria, *E. coli* strain BL21 or *E. coli* strain BL21(DE3), were transformed with recombinant pET expression plasmids carrying the cloned *H. pylori*

sequences according to standard methods (Current Protocols in Molecular, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). Briefly, 1 microliter of ligation reaction was mixed with 50 microliters of electrocompetent cells and subjected to a high voltage pulse, after which, samples were incubated in 0.45 milliliters SOC medium (0.5% yeast extract, 2.0 % tryptone, 10 mM NaCl, 2.5 mM KCl, 10 mM MgCl₂, 10 mM MgSO₄ and 20, mM glucose) at 37°C with shaking for 1 hour. Samples were then spread on LB agar plates containing 25 microgram/ml kanamycin sulfate for growth overnight. Transformed colonies of BL21 were then picked and analyzed to evaluate cloned inserts as described below.

10

Identification of recombinant pET expression plasmids carrying H. pylori sequences

Individual BL21 clones transformed with recombinant pET-28b-H.pylori ORFs were analyzed by PCR amplification of the cloned inserts using the same forward and reverse primers, specific for each *H. pylori* sequence, that were used in the original PCR amplification cloning reactions. Successful amplification verified the integration of the *H. pylori* sequences in the expression vector (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994).

Isolation and Preparation of plasmid DNA from BL21 transformants

Individual clones of recombinant pET-28b vectors carrying properly cloned *H. pylori* ORFs were picked and incubated in 5 mls of LB broth plus 25 microgram/ml kanamycin sulfate overnight. The following day plasmid DNA was isolated and purified using the Qiagen plasmid purification protocol (Qiagen Inc., Chatsworth, CA, USA).

Expression of recombinant H. pylori sequences in E. coli

The pET vector can be propagated in any *E. coli* K-12 strain e.g. HMS174, HB101, JM109, DH5, etc. for the purpose of cloning or plasmid preparation. Hosts for expression include *E. coli* strains containing a chromosomal copy of the gene for T7 RNA polymerase. These hosts are lysogens of bacteriophage DE3, a lambda derivative that carries the lacI gene, the lacUV5 promoter and the gene for T7 RNA polymerase. T7 RNA polymerase is induced by addition of isopropyl-B-D-thiogalactoside (IPTG), and the T7 RNA polymerase transcribes any target plasmid, such as pET-28b, carrying a T7 promoter and a gene of interest. Strains used include: BL21(DE3) (Studier, F.W., Rosenberg, A.H., Dunn, J.J., and Dubendorff, J.W. (1990) Meth. Enzymol. 185, 60-89).

To express recombinant *H. pylori* sequences, 50 nanograms of plasmid DNA isolated as described above was used to transform competent BL21(DE3) bacteria as described above (provided by Novagen as part of the pET expression system kit). The lacZ gene (beta-galactosidase) was expressed in the pET-System as described for the *H. pylori* recombinant constructions. Transformed cells were cultured in SOC medium for 1 hour,

-97-

and the culture was then plated on LB plates containing 25 micrograms/ml kanamycin sulfate. The following day, bacterial colonies were pooled and grown in LB medium containing kanamycin sulfate (25 micrograms/ml) to an optical density at 600 nm of 0.5 to 1.0 O.D. units, at which point, 1 millimolar IPTG was added to the culture for 3 hours to induce gene expression of the *H. pylori* recombinant DNA constructions .

After induction of gene expression with IPTG, bacteria were pelleted by centrifugation in a Sorvall RC-3B centrifuge at 3500 x g for 15 minutes at 4°C. Pellets were resuspended in 50 milliliters of cold 10 mM Tris-HCl, pH 8.0, 0.1 M NaCl and 0.1 mM EDTA (STE buffer). Cells were then centrifuged at 2000 x g for 20 min at 4°C. Wet pellets were weighed and frozen at -80°C until ready for protein purification.

III. Purification of recombinant proteins from *E. coli*

Analytical Methods

The concentrations of purified protein preparations were quantified spectrophotometrically using absorbance coefficients calculated from amino acid content (Perkins, S.J. 1986 Eur. J. Biochem. 157, 169-180). Protein concentrations were also measured by the method of Bradford, M.M. (1976) Anal. Biochem. 72, 248-254, and Lowry, O.H., Rosebrough, N., Farr, A.L. & Randall, R.J. (1951) J. Biol. Chem. 193, pages 265-275, using bovine serum albumin as a standard.

SDS-polyacrylamide gels (12% or 4.0 to 25 % acrylamide gradient gels) were purchased from BioRad (Hercules, CA, USA), and stained with Coomassie blue. Molecular weight markers included rabbit skeletal muscle myosin (200 kDa), *E. coli* (-galactosidase (116 kDa), rabbit muscle phosphorylase B (97.4 kDa), bovine serum albumin (66.2 kDa), ovalbumin (45 kDa), bovine carbonic anhydrase (31 kDa), soybean trypsin inhibitor (21.5 kDa), egg white lysozyme (14.4 kDa) and bovine aprotinin (6.5 kDa).

1. Purification of soluble proteins

All steps were carried out at 4°C. Frozen cells were thawed, resuspended in 5 volumes of lysis buffer (20 mM Tris, pH 7.9, 0.5 M NaCl, 5 mM imidazole with 10% glycerol, 0.1 % 2-mercaptoethanol, 200 µg/ml lysozyme, 1 mM phenylmethylsulfonyl fluoride (PMSF), and 10 µg/ml each of leupeptin, aprotinin, pepstatin, L-1-chloro-3-[4-tosylamido]-7-amino-2-heptanone (TLCK), L-1-chloro-3-[4-tosylamido]-4-phenyl-2-butanone (TPCK), and soybean trypsin inhibitor, and ruptured by several passages through a small volume microfluidizer (Model M-110S, Microfluidics International Corporation, Newton, MA). The resultant homogenate was made 0.1 % Brij 35, and centrifuged at 100,000 x g for 1 hour to yield a clear supernatant (crude extract).

Following filtration through a 0.8 µm Supor filter (Gelman Sciences, FRG) the crude extract was loaded directly onto a Ni²⁺-nitrilotriacetate-agarose (NTA) with a 5 milliliter bed volume (Hochuli, E., Dbeli, H., and Schacheer, A. (1987) J. Chromatography

411, 177-184) pre-equilibrated in lysis buffer containing 10 % glycerol, 0.1 % Brij 35 and 1 mM PMSF. The column was washed with 250 ml (50 bed volumes) of lysis buffer containing 10 % glycerol, 0.1 % Brij 35, and was eluted with sequential steps of lysis buffer containing 10 % glycerol, 0.05 % Brij 35, 1 mM PMSF, and 20, 100, 200, and 500 mM imidazole in succession. Fractions were monitored by absorbance at OD₂₈₀ nm, and peak fractions were analyzed by SDS-PAGE. Fractions containing the recombinant protein eluted at 100 mM imidazole.

Recombinant protein 14640637 (SEQ ID NO: 447) and proteins, beta-galactosidase (lacZ) and peptidyl-prolyl cis-trans isomerase (ppiB)

Fractions containing the recombinant proteins from the Ni²⁺-NTA-agarose columns were pooled and then concentrated to approximately 5 ml by centrifugal filtration (Centriprep-10, Amicon, MA), and loaded directly onto a 180-ml column (1.6 X 91 cm) of Sephacryl S-100 HR gel filtration medium equilibrated in Buffer A (10 mM Hepes, pH 7.5, 150 mM NaCl, 0.1 mM EGTA) and run in Buffer A at 18 ml/h. Fractions containing the recombinant protein were identified by absorbance at 280 nm and analyzed by SDS-PAGE. Fractions were pooled and concentrated by centrifugal filtration.

Recombinant protein 7116626 (SEQ ID NO: 865)

Fractions containing the recombinant protein from the Ni²⁺-NTA-agarose column were pooled and dialyzed overnight against 1 liter of dialysis buffer (10 mM MOPS, pH 6.5, 50 mM NaCl, 0.1 mM EGTA, 0.02% Brij 35 and 1 mM PMSF). In the morning, a fine white precipitate was removed by centrifugation and the resulting supernatant was loaded onto an 8 ml (8 x 75 mm) MonoS high performance liquid chromatography column (Pharmacia Biotechnology, Inc., Piscataway, NJ, USA) equilibrated in buffer B (10 mM MOPS, pH 6.5, 0.1 mM EGTA) containing 50 mM NaCl. The column was washed with 10 bed volumes of buffer B containing 50 mM NaCl, and developed with a 50-ml linear gradient of increasing NaCl (50 to 500 mM). Recombinant protein 7116626 (SEQ ID NO: 865) eluted as a sharp peak at 300 mM NaCl.

2. Purification of insoluble proteins from inclusion bodies

The following steps were carried out at 4°C. Cell pellets were resuspended in lysis buffer with 10% glycerol 200 µg/ml lysozyme, 5 mM EDTA, 1mM PMSF and 0.1 % -mercaptoethanol. After passage through the cell disrupter, the resulting homogenate was made 0.2 % deoxycholate, stirred 10 minutes, then centrifuged at 20,000 x g, for 30 min. The pellets were washed with lysis buffer containing 10 % glycerol, 10 mM EDTA, 1% Triton X-100, 1 mM PMSF and 0.1% -mercaptoethanol, followed by several washes with lysis buffer containing 1 M urea, 1 mM PMSF and 0.1 % 2-mercaptoethanol. The resulting

white pellet was composed primarily of inclusion bodies, free of unbroken cells and membranous materials..

5 *Recombinant proteins 26054702 (SEQ ID NO: 649), 16225006 (SEQ ID NO: 465),
30100332 (SEQ ID NO: 685), 4721061 (SEQ ID NO: 812)*

10 The following steps were carried out at room temperature. Purified inclusion bodies were dissolved in 20 ml 8.0 M urea in lysis buffer with 1 mM PMSF and 0.1 % 2-mercaptoethanol, and incubated at room temperature for 1 hour. Materials that did not dissolve were removed by centrifugation. The clear supernatant was filtered, then loaded
15 onto a Ni^{2+} -NTA agarose column pre-equilibrated in 8.0 M urea in Lysis Buffer. The column was washed with 250 ml (50 bed volumes) of lysis buffer containing 8 M urea, 1.0 mM PMSF and 0.1 % 2-mercaptoethanol, and developed with sequential steps of lysis buffer containing 8M urea, 1 mM PMSF, 0.1 % 2-mercaptoethanol and 20, 100, 200, and 500 mM imidazole in succession. Fractions were monitored by absorbance at OD₂₈₀ nm,
and peak fractions were analyzed by SDS-PAGE. Fractions containing the recombinant protein eluted at 100 mM imidazole.

20 *Recombinant proteins 29479681 (SEQ ID NO: 677), 978477 (SEQ ID NO: 880), 26380318 (SEQ ID NO: 658)*

20 The pellet containing the inclusion bodies was solubilized in buffer B containing 8 M urea, 1 mM PMSF and 0.1 % 2-mercaptoethanol, and incubated for 1 hour at room temperature. Insoluble materials were removed by centrifugation at 20,000 x g for 30 min, and the cleared supernatant was loaded onto a 15 ml (1.6 x 7.5 cm) SP-Sepharose column pre-equilibrated in buffer B, 6 M urea, 1 mM PMSF, 0.1 % 2-mercaptoethanol. After
25 washing the column with 10 bed volumes, the column was developed with a linear gradient from 0 to 500 mM NaCl.

Dialysis and concentration of protein samples

30 Urea was removed slowly from the protein samples by dialysis against Tris-buffered saline (TBS; 10 mM Tris pH 8.0, 150 mM NaCl) containing 0.5 % deoxycholate (DOC) with sequential reduction in urea concentration as follows; 6M, 4M, 3M, 2M, 1M, 0.5 M and finally TBS without any urea. Each dialysis step was conducted for a minimum of 4 hours at room temperature.

35 After dialysis, samples were concentrated by pressure filtration using Amicon stirred-cells. Protein concentrations were measured using the methods of Perkins (1986 Eur. J. Biochem. 157, 169-180), Bradford ((1976) Anal. Biochem. 72, 248-254) and Lowry ((1951) J. Biol. Chem. 193, pages 265-275).

The recombinant proteins purified by the methods described above are summarized in Table 5 below.

TABLE 5

J99 Sequence Identifier	Homolog Identified by Blast	Gene symbol of Homolog	Bacterial cell fraction used to purify recombinant proteins	Method of purification	Relative MW on SDS-PAGE gel	Final concentration of purified protein	Composition of buffer
Outer Membrane Proteins							
16225006 (SEQ ID NO: 465)	P28635	YEAC	Inclusion bodies	His-Tag	18 kDa	5 mg/ml	B
26054702 (SEQ ID NO: 649)	P15929	flgH	Inclusion bodies	His-Tag	37 kDa	1.18 mg/ml	B
						----	as dry pellet
7116626 (SEQ ID NO: 865)	P26093	e(P4)	Soluble fraction	His-Tag	29 kDa	0.8 mg/ml	A
						1.85 mg/ml	C
29479681 (SEQ ID NO: 677)	P13036	fecA	Inclusions bodies	SP-Sepharose	23 kDa	2.36 mg/ml	B
						0.5 mg/ml	B
14640637 (SEQ ID NO: 447)	P16665	TPF1	Soluble fraction	His-Tag	17 kDa	2.4 mg/ml	as dry pellet A
				gel filtration S100 HR			

TABLE 5 (continued)

Periplasmic/Secreted Protein			Inclusion bodies	His-Tag		2.88 mg/ml	B
3010032 (SEQ ID NO: 685)	P23847	dppA					
4721061 (SEQ ID NO: 812)	P36175	GCP	Inclusion bodies	His-Tag	38 kDa	2.8 mg/ml	B
Other Surface Proteins							
4821082 (SEQ ID NO: 820)	P08089	M protein	Inclusion bodies	His-Tag	20 kDa	1.16 mg/ml	B
978477 (SEQ ID NO: 880)	L28919	FBP54	Inclusion bodies	SP-Sepharose	44 kDa	2.56 mg/ml	B
Inner Membrane Proteins							
26380318 (SEQ ID NO: 658)	P15933	flgG	Inclusion bodies	SP-Sepharose	11 kDa	22 mg/ml	B
Control Proteins with His-Tag							
	P00722	lacZ	Soluble fraction	His-Tag gel filtration S200 HR	116 kDa	10 mg/ml	A
		ppiB	Soluble fraction	His-Tag gel filtration S100 HR	21 kDa	4.4 mg/ml	A
Buffer compositions:							
A= 10 mM Hepes pH 7.5, 150 mM NaCl, 0.1 mM EGTA							
B= 10 mM Tris pH 8.0, 150 mM NaCl, 0.5 % DOC							
C= 10 mM MOPS pH 6.5, 300 mM NaCl, 0.1 EGTA							

-102-

IV. Analysis of *H. pylori* proteins as Vaccine candidates

To investigate the immunomodulatory effect of *H. pylori* proteins, a mouse/*H. pylori* model was used. This model mimics the human *H. pylori* infection in many respects. The focus is on the effect of oral immunization in *H. pylori* infected animals in order to test the concept of therapeutic oral immunotherapy.

Animals

Female SPF BALB/c mice were purchased from Bomholt Breeding center (Denmark). They were kept in ordinary makrolon cages with free supply of water and food. The animals were 4-6 weeks old at arrival.

Infection

After a minimum of one week of acclimatization, the animals were infected with a type 2 strain (VacA negative) of *H. pylori* (strain 244, originally isolated from an ulcer patient). In our hands, this strain has earlier proven to be a good colonizer of the mouse stomach. The bacteria were grown overnight in Brucella broth supplemented with 10 % fetal calf serum, at 37°C in a microaerophilic atmosphere (10% CO₂, 5% O₂). The animals were given an oral dose of omeprazole (400 µmol/kg) and 3-5 h after this an oral inoculation of *H. pylori* in broth (approximately 10⁸ cfu/animal). Positive take of the infection was checked in some animals 2-3 weeks after the inoculation.

Antigens

Recombinant *H. pylori* antigens were chosen based on their association with externally exposed *H. pylori* cell membrane. These antigens were selected from the following groups: (1.) Outer Membrane Proteins; (2.) Periplastic/Secreted proteins; (3.) Outer Surface proteins; and (4.) Inner Membrane proteins. All recombinant proteins were constructed with a hexa-HIS tag for purification reasons and the non-*Helicobacter pylori* control protein (β-galactosidase from *E. coli*; LacZ), was constructed in the same way.

All antigens were given in a soluble form, i.e. dissolved in either a HEPES buffer or in a buffer containing 0.5% Deoxycholate (DOC).

The antigens are listed in Table 6 below.

Table 6

Helicobacter pylori proteins

35

Outer membrane Proteins

SEQ ID NO:447

SEQ ID NO:677

SEQ ID NO:865

40

SEQ ID NO:812

SEQ ID NO:465

Periplastic/Secreted proteins

SEQ ID NO:685

5 **Other cell envelope proteins**

SEQ ID NO:820

SEQ ID NO:880

Flagella-associated proteins

10 SEQ ID NO:658

Control proteins β -galactosidase (LacZ)15 **Immunizations**

Ten animals in each group were immunized 4 times over a 34 day period (day 1, 15, 25 and 35). Purified antigens in solution or suspension were given at a dose of 100 μ g/mouse. As an adjuvant, the animals were also given 10 μ g/mouse of Cholera toxin (CT) with each immunization. Omeprazole (400 μ mol/kg) was given orally to the animals 3-5 h prior to immunization as a way of protecting the antigens from acid degradation. Infected control animals received HEPES buffer + CT or DOC buffer + CT. Animals were sacrificed 2-4 weeks after final immunization. A general outline of the study is shown in Table 7 below.

25 **Table 7****Study outline, therapeutic immunization:**

Mice were all infected with *H. pylori* strain Ah244 at day 30. Proteins are listed by their SeqID #'s.

30	<u>Substance</u>	<u>Mouse strain</u> n=10	<u>Dose/mouse</u>	<u>Dates for dosing</u>
	1. Controls, PBS	Balb/c	0,3 ml	0, 14, 24, 34
	2. Cholera toxin, 10 μ g	Balb/c	0,3 ml	0, 14, 24, 34
35	3. Protein 447, 100 μ g + CT 10 μ g	Balb/c	0,3 ml	0, 14, 24, 34
	4. Protein 465, 100 μ g + CT 10 μ g	Balb/c	0,3 ml	0, 14, 24, 34
	5. Protein 649, 100 μ g + CT 10 μ g	Balb/c	0,3 ml	0, 14, 24, 34
	6. Protein 658, 100 μ g + CT 10 μ g	Balb/c	0,3 ml	0, 14, 24, 34
	7. Protein 677, 100 μ g + CT 10 μ g	Balb/c	0,3 ml	0, 14, 24, 34
40	8. Protein 685, 100 μ g + CT 10 μ g	Balb/c	0,3 ml	0, 14, 24, 34
	9. Protein 812, 100 μ g + CT 10 μ g	Balb/c	0,3 ml	0, 14, 24, 34
	10. Protein 820, 100 μ g + CT 10 μ g	Balb/c	0,3 ml	0, 14, 24, 34
	11. Protein 880, 100 μ g + CT 10 μ g	Balb/c	0,3 ml	0, 14, 24, 34
	12. Protein 865, 100 μ g + CT 10 μ g	Balb/c	0,3 ml	0, 14, 24, 34

Analysis of infection

Mucosal infection: The mice were sacrificed by CO₂ and cervical dislocation. The abdomen was opened and the stomach removed. After cutting the stomach along the greater curvature, it was rinsed in saline. The mucosa from the antrum and corpus of an area of 25mm² was scraped separately with a surgical scalpel. The mucosa scraping was suspended in Brucella broth and plated onto Blood Skirrow selective plates. The plates were incubated under microaerophilic conditions for 3-5 days and the number of colonies was counted. The identity of *H. pylori* was ascertained by urease and catalase test and by direct microscopy or Gram staining.

The urease test was performed essentially as follows. The reagent, Urea Agar Base Concentrate, was purchased from DIFCO Laboratories, Detroit, MI (Catalog # 0284-61-3). Urea agar base concentrate was diluted 1:10 with water. 1 ml of if the diluted concentrate was mixed with 100-200 µl of actively growing *H. pylori* cells. Color change to magenta indicated that cells were urease positive.

The catalase test was performed essentially as follows. The reagent, N,N,N',N'-Tetramethyl-p-Phenylenediamine, was purchased from Sigma, St. Louis, MO (Catalog # T3134). A solution of the reagent (1% w/v in water) was prepared. *H. pylori* cells were swabbed onto Whatman filter paper and overlaid with the 1% solution. Color change to dark blue indicated that the cells were catalase positive.

Serum antibodies: From all mice serum was prepared from blood drawn by heart puncture. Serum antibodies were identified by regular ELISA techniques, where the specific antigens of *Helicobacter pylori* were plated.

Mucosal antibodies: Gentle scrapings of a defined part of the corpus and of 4 cm of duodenum were performed in 50% of the mice in order to detect the presence of antibodies in the mucous. The antibody titers were determined by regular ELISA technique as for serum antibodies.

Statistical analysis: Wilcoxon-Mann-Whitney sign rank test was used for determination of significant effects of the antigens on *Helicobacter pylori* colonization. P<0.05 was considered significant. Because the antrum is the major colonization site for *Helicobacter* most emphasis was put upon changes in the antral colonization.

Results

Antibodies in sera: All antigens tested given together with CT gave rise to a measurable specific titer in serum. The highest responses were seen with SEQ ID NOs:865, 812, 658, 447, and 820 (see Figure 1).

Antibodies in mucus: In the mucus scrapings, specific antibodies against all antigens tested were seen. By far the strongest response was seen with SEQ ID NOs:685, followed by 447, 865, and 658 (see Figure 2).

Therapeutic immunization effects:

All control animals (BALB/c mice) were well colonized with *H. pylori* (strain AH244) in both antrum and corpus of the stomach. Of the antigens tested 3 proteins (SEQ ID NOs: 812, 820, and 447) gave a good and significant reduction and/or eradication of the *H. pylori* infection. The degree of colonization of the antrum was lower following immunization with SEQ ID NOs: 880, 658, and 865 compared to control. The effect of SEQ ID NOs: 465, 677, and 685 did not differ from control. The control protein lacZ, i.e. the non-*H. pylori* protein, had no eradication effect and in fact had higher *Helicobacter* colonization compared to the HEPES + CT control. All data are shown in Figures 3 and 4 for proteins dissolved in HEPES and DOC respectively. Data is shown as geometric mean values. n=8-10 Wilcoxon-Mann-Whitney sign rank test * = p<0.05; x/10 = number of mice showing eradication of *H. pylori* over the total number of mice examined.

The data presented indicate that all of the *H. pylori* associated proteins included in this study, when used as oral immunogens in conjunction with the oral adjuvant CT, resulted in stimulation of an immune response as measured by specific serum and mucosal antibodies. A majority of the proteins led to a reduction, and in some cases complete clearance of the colonization of *H. pylori* in this animal model. It should be noted that the reduction or clearance was due to heterologous protection rather than homologous protection (the polypeptides were based on the *H. pylori* J99 strain sequence and used in the therapeutic immunization studies against a different (AH244) challenge strain), indicating the vaccine potential against a wide variety of *H. pylori* strains.

The highest colonization in the antrum was seen in animals treated with the non-*Helicobacter* protein LacZ, indicating that the effects seen with the *Helicobacter pylori* antigens were specific.

Taken together these data strongly support the use of these *H. pylori* proteins in a pharmaceutical formulation for the use in humans to treat and/or prevent *H. pylori* infections.

V. Sequence Variance Analysis of genes in *Helicobacter pylori* strains

Four genes were cloned and sequenced from several strains of *H. pylori* to compare the DNA and deduced amino acid sequences. This information was used to determine the sequence variation between the *H. pylori* strain, J99, and other *H. pylori* strains isolated from human patients.

Preparation of Chromosomal DNA.

Cultures of *H. pylori* strains (as listed in Table 10) were grown in BLBB (1% Tryptone, 1% Peptamin 0.1% Glucose, 0.2% Yeast Extract 0.5% Sodium Chloride, 5% Fetal Bovine Serum) to an OD₆₀₀ of 0.2. Cells were centrifuged in a Sorvall RC-3B at 3500 x g at 4°C for 15 minutes and the pellet resuspended in 0.95 mls of 10 mM Tris-HCl,

-106-

0.1 mM EDTA (TE). Lysozyme was added to a final concentration of 1mg/ml along with, SDS to 1% and RNase A + T1 to 0.5mg/ml and 5 units/ml respectively, and incubated at 37°C for one hour. Proteinase K was then added to a final concentration of 0.4mg/ml and the sample was incubated at 55 C for more than one hour. NaCl was added to the sample to a concentration of 0.65 M, mixed carefully, and 0.15 ml of 10% CTAB in 0.7M NaCl (final is 1% CTAB/70mM NaCl) was added followed by incubation at 65°C for 20 minutes. At this point, the samples were extracted with chloroform:isoamyl alcohol, extracted with phenol, and extracted again with chloroform:isoamyl alcohol. DNA was precipitated with either EtOH (1.5 x volumes) or isopropanol (0.6 x volumes) at -70°C for 10 minutes, washed in 70% EtOH and resuspended in TE.

PCR Amplification and cloning.

Genomic DNA prepared from twelve strains of *Helicobacter pylori* was used as the source of template DNA for PCR amplification reactions (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). To amplify a DNA sequence containing an *H. pylori* ORF, genomic DNA (10 nanograms) was introduced into a reaction vial containing 2 mM MgCl₂, 1 micromolar synthetic oligonucleotide primers (forward and reverse primers, see Table 8) complementary to and flanking a defined *H. pylori* ORF, 0.2 mM of each deoxynucleotide triphosphate; dATP, dGTP, dCTP, dTTP and 0.5 units of heat stable DNA polymerase (Amplitaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA) in a final volume of 20 microliters in duplicate reactions.

Table 8

Oligonucleotide primers used for PCR amplification of *H. pylori* DNA sequences.

Outer membrane Proteins	Forward primer 5' to 3'	Reverse Primer 5' to 3'
SEQ ID NO:649 (for strains AH4, AH15, AH61, 5294, 5640, AH18, and AH244)	5'-TTAACCATGGTGAAAAGC GATA-3' (SEQ ID NO:1919)	5'-TAGAATTCGCCTCTAAACT TTAG-3' (SEQ ID NO:1920)
SEQ ID NO:649 (for strains AH5, 5155, 7958, AH24, and J99)	5'-TTAACCATGGTGAAAAGC GATA-3' (SEQ ID NO:1921)	5'-TAGAATTCGCATAACGATCA ATC-3' (SEQ ID NO:1922)
SEQ ID NO:865	5'-ATATCCATGGTGAGTTTGA TGA-3' (SEQ ID NO:1923)	5'-ATGAATTCAATTTTTATTTT GCCA-3' (SEQ ID NO:1924)
SEQ ID NO:677	5'-AATTCCATGGCTATCCAAA TCCG-3' (SEQ ID NO:1925)	5'-ATGAATTCGCCAAAATCGTA GTATT-3' (SEQ ID NO:1926)
SEQ ID NO:764	5'-GATACCATGGAATTTATGA AAAAG-3' (SEQ ID NO:1927)	5'-TGAATTCGAAAAAGTGAGT TATAC-3' (SEQ ID NO:1928)

-107-

The following thermal cycling conditions were used to obtain amplified DNA products for each ORF using a Perkin Elmer Cetus/ GeneAmp PCR System 9600 thermal cycler:

- 5 Sequences (by SEQ ID NO:) 865 and 764;
Denaturation at 94°C for 2 min,
2 cycles at 94°C for 15 sec, 30°C for 15 sec and 72°C for 1.5 min
23 cycles at 94°C for 15 sec, 55°C for 15 sec and 72°C for 1.5 min
Reactions were concluded at 72°C for 6 minutes.
- 10 Sequence (by SEQ ID NO:) 649 for strains AH5, 5155, 7958, AH24, and J99;
Denaturation at 94°C for 2 min,
2 cycles at 94°C for 15 sec, 30°C for 15 sec and 72°C for 1.5 min
25 cycles at 94°C for 15 sec, 55°C for 15 sec and 72°C for 1.5 min
- 15 Reaction was concluded at 72°C for 6 minutes.
- Sequences (by SEQ ID NO:) 677 and 649 for strains AH4, AH15, AH61, 5294, 5640, AH18, and Hp244 ;
Denaturation at 94°C for 2 min,
20 2 cycles at 94°C for 15 sec, 30°C for 20 sec and 72°C for 2 min
25 cycles at 94°C for 15 sec, 55°C for 20 sec and 72°C for 2 min
Reactions were concluded at 72°C for 8 minutes.
- 25 Upon completion of thermal cycling reactions, each pair of samples were combined and used directly for cloning into the pCR cloning vector as described below.

Cloning of H. pylori DNA sequences into the pCR TA cloning vector.

- All amplified inserts were cloned into the pCR 2.1 (pCRII in the case of *H. pylori* sequence 865) vector by the method described in the Original TA cloning kit (Invitrogen, San Diego, CA). Products of the ligation reaction were then used to transform the TOP10F' (INVaF' in the case of *H. pylori* sequence 865) strain of *E. coli* as described below.
- 30

Transformation of competent bacteria with recombinant plasmids

- 35 Competent bacteria. *E. coli* strain TOP10F' or *E. coli* strain INVaF' were transformed with recombinant pCR expression plasmids carrying the cloned *H. pylori* sequences according to standard methods (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). Briefly, 2 microliters of 0.5 micromolar BME was added to each vial of 50 microliters of competent cells.

-108-

Subsequently, 2 microliters of ligation reaction was mixed with the competent cells and incubated on ice for 30 minutes. The cells and ligation mixture were then subjected to a "heat shock" at 42°C for 30 seconds, and were subsequently placed on ice for an additional 2 minutes, after which, samples were incubated in 0.45 milliliters SOC medium (0.5% yeast extract, 2.0 % tryptone, 10 mM NaCl, 2.5 mM KCl, 10 mM MgCl₂, 10 mM MgSO₄ and 20, mM glucose) at 37°C with shaking for 1 hour. Samples were then spread on LB agar plates containing 25 microgram/ml kanamycin sulfate or 100 micrograms/ml ampicillin for growth overnight. Transformed colonies of TOP10F' or INVaF' were then picked and analyzed to evaluate cloned inserts as described below.

10 *Identification of recombinant PCR plasmids carrying H. pylori sequences*

Individual TOP10F' or INVaF' clones transformed with recombinant pCR-*H. pylori* ORFs were analyzed by PCR amplification of the cloned inserts using the same forward and reverse primers, specific for each *H. pylori* sequence, that were used in the original PCR amplification cloning reactions. Successful amplification verified the integration of the *H. pylori* sequences in the cloning vector (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994).

Individual clones of recombinant pCR vectors carrying properly cloned *H. pylori* ORFs were picked for sequence analysis. Sequence analysis was performed on ABI Sequencers using standard protocols (Perkin Elmer) using vector-specific primers (as found in PCR2.1, Invitrogen, San Diego, CA) and sequencing primers specific to the ORF as listed in Table 9 below.

Table 9

Oligonucleotide primers used for sequencing of *H. pylori* DNA sequences.

Outer membrane Proteins	Forward primers 5' to 3'	Reverse Primers 5' to 3'
SEQ ID NO:649	5'-CCCTTCATTTTAGAAATCG-3' (SEQ ID NO:1929) 5'-ATTTCAACCAATTCAATGCG-3' (SEQ ID NO:1930) 5'-GCCCCTTTTGATTTGAAGCT-3' (SEQ ID NO:1931) 5'-TCGCTCCAAGATACCAAGAAGT-3' (SEQ ID NO:1932) 5'-CTTGAATTAGGGGCAAAGATCG-3' (SEQ ID NO:1933) 5'-ATGCGTTTTTACCCAAAGAAGT-3' (SEQ ID NO:1934) 5'-ATAACGCCACTTCCTTATTGGT-3' (SEQ ID NO:1935)	5'-CTTTGGGTAAAAACGCATC-3' (SEQ ID NO:1936) 5'-CGATCTTTGATCCTAATTCA-3' (SEQ ID NO:1937) 5'-ATCAAGTTGCCTATGCTGA-3' (SEQ ID NO:1938)
SEQ ID NO:865	5'-TTGAACACTTTTGATTATGCGG-3' (SEQ ID NO:1939) 5'-GGATTATGCGATTGTTTTACAAG-3' (SEQ ID NO:1940)	5'-GTCTTTAGCAAAAATGGCGTC-3' (SEQ ID NO:1941) 5'-AATGAGCGTAAGAGAGCC TTC-3' (SEQ ID NO:1942)
SEQ ID NO:677	5'-CTTATGGGGGTATTGTCA-3' (SEQ ID NO:1943) 5'-AGCATGTGGGTATCCAGC-3' (SEQ ID NO:1944)	5'-AGGTTGTTGCCTAAAGACT-3' (SEQ ID NO:1945) 5'-CTGCCTCCACCTTTGATC-3' (SEQ ID NO:1946)
SEQ ID NO:764	5'-ACCAATATCAATTGGCACT-3' (SEQ ID NO:1947) 5'-ACTTGGAAGAGCTCTGCA-3' (SEQ ID NO:1948)	5'-CTTGCTTGTCATATCTAGC-3' (SEQ ID NO:1949) 5'-GTTGAAGTGTTGGTGCTA-3' (SEQ ID NO:1950)
	5'-CAAGCAAGTGGTTTGGTTTAG-3' (SEQ ID NO:1951) 5'-TGGAAAGAGCAAATCATTGAAG-3' (SEQ ID NO:1952)	5'-GCCCATAATCAAAAAGCCCAT-3' (SEQ ID NO:1953) 5'-CTAAAACCAACCACCTTGCTT-3' (SEQ ID NO:1954)
Vector Primers	5'-GTAAAACGACGGCCAG-3' (SEQ ID NO:1955)	5'-CAGGAAACAGCTATGAC-3' (SEQ ID NO:1956)

5 Results

To establish the PCR error rate in these experiments, five individual clones of SEQ ID NO:649, prepared from five separate PCR reaction mixtures from *H. pylori* strain J99, were sequenced over a total length of 897 nucleotides for a cumulative total of 4485 bases of DNA sequence. DNA sequence for the five clones was compared to the DNA sequence of SEQ ID NO:649 obtained previously by a different method, i.e., random shotgun cloning and sequencing. The PCR error rate for the experiments described herein was determined to be 2 base changes out of 4485 bases, which is equivalent to an estimated error rate of less than or equal to 0.04%.

-110-

DNA sequence analysis was performed on four different open reading frames identified as genes and amplified by PCR methods from a dozen different strains of the bacterium *Helicobacter pylori*. The deduced amino acid sequences of three of the four open reading frames that were selected for this study showed statistically significant
5 BLAST homology to defined proteins present in other bacterial species. Those ORFs included: SEQ ID NO:649, homologous to the val A & B genes encoding an ABC transporter in *F. novicida*; SEQ ID NO:865, homologous to lipoprotein e (P4) present in the outer membrane of *H. influenzae*; SEQ ID NO:677, homologous to fecA, an outer membrane receptor in iron (III) dicitrate transport in *E. coli*. SEQ ID NO:764 was
10 identified as an unknown open reading frame, because it showed low homology with sequences in the public databases.

To assess the extent of conservation or variance in the ORFs across various strains of *H. pylori*, changes in DNA sequence and the deduced protein sequence were compared to the DNA and deduced protein sequences found in the J99 strain of *H. pylori* (see Table
15 10 below). Results are presented as percent identity to the J99 strain of *H. pylori* sequenced by random shotgun cloning. To control for any variations in the J99 sequence each of the four open reading frames were cloned and sequenced again from the J99 bacterial strain and that sequence information was compared to the sequence information that had been
20 collected from inserts cloned by random shotgun sequencing of the J99 strain. The data demonstrate that there is variation in the DNA sequence ranging from as little as 0.12 % difference (SEQ ID NO:764, J99 strain) to approximately 7% change (SEQ ID NO:649, strain AH5). The deduced protein sequences show either no variation (SEQ ID NO:764, strains AH18 and AH24) or up to as much as 7.66% amino acid changes (SEQ ID NO:649, Strain AH5).

25

-111-

Table 10Multiple Strain DNA Sequence analysis of *H. pylori* Vaccine Candidates

<u>J99 Seq. ID #:</u>	649	649	865	865	677	677	764	764
Length of	248 a.a.	746 nt.	232 a.a.	696 nt.	182 a.a.	548 nt.	273 a.a.	819 nt.
Region								
Sequenced:								

Strain
Tested

	AA identity	Nuc. identity	AA identity	Nuc. identity	AA identity	Nuc. identity	AA identity	Nuc. identity
J99	100.00%	100.00%	100.00%	100.00%	100.00%	100.00%	99.63%	99.88%
AH244	95.16%	95.04%	n.d.	n.d.	99.09%	96.71%	98.90%	96.45%
AH4	95.97%	95.98%	97.84%	95.83%	n.d.	n.d.	97.80%	95.73%
AH5	92.34%	93.03%	98.28%	96.12%	98.91%	96.90%	98.53%	95.73%
AH15	95.16%	94.91%	97.41%	95.98%	99.82%	97.99%	99.63%	96.09%
AH61	n.d.	n.d.	97.84%	95.98%	99.27%	97.44%	n.d.	n.d.
5155	n.d.	n.d.	n.d.	n.d.	99.45%	97.08%	98.53%	95.60%
5294	94.35%	94.37%	98.28%	95.40%	99.64%	97.26%	97.07%	95.48%
7958	94.35%	94.10%	97.84%	95.40%	n.d.	n.d.	99.63%	96.46%
5640	95.16%	94.37%	97.41%	95.69%	99.09%	97.63%	98.53%	95.48%
AH18	n.d.	n.d.	98.71%	95.69%	99.64%	97.44%	100.00%	95.97%
AH24	94.75%	95.04%	97.84%	95.40%	99.27%	96.71%	100.00%	96.46%

n.d. = not done

5 VI. Experimental Knock-Out Protocol for the Determination of Essential *H. pylori* Genes as Potential Therapeutic Targets

Therapeutic targets are chosen from genes whose protein products appear to play key roles in essential cell pathways such as cell envelope synthesis, DNA synthesis, transcription, translation, regulation and colonization/virulence.

- 10 The protocol for the deletion of portions of *H. pylori* genes/ORFs and the insertional mutagenesis of a kanamycin-resistance cassette in order to identify genes which are essential to the cell is modified from previously published methods (Labigne-Roussel et al., 1988, J. Bacteriology 170, pp. 1704-1708; Cover et al., 1994, J. Biological Chemistry 269, pp. 10566-10573; Reyrat et al., 1995, Proc. Natl. Acad. Sci. 92, pp 8768-8772). The
- 15 result is a gene "knock-out."

Identification and Cloning of *H. pylori* Gene Sequences

- The sequences of the genes or ORFs (open reading frames) selected as knock-out targets are identified from the *H. pylori* genomic sequence and used to design primers to
- 20 specifically amplify the genes/ORFs. All synthetic oligonucleotide primers are designed with the aid of the OLIGO program (National Biosciences, Inc., Plymouth, MN 55447, USA), and can be purchased from Gibco/BRL Life Technologies (Gaithersburg, MD, USA). If the ORF is smaller than 800 to 1000 base pairs, flanking primers are chosen outside of the open reading frame.

-112-

Genomic DNA prepared from the *Helicobacter pylori* HpJ99 strain (ATCC 55679) is used as the source of template DNA for amplification of the ORFs by PCR (polymerase chain reaction) (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). For the preparation of genomic DNA from *H. pylori*, see

5 Example I. PCR amplification is carried out by introducing 10 nanograms of genomic HpJ99 DNA into a reaction vial containing 10 mM Tris pH 8.3, 50 mM KCl, 2 mM MgCl₂, 2 microMolar synthetic oligonucleotide primers (forward=F1 and reverse=R1), 0.2 mM of each deoxynucleotide triphosphate (dATP, dGTP, dCTP, dTTP), and 1.25 units of heat

10 stable DNA polymerase (Amplitaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA) in a final volume of 40 microliters. The PCR is carried out with Perkin Elmer Cetus/GeneAmp PCR System 9600 thermal cyclers.

Upon completion of thermal cycling reactions, each sample of amplified DNA is visualized on a 2% TAE agarose gel stained with Ethidium Bromide (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994) to

15 determine that a single product of the expected size had resulted from the reaction. Amplified DNA is then washed and purified using the Qiaquick Spin PCR purification kit (Qiagen, Gaithersburg, MD, USA).

PCR products are cloned into the pT7Blue T-Vector (catalog#69820-1, Novagen, Inc., Madison, WI, USA) using the TA cloning strategy (Current Protocols in Molecular

20 Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). The ligation of the PCR product into the vector is accomplished by mixing a 6 fold molar excess of the PCR product, 10 ng of pT7Blue-T vector (Novagen), 1 microliter of T4 DNA Ligase Buffer (New England Biolabs, Beverly, MA, USA), and 200 units of T4 DNA Ligase (New England Biolabs) into a final reaction volume of 10 microliters. Ligation is allowed to

25 proceed for 16 hours at 16°C.

Ligation products are electroporated (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994) into electroporation-competent XL-1 Blue or DH5- α *E. coli* cells (Clontech Lab., Inc. Palo Alto, CA, USA). Briefly, 1 microliter of ligation reaction is mixed with 40 microliters of electrocompetent cells and subjected to

30 a high voltage pulse (25 microFarads, 2.5 kV, 200 ohms) after which the samples are incubated in 0.45 ml SOC medium (0.5% yeast extract, 2% tryptone, 10 mM NaCl, 2.5 mM KCl, 10 mM MgCl₂, 10 mM MgSO₄ and 20 mM glucose) at 37°C with shaking for 1 hour. Samples are then spread onto LB (10 g/l bacto tryptone, 5 g/l bacto yeast extract, 10 g/l sodium chloride) plates containing 100 microgram/ml of Ampicillin, 0.3% X-gal, and 100

35 microgram/ml IPTG. These plates are incubated overnight at 37°C. Ampicillin-resistant colonies with white color are selected, grown in 5 ml of liquid LB containing 100 microgram/ml of Ampicillin, and plasmid DNA is isolated using the Qiagen miniprep protocol (Qiagen, Gaithersburg, MD, USA).

-113-

To verify that the correct *H. pylori* DNA inserts had been cloned, these pT7Blue plasmid DNAs are used as templates for PCR amplification of the cloned inserts, using the same forward and reverse primers used for the initial amplification of the J99 *H. pylori* sequence. Recognition of the primers and a PCR product of the correct size as visualized on a 2% TAE, ethidium bromide stained agarose gel are confirmation that the correct inserts had been cloned. Two to six such verified clones are obtained for each knock-out target, and frozen at -70°C for storage. To minimize errors due to PCR, plasmid DNA from these verified clones are pooled, and used in subsequent cloning steps.

The sequences of the genes/ORFs are again used to design a second pair of primers which flank the region of *H. pylori* DNA to be either interrupted or deleted (up to 250 basepairs) within the ORFs but are oriented away from each other. The pool of circular plasmid DNAs of the previously isolated clones are used as templates for this round of PCR. Since the orientation of amplification of this pair of deletion primers is away from each other, the portion of the ORF between the primers is not included in the resultant PCR product. The PCR product is a linear piece of DNA with *H. pylori* DNA at each end and the pT7Blue vector backbone between them which, in essence, results in the deletion of a portion of the ORFs. The PCR product is visualized on a 1% TAE, ethidium bromide stained agarose gel to confirm that only a single product of the correct size has been amplified.

A Kanamycin-resistance cassette (Labigne-Roussel et al., 1988 J. Bacteriology 170, 1704-1708) is ligated to this PCR product by the TA cloning method used previously (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., editors, 1994). The Kanamycin cassette containing a *Campylobacter* kanamycin resistance gene is obtained by carrying out an EcoRI digestion of the recombinant plasmid pCTB8:kan (Cover et al., 1994, J. Biological Chemistry 269, pp. 10566-10573). The proper fragment (1.4 kb) is isolated on a 1% TAE gel, and isolated using the QIAquick gel extraction kit (Qiagen, Gaithersburg, MD, USA). The fragment is end repaired using the Klenow fill-in protocol, which involved mixing 4ug of the DNA fragment, 1 microliter of dATP, dGTP, dCTP, dTTP at 0.5 mM, 2 microliter of Klenow Buffer (New England Biolabs) and 5 units of Klenow DNA Polymerase I Large (Klenow) Fragment (New England Biolabs) into a 20 microliter reaction, incubating at 30°C for 15 min, and inactivating the enzyme by heating to 75°C for 10 minutes. This blunt-ended Kanamycin cassette is then purified through a QIAquick column (Qiagen, Gaithersburg, MD, USA) to eliminate nucleotides. The "T" overhang is then generated by mixing 5 micrograms of the blunt-ended kanamycin cassette, 10 mM Tris pH 8.3, 50 mM KCl, 2 mM MgCl₂, 5 units of DNA Polymerase (Amplitaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA), 20 microliters of 5 mM dTTP, in a 100 microliter reaction and incubating the reaction for 2 hours at 37°C. The "Kan-T" cassette is purified using a QIAquick column (Qiagen, Gaithersburg, MD, USA). The PCR product of the deletion primers (F2 and R2) is ligated

-114-

to the Kan-T cassette by mixing 10 to 25 ng of deletion primer PCR product, 50 - 75 ng Kan-T cassette DNA, 1 microliter 10x T4 DNA Ligase reaction mixture, 0.5 microliter T4 DNA Ligase (New England Biolabs, Beverly, MA, USA) in a 10 microliter reaction and incubating for 16 hours at 16°C.

- 5 The ligation products are transformed into XL-1 Blue or DH5- α *E.coli* cells by electroporation as described previously. After recovery in SOC, cells are plated onto LB plates containing 100 microgram/ml Ampicillin and grown overnight at 37°C. These plates are then replica plated onto plates containing 25 microgram/ml Kanamycin and allowed to grow overnight. Resultant colonies have both the Ampicillin resistance gene present in the
- 10 pT7Blue vector, and the newly introduced Kanamycin resistance gene. Colonies are picked into LB containing 25 microgram/ml Kanamycin and plasmid DNA is isolated from the cultured cells using the Qiagen miniprep protocol (Qiagen, Gaithersburg, MD, USA).

- Several tests by PCR amplification are conducted on these plasmids to verify that the Kanamycin is inserted in the *H. pylori* gene/ORF, and to determine the orientation of
- 15 the insertion of the Kanamycin-resistance gene relative to the *H. pylori* gene/ORF. To verify that the Kanamycin cassette is inserted into the *H. pylori* sequence, the plasmid DNAs are used as templates for PCR amplification with the set of primers originally used to clone the *H. pylori* gene/ORFs. The correct PCR product is the size of the deleted gene/ORF but increased in size by the addition of a 1.4 kilobase Kanamycin cassette. To
- 20 avoid potential polar effects of the kanamycin resistance cassette on *H. pylori* gene expression, the orientation of the Kanamycin resistance gene with respect to the knock-out gene/ORF is determined and both orientations are eventually used in *H. pylori* transformations (see below). To determine the orientation of insertion of the kanamycin resistance gene, primers are designed from the ends of the kanamycin resistance gene
- 25 ("Kan-1" 5'-ATCTTACCTATCACCTCAAAT-3', and "Kan-2" 5'-AGACAGCAACATCTTTGTGAA-3'). By using each of the cloning primers in conjunction with each of the Kan primers (4 combinations of primers), the orientation of the Kanamycin cassette relative to the *H.pylori* sequence is determined. Positive clones are classified as either in the "A" orientation (the same direction of transcription is present
- 30 for both the *H. pylori* gene and the Kanamycin resistance gene), or in the "B" orientation (the direction of transcription for the *H.pylori* gene is opposite to that of the Kanamycin resistance gene). Clones which share the same orientation (A or B) are pooled for subsequent experiments and independently transformed into *H. pylori*.

35 *Transformation of Plasmid DNA into H. pylori cells*

Two strains of *H. pylori* are used for transformation: ATCC 55679, the clinical isolate which provided the DNA from which the *H. pylori* sequence database is obtained, and AH244, an isolate which had been passaged in, and has the ability to colonize the mouse stomach. Cells for transformation are grown at 37°C, 10% CO₂, 100% humidity,

-115-

either on Sheep-Blood agar plates or in Brucella Broth liquid. Cells are grown to exponential phase, and examined microscopically to determine that the cells are "healthy" (actively moving cells) and not contaminated. If grown on plates, cells are harvested by scraping cells from the plate with a sterile loop, suspended in 1 ml of Brucella Broth, spun
5 down (1 minute, top speed in eppendorf microfuge) and resuspended in 200 microliters Brucella Broth. If grown in Brucella Broth liquid, cells are centrifuged (15 minutes at 3000 rpm in a Beckman TJ6 centrifuge) and the cell pellet resuspended in 200 microliters of Brucella broth. An aliquot of cells is taken to determine the optical density at 600 nm, in order to calculate the concentration of cells. An aliquot (1 to 5 OD₆₀₀ units/25 microliter)
10 of the resuspended cells is placed onto a prewarmed Sheep-Blood agar plate, and the plate is further incubated at 37°C, 6% CO₂, 100% humidity for 4 hours. After this incubation, 10 microliters of plasmid DNA (100 micrograms per microliter) is spotted onto these cells. A positive control (plasmid DNA with the ribonuclease H gene disrupted by kanamycin resistance gene) and a negative control (no plasmid DNA) are done in parallel. The plates
15 are returned to 37°C, 6% CO₂ for an additional 4 hours of incubation. Cells are then spread onto that plate using a swab wetted in Brucella broth, and grown for 20 hours at 37°C, 6% CO₂. Cells are then transferred to a Sheep-Blood agar plate containing 25 micrograms/ml Kanamycin, and allowed to grow for 3 to 5 days at 37°C, 6% CO₂, 100% humidity. If colonies appear, they are picked and regrown as patches on a fresh Sheep-
20 Blood agar plate containing 25 micrograms/ml Kanamycin.

Three sets of PCR tests are done to verify that the colonies of transformants have arisen from homologous recombination at the proper chromosomal location. The template for PCR (DNA from the colony) is obtained by a rapid boiling DNA preparation method as follows. An aliquot of the colony (stab of the colony with a toothpick) is introduced into
25 100 microliters of 1% Triton X-100, 20 mM Tris, pH 8.5, and boiled for 6 minutes. An equal volume of phenol : chloroform (1:1) is added and vortexed. The mixture is microfuged for 5 minutes and the supernatant is used as DNA template for PCR with combinations of the following primers to verify homologous recombination at the proper chromosomal location.

30 TEST 1. PCR with cloning primers originally used to amplify the gene/ORF. A positive result of homologous recombination at the correct chromosomal location should show a single PCR product whose size is expected to be the size of the deleted gene/ORF but increased in size by the addition of a 1.4 kilobase Kanamycin cassette. A PCR product of just the size of the gene/ORF is proof that the gene had not been knocked out and that
35 the transformant is not the result of homologous recombination at the correct chromosome location.

TEST 2. PCR with F3 (primer designed from sequences upstream of the gene/ORF and not present on the plasmid), and either primer Kan-1 or Kan-2 (primers designed from the ends of the kanamycin resistance gene), depending on whether the plasmid DNA used

-116-

was of "A" or "B" orientation. Homologous recombination at the correct chromosomal location will result in a single PCR product of the expected size (i.e., from the location of F3 to the insertion site of kanamycin resistance gene). No PCR product or PCR product(s) of incorrect size(s) will prove that the plasmid had not integrated at the correct site and that the gene had not been knocked out.

TEST 3. PCR with R3 (primer designed from sequences downstream of the gene/ORF and not present on the plasmid) and either primer Kan-1 or Kan-2, depending on whether the plasmid DNA used was of "A" or "B" orientation. Homologous recombination at the correct chromosomal location will result in a single PCR product of the expected size (i.e., from the insertion site of kanamycin resistance gene to the downstream location of R3). Again, no PCR product or PCR product(s) of incorrect size(s) will prove that the plasmid had not integrated at the correct site and that the gene had not been knocked out.

Transformants showing positive results for all three tests above indicate that the gene is not essential for survival *in vitro*.

A negative result in any of the three above tests for each transformant indicates that the gene had not been disrupted, and that the gene is essential for survival *in vitro*.

In the event that no colonies result from two independent transformations while the positive control with the disrupted ribonuclease H plasmid DNA produces transformants, the plasmid DNA is further analyzed by PCR on DNA from transformant populations prior to plating for colony formation. This will verify that the plasmid can enter the cells and undergo homologous recombination at the correct site. Briefly, plasmid DNA is incubated according to the transformation protocol described above. DNA is extracted from the *H. pylori* cells immediately after incubation with the plasmid DNAs and the DNA is used as template for the above TEST 2 and TEST 3. Positive results in TEST 2 and TEST 3 would verify that the plasmid DNA could enter the cells and undergo homologous recombination at the correct chromosomal location. If TEST 2 and TEST 3 are positive, then failure to obtain viable transformants indicates that the gene is essential, and cells suffering a disruption in that gene are incapable of colony formation

VII. High-throughput drug screen assay

Cloning, expression and protein purification

Cloning, transformation, expression and purification of the *H. pylori* target gene and its protein product, e.g., an *H. pylori* enzyme, to be used in a high-throughput drug screen assay, is carried out essentially as described in Examples II and III above. Development and application of a screening assay for a particular *H. pylori* gene product, peptidyl-propyl *cis-trans* isomerase, is described below as a specific example.

-117-

Enzymatic Assay

The assay is essentially as described by Fisher (Fischer, G., et.al. (1984) *Biomed. Biochim. Acta* 43:1101-1111). The assay measures the *cis-trans* isomerization of the Ala-Pro bond in the test peptide N-succinyl-Ala-Ala-Pro-Phe-p-nitroanilide (Sigma # S-7388, lot # 84H5805). The assay is coupled with α -chymotrypsin, where the ability of the protease to cleave the test peptide occurs only when the Ala-Pro bond is in *trans*. The conversion of the test peptide to the trans isomer in the assay is followed at 390 nm on a Beckman Model DU-650 spectrophotometer. The data are collected every second with an average scanning of time of 0.5 second. Assays are carried out in 35 mM Hepes, pH 8.0, in a final volume of 400 μ l, with 10 μ M α -chymotrypsin (type 1-5 from bovine Pancreas, Sigma # C-7762, lot 23H7020) and 10 nM PPLase. To initiate the reaction, 10 μ l of the substrate (2 mM N-Succinyl-Ala-Ala-Pro-Phe-p-nitroanilide in DMSO) is added to 390 μ l of reaction mixture at room temperature.

15 Enzymatic assay in crude bacterial extract.

A 50 ml culture of *Helicobacter pylori* (strain J99) in Brucella broth is harvested at mid-log phase ($OD_{600\text{ nm}} \sim 1$) and resuspended in lysis buffer with the following protease inhibitors: 1 mM PMSF, and 10 μ g/ml of each of aprotinin, leupeptin, pepstatine, TLCK, TPCK, and soybean trypsin inhibitor. The suspension is subjected to 3 cycles of freeze-thaw (15 minutes at -70°C , then 30 minutes at room temperature), followed by sonication (three 20 second bursts). The lysate is centrifuged (12,000 g x 30 minutes) and the supernatant is assayed for enzymatic activity as described above.

Many *H. pylori* enzymes can be expressed at high levels and in an active form in *E. coli*. Such high yields of purified proteins provide for the design of various high throughput drug screening assays.

EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments and methods described herein. Such equivalents are intended to be encompassed by the scope of the following claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Astra Aktiebolag
- (B) STREET: S-151 85
- (C) CITY: Sodertalje
- (D) STATE:
- (E) COUNTRY: Sweden
- (F) POSTAL CODE (ZIP):

- (ii) TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS

- (iii) NUMBER OF SEQUENCES: 1956

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 8-mm cartridge tape
- (B) COMPUTER: SPARC station LX
- (C) OPERATING SYSTEM: SunOS Release 4.1.3
- (D) SOFTWARE: tar

(v) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/US96/09122
- (B) FILING DATE: June 6, 1996

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/630,405
- (B) FILING DATE: 01-APR-1996

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/561,469
- (B) FILING DATE: 17-NOV-1995

(viii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/487,032
- (B) FILING DATE: 07-JUNE-1995

(ix) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: LAHIVE & COCKFIELD
- (B) STREET: 60 State Street, Suite 510
- (C) CITY: Boston
- (D) STATE: Massachusetts
- (E) COUNTRY: USA
- (F) ZIP: 02109-1875

(x) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Mandragouras, Amy E.
- (B) REGISTRATION NUMBER: 36,207
- (C) REFERENCE/DOCKET NUMBER: GTN-001C5PC

(xi) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (617)227-7400
- (B) TELEFAX: (617)227-5941

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

ATGTGTTCTC	AGGAAATTTT	ATCAAGCTTG	CAAACCATTA	TTGCCGAACA	ATTTTCTATA	60
AATATCATCA	CTCAGCTTGC	TAATAAACTC	ACACAAGTTA	AAAATCTAAA	TTTTTTTGAG	120
AATAAGACC	ATACTATCAA	GCTTAACACT	ATCCATAACG	GACTGCACAT	CCGCCCCCTA	180
AAATTATGTC	GTAATCTTTT	TTTCAATCTA	CAACGCATTA	TAGGGCTTAT	CAGTCTGTTT	240
GGGATATTAT	TTTCCATTAG	TATTTATCTA	CCCTTTATAA	TGATTTTTCG	AACAGTGCCT	300
TGTATTCTCA	TTTCCAACCA	TATAGCAAAA	AAACATAGTG	CTTCCATAGA	TAAACTTCAA	360
GACCAAAAAG	AAAGCATGCA	AAATTACTTA	TACTCTGGAC	TAGATAACCA	AAAGAACAAG	420
GACAACCTAT	TATTTAACTT	CATGCTAAAT	TTTCACCATA	AATTTATTGA	AACAAAAGAA	480
TTGTATCTCA	ATAATTTTGT	GAAAGTAGCC	CAAAAAAAGT	TAATATTTAC	CATATATGCT	540
GATGTTTTAA	TCACCACTCT	AAGTATTGCA	CTATTTTTC	TAATGGTTTT	TATTATCCTT	600
TCAAAATTAA	TGGGTGTGGG	AGCAATTGCT	GGGTATATCC	AAGCATTTAG	CTCTACCCAA	660
CAACAACTAC	AAGATTTATC	ATTTTATGGA	AAGTGGTTTT	TTGCTATCAA	TAAATACTTT	720
GAAAATTATT	TCTGTATTTT	AGATTACAAA	ATACCGAAAC	CAGAAACACA	AATCAAATTA	780
GAAGAAAAAA	TCCATAGCAT	TACATTTGAA	AATATTAGTT	TCTCTTATCC	TAATTCAAAA	840
CTTATTTTTG	AAAACCTTAA	TCTCTCTTTA	CACTCTAATA	AAATTTATGC	ATTAGTCGGC	900
AAGAATGCTA	GCGGAAAAAG	CACGCTGATT	AAATTATTAT	TAGGTTTTTA	TACCCCAAAT	960
TCAGGTCAAA	TTATCATTAA	TAACAAATAC	CCATTACAAG	ACTTGGAAGT	AAATAGCTAC	1020
CATCAACAAA	TGAGTGCCAT	ATTTCAAGAT	TTTTCTCTTT	ATGCTGGGTA	TAGCATTGAT	1080
GATAATCTTT	TTATGCAAAA	CAATATCACT	AAAGAGCAAT	TGAAGCAAAA	AAGAGAAATA	1140
CTAAAATCTT	TTGATGAGAA	TTTTCAAAAT	TGCTCTAATG	ATTGCAACAA	CACACTATTT	1200
GGAGCGCAAT	ATAATGGGGT	AGATTTTCTT	TTAGGTCAAA	AGCAACGCAT	AGCTACCATG	1260
AGAGCCTTTT	TAAAACCAAG	TAATTGCATT	GTTTTAGATG	AGCCAAGCAG	CGCCATCGAT	1320
CCCATATG	AAAAAGAGTT	TTTAGATTTT	ATTTTTTAAA	AATCGCAATC	TAAGATGGCT	1380
TTAATTATTA	CACACCGCAT	GAATAGTGTC	AAGCAAGCTA	ATGAAATTAT	CGTGTTAGAT	1440
CAAGGCAAAC	TAATAGAACA	GGGCAACTTT	GAAACCCTTA	TGAAAAAACA	GGGATTATTT	1500
TGCGAATTGT	TTTTGAAACA	ACAATAC				1527

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

120

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

ATGGAGCGCA	AGACGCTCCA	GAGCATTTTA	TGTTTAATAA	AAAAAGAAAT	GATGAGACCA	60
AAAGGTATTG	TAATGAATTG	TTGCAGGSCT	TGGAAACACC	AGGTTCTTAA	GCAAAGCAGG	120
ACAGGTTTAG	TGGTGTGAG	CATTATCTCT	TCTACAGCCC	CCTTTATTGG	TTTGTTTGGG	180
ACGGTAGTTG	AAATTTTAGA	AGCGTTTAAC	AATTTGGGCG	CGTTAGGTCA	AGCTTCTTTT	240
GGAGTGATCG	CACCCATTAT	TTCTAAGGCG	CTTATCGCCA	CCGCTGCAGG	GATTTTAGCA	300
GCCATTCCAG	CCTATTCTTT	TTACTTGATC	TTAAAGCGCA	AGGTGTATGA	TTTATCGGTT	360
TATGTGCAGA	TGCAAGTGGA	TATTTGTCT	TCTAAAAAA			399

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 474 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

ATGCATGAAC	GCATTGAAAG	AGGTATTGGA	AATAATGAAT	GTAAAGAAAT	TTTTGGCAAT	60
GAACTCAAAC	AAAGAAAGAC	AAAATTGATT	GAAGACATAG	AACGGCGGTT	CAAAGAATGC	120
GAGGAACAAT	TCCGTGGAAG	TGTAGGAAAA	AATATTGAAC	AACTTGAAGA	AAGAGTTAAA	180
GATTCTCTAG	CGATTATAAA	ACGCATCAAT	AACCTTGGTC	TTAATCCTAA	TTCTAATTTT	240
AATATGGATA	GCGGCATTGA	TACAATAGGC	TTATTTAGTT	CAATAGGAGG	TTTGGTGTTG	300
CTTCTATTGA	CGCCTGTAGT	AGGTGAGTTT	GCGTTAATTG	CAGGAGTGGG	TTTAGCATTG	360
GTGGGGGTAG	GTAAATCAAT	ATGGAGTTTT	TTTGATTGAG	ATTATAAAAA	ATCCCAACAA	420
AGAAAAGAAG	TGGATAAGAA	TTTACATCAA	ATTTGCGAAA	AATTGTGCAG	GATG	474

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

121

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

ATGCCTGGCG TGTATCAAAT GAGTATAGAG CCTCTTTTAA AAGAATGCGA AGAATTAGTG	60
GGTTTAGGCA TAAAAGCCGT TTTATTGTTT GGCATTCCTA AACATAAGGA CGCTACAGGA	120
AGCCATGCGT TAAATAAGGA TCACATTGTC GCAAAAGCTA CGAGAGAAAT TAAAAACGA	180
TTTAAGGATT TGATCGTTAT AGCGGATTG TGTTTTGCG AATACACCGA CCATGGGCAT	240
TGCGGGATTT TAGAAAACGC TTCTGTGTCT AACGATAAAA CGCTAAAGAT TTAAATCTT	300
CAAGGGCTTA TTTTGCTGAA AGCGGTGTGG ATATTC	336

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

GTGGAAAACA ACAAGAGTTT AAAGCATGCG AATGAGTTAA GGGATAAGCG AGATGAATTA	60
GAGTTTCATT TCGGAGAGCT TTTCGGGGGG AATGTTTTTA AAAGCAGCAT TAAAACCCAT	120
TCGCTCACAG ATAAAGACTC AGCGGACTTT GATGAGAGCT ATACCTTAA TATCGGGCAT	180
GGGYTCAATA TSATA	195

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1857 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

SUBSTITUTE SHEET (RULE 26)

122

(A) NAME/KEY: misc_feature
(B) LOCATION 1...1857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

GTGTTTGTGG	CAAGCAAACA	AGCTGACGAA	CAAAAAAAGC	TAGTTATAGA	GCAAGAGGTT	60
CAAAAGCGGC	AGTTTCAAAA	AATAGAAGAA	CTTAAAGCAG	ACATGCAAAA	GGGTGTCAAT	120
CCCTTTTTTA	AAGTCTTGTT	TGATGGGGGG	AATAGGTTGT	TTGGTTTCCC	TGAAACTTTT	180
ATTTATCTT	CTATATTTAT	ATTGTTTGTA	ACAATTGTAT	TATCTGTTAT	TCTTTTTCAA	240
GCCTATGAAC	CTGTTTGTAT	TGTAGCGATT	GTTATTGTGC	TTGTAGCTCT	TGGATTCAAG	300
AAAGATTACA	GGCTTTATCA	AAGAATGGAG	CGAGCGATGA	AATTTAAAAA	ACCTTTTTTG	360
TTTAAGGGCG	TGAAAAACAA	AGCGTTCATG	AGCATTTTTT	CCATGAAGCC	TAGTAAAGAA	420
ATGGCTAATG	ACATCCACTT	AAATCCAAAC	AGAGAAGACA	GGCTTGTGAG	CGCTGCAAAAC	480
TCCTATCTAG	CGAATAACTA	TGAATGTTTT	TTAGATGATG	GGGTGATCCT	TACTAACAAC	540
TATTTCTCTT	TAGGCACAAT	CAAAATTGGGG	GGCATTGATT	TTTTAACCAC	TTCCAAAAAA	600
GATCTCATAG	AGTTACACGC	TTCTATTTAT	AGCGTTTTTA	GGAATTTTGT	TACCCCTGAA	660
TTCAAATTTT	ATTTTCACAC	TGTTAAAAAG	AAAATCGTTA	TTGATGAAAC	CAATAGGGAT	720
TATGGTCTTA	TTTTTTCTAA	TGATTTTCATG	CGAGCCTATA	ATGAGAAGCA	AAAGAGAGAA	780
AGTTTTTATG	ATATTAGTTT	TTATCTCACC	ATAGAGCAAG	ATTTATTAGA	CACTCTCAAT	840
GAACCCGTTA	TGAATAAAAA	GCATTTTGCA	GACAATAATT	TTGAAGAGTT	TCAAAGGATT	900
ATTAGAGCCA	AGCTTGAAAA	CTTCAAAGAT	AGGATAGAGC	TCATAGAAGA	GCTACTGAGT	960
AAATACCACC	CCACTAGATT	AAAAGAATAC	ACTAAAGATG	GCATTATTTA	CTCCAAACAA	1020
TGCGAATTTT	ACAATTTTCT	TGTGGGAATG	AATGAAGCCC	CTTTTATTTG	CAACAGAAAA	1080
GACTTGTATC	TCAAGGAAAA	AATGCATGGT	GGGGTGAAAG	AAGTTTATTT	TGCCAATAAG	1140
CATGGAAAAA	TCTTAAATGA	CGATTTGAGT	GAAAAATATT	TTAGCGCTAT	TGAGATCAGT	1200
GAATACGCCC	CTAAATCACA	GAGCGATTG	TTTGATAAAA	TCAACGCTCT	AGACAGCGAA	1260
TTTATCTTTA	TGCATGCTTA	TTGCGCTAAA	AACTCACAAG	TTTTAAAGGA	CAAAC TAGCT	1320
TTCACTCTTA	GAAGGATTAT	TATTAGTGGA	GGCTCCAAAG	AGCAAGGCAT	GACTTTGGGT	1380
TGCTTGAGCG	AATTAGTGGG	TAATGGTGAT	ATTACGCTAG	GCAGTTATGG	TAATCTTTTA	1440
GTGCTGTTTG	CTGATAGCTT	TGAAAAAATG	AAACAAAGCG	TTAAGGAATG	CGTCTCTAGT	1500
CTTAACGCTA	AAGGTTTTTT	AGCCAACGCA	GCGACTTTCT	CTATGGAAAA	TTACTTTTTT	1560
GCCAAACATT	GCTCTTTTAT	CACGCTTCCT	TTTTATTTTG	ATGTAACCTC	TAACAATTTT	1620
GCTGATTTCA	TAGCGATGAG	AGCGATGAGT	TTTGATGGCA	AAGAAGACAA	TAACGCTTGG	1680
GGCAATAGCG	TGATGACGTT	AAAAAGCGAG	ATCAATTCGC	CTTTTTATTT	GAACCTCCAC	1740
ATGCCCACTG	ATTTTGGTTC	AGCTTCAGCA	GGACACACTT	TGATACTTGG	CTCAACCGGT	1800
TCAGGTAAGA	ACAGTGTTTA	TGTCCATGAC	TCTAAACGCT	ATGGGGCAAT	TTGCCTA	1857

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

GTGAAACAT	CGTGTGTTGGT	TACAATAGGG	AGGATCCGGG	GCGTTTTTAT	CATTAAGGCG	60
CAGTTGTGTC	TCGTGAGGG	AGGTTTTATG	AATTTTACCG	CTTATAACAC	GAAGACGCCA	120
GGGCATTTGC	ATTGTATGT	GCATAAGGGG	CATACGGAAT	TAGGCGAGGG	TGAAAGGCTG	180
ATTAAACTT	TATCCATGAA	ATTAGCGCAA	GGGTGCGCTA	AAGAATGGAG	GGTTTTCCCT	240

123

AGCAATGAAT GGCCTAAGGA ATTTAATATT TTAGCTTTAC CTTATGAAGT GTTTGCAAAA 300
 GAGCGCGGGA GCTCTTGGGC GAAGCATTTA 330

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

GTGGCTAAAG ACATCATCAG CGAGTCTCAA AACCTTTGCG CAAGAAAATT CCGCCGTTTG 60
 TATGCGTTAT TGAAAGAAAA TGAAATGCTC ATTGCGATCG GATCTTATCA AATGGGGAAC 120
 GATAAAGAGC TTGATGAAGC GATTAAGAAA AAGGCTCTAA TGGAGCAATT TTTAGTGCAA 180
 GATGAAAACG CTTTACYAGC CTTT 204

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

ATGAAATCAC GCCCAATCCT CGCACAGCT TACGCGCTCC AAATGATGGT CAAACAGATC 60
 GCTTTTTTAG AAACCATTTT AGTGGAACAC GAGCAAGACG CTTTGATTTT GGAAAAATCT 120
 TTGATCAAGC AGCTCAAGCC TAAATACAAC ATTCTTTTAA GAGACGATAA AACTTACCCT 180
 TATATTTACA TGGATTTTTC TATTGATTTT CCTATCCCTT TAATCACACG AAAAATCTTA 240
 AAACAGCCTG GCGTTAAATA TTTTGGCCCT TTTACGAGCG GGGCTAAGGA TATTTTGGAC 300
 AGCTTGTATG AATTGCTCCC TTTGGTTCAA AAGAAAAATT GCATCAAGGA TAAAAAGGCA 360
 TGCATGTTTT ATCAAATAGA GCGTTGTAAA GCCCCATGCG AGGATAAAAT CACTAAAGAA 420
 GAATATTTAA AAATCGCTAA AGAATGTTTA GAAATGATTG AAAATAAAGA CAGGCTCATC 480
 AAAGAGCTTG AATTGAAAAT GGAGCGCCTT TCTAGTAACT TGCCTTTTGA AGAAGCCTTA 540

124

ATTTATAGGG	ATAGGATTGC	AAAAATCCAA	AAAAATCGCCC	CTTTCACCTTG	CATGGATTTA	600
GCCAAACTCT	ACGATTTGGA	TATTTTGGCT	TTTTATGGTG	GGAACAACAA	GGCGGTGTTA	660
GTGAAAATGT	TCATGCGTGG	GGGTAAAATC	ATTTCTTCAG	CGTTTGAAAA	AATCCACTCT	720
CTCAACGGGT	TTGACACTGA	TGAAGCGATG	AAACAAGCCA	TTATCAATCA	TTACCAATCG	780
CATTTGCCTT	TGATGCCTGA	ACAAATCTTA	TTGAGCGCTT	GTTCTAATGA	AACGCTTAAA	840
GAATTGCAAG	AGTTTATCTC	TCACCAATAT	TCTAAAAAAA	TCGCTCTTAG	CATTCCTAAA	900
AAGGGTGATA	AGCTCGCTTT	AATAGAAATC	GCTATGAAAA	ACGCTCAAGA	GATTTTTAGC	960
CAAGAAAAAA	CCTCTAATGA	AGATCGGATC	TTAGAAGAAG	CGCGATCGCT	CTTCAATTTA	1020
GAGTGCCTGC	CTTATAGGGT	AGAAATCTTT	GACACAAGCC	ACCATTCAAA	CAGCCAATGC	1080
GTGGGGGGAA	TGGTCGTGTA	TGAAAACAAT	GCATTTCAAA	AAGACTCTTA	TCGGCGCTAC	1140
CATCTAAAAG	GCTCTAACGA	ATATGATCAA	ATGAGCGAAT	TGCTCACCAG	AAGGGCTTTA	1200
GACTTTGCTA	AAGAGCCACC	GCCTAATTTG	TGGGTGATAG	ATGGAGGGAG	GGCGCAATTA	1260
AACATCGCTT	TAGAAATTTT	AAAAAGCAGC	GGGAGTTTGT	TAGAAGTGAT	CGCTATTTCT	1320
AAAGAAAAAA	GGGGATTG					1338

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

GTGAGTTTGG	GGGCGTTTCA	GGGGTATTAT	GGAGGGCTAG	TGGATTTAGT	GGGGCAAAGG	60
TTGAGCGAAA	TTTGGAGCGC	GATCCCCATG	CTTTTATTAC	TCATTGTGAT	TTCTAGCGCG	120
TTCAATTCTA	ATTTTGGGAT	CATCTTGTTT	TTAGTCTTGC	TCTTTAGCTG	GATGGGGCTT	180
TCTCAAGTCG	TGCGCACGGA	GTTTTTAAAA	GCAAGGAATA	TGGAATACAC	CAAAGCCGCT	240
AGAGCGTTGG	GG					252

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

125

(B) LOCATION 1...120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

ATGAGTGAAG CCTATTTTTT ACACCATAAA AACGCTTCTC AAGTGTCTCT TAATGAACAA	60
GTITTAACG TTATGAAACA AGTTCAATTG GATGAAAATT TTTGGAATGT TTCTCTTATG	120

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

GTGATCCTGA TATTTATCAT CGTGGTGGAA GATCAGAAAG GCATTTTCCC TATCGCAGCG	60
TCAAAAAGAA AAAGCCAAAG CTCGTGTGATC ATTGAAGACG TGTGCTTCAG CAAAGAGGAT	120
TTTGTAGAAG GGGCAAAAGC GATTGAGGGG CTTTTAAAAA AACATGGCTT TAAGGATAAT	180
GGCATTATTT TTGGGCATGC GTTAAGCGGG AATTTGCACT TTGTCGTTAC GCCGATTCTA	240
GAAAATGAAG CTGAAAGAAA AGCGTTTGAA AATTTAGTTT CTGAGATGTT TTTAATGGTG	300
AGCAAAAGCT CTGGCTCTAT TAAAGCCGAA CATGGCACAG GCAGGATGGT AGCCCCTTTT	360
GTGGAATGG AGTGGGGAGA AAAAGCTTAT AAGATCCACA AACAAATCAA GGAATTGTTT	420
GATCCTAATG GCCTTTAAA CCCTGATGTG ATCATCACAA ACGATAAAGA AATCCACACT	480
AAAAATTTAA AGAGCATTTA CCCTATTGAA GAGCATTTGG ACATGTGCAT GGAATGTGGG	540
TTTTGTGAAA GGATCTGCCC CAGTAAAGAT TTATCCTTAA CGCCACGACA ACGCATCGTC	600
ATCCACAGAG AGGTAGAGCG TTTGAAAGAA AGGGTAAGTC ATGGTCATGA TGAAGATCAG	660
GTTTTACTAG ATGAGCTTTT AAAAGAGTCT GAATACTAG CGCATGCCAC TTGCGCGGTG	720
TGCCATATGT GTTCCACTTT ATGCCCTTTA GGGATTGATA CCGGGAGYAT CGCTTTAAAT	780
CATTATCAAA AAAACCCTAA AGGCGAAAAG ATCGCTTCAA AGATTCTTAA ATCACATGCA	840
AACGACCACA AGCGTGGCTC GTTTTCTTT AAAARGCGCT TTCGTGGTTT CAAAAACTCA	900

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

126

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13

ATGAAAGAAA AAAACTTTTG GCCTTTAGGA ATCATGAGCG TGCTTATTTT TGGGCTTGGG	60
ATCGTGGTGT TTTTAGTGGT GTTTGCCCTA AAAAATTCGC CTAAAAATGA TTTAGTGTAT	120
TTCAAGGGTC ATAACGAAGT GGATTIAAAC TTAAACGCCA TGCTTAAAC TTATGAAAAC	180
TTTAAATCCA ATTATCGTTT TTCAGTGGGT TTAAAGCCTC TTACCGAAAG CCCTAAAACC	240
CCCATTTTGC CCTATTTTTC TAAAGGCACG CATGGGGATA AAAAAATCCA AGAAAACCTT	300
TTAAACAACG CTTTGATTTT AGAAAAGTCC AACACGCTTT ATGCACAATT GCAACCGCTC	360
AAACCCGCTT TAGATTCGCC AAATATTCAA GTGTATTTAG CGTTCATATCC CAGCCAATCC	420
CAGCCCAGAT TATTAGGAAC GCTTGATTGT AAAAACGCAT GCGAACCTTT AAAATTTGAT	480
TTGTTAGAGG GCGATAAAGT GGGGCGCTAT AAGATCCTTT TTAAATTTGT TTTTAAAAAT	540
AAAGAAGAAT TGATTTTGGA GCAACTGCTT TTTTAAAGTA GCATGGCTTG TATGGGTATA	600
TCAATTTTAA AAAACGCTAA AGCATTTTTT AAATACAAAA TA	642

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14

ATGCCCATTA AAGGCTCTTT TTTAGCCAGA AACCGCCTGG TGATCGCTTT AACCGATGCG	60
GTGATTATCC CCAAGCGGA TTTAAAAAGC GGCTCTATGA GCAGTGCGAG ATTAGCCCAG	120
AAATACCAAA AACCTTGTT TGTTTTACCC CAACGCCTGA ATGAGAGCGA CGGCACTAAT	180
GAGCTTTTAG AAAAAGGCA GGCTCAAGGG ATATTTAATA TTCAAAATTT TATAAACACC	240
CTTTTAAAAG ATTACATTT AAAAGAAATG CCTGAAATGA AAGATGAATT TTTAGAATAT	300
TGCGCGAAAA ACCCTAGCTA TGAAGAAGCG TATCTCAAAT TTGGGGATAA GCTTTTAGAA	360
TACGAGCTGT TGGTAAGAT TAAGCGCATC AATCATCTCG TGGTGTAGC A	411

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

127

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

ATGGTAGTAG	AATTAAAAA	CATTGAAAAG	ATTTATGAAA	ACGGGTTTCA	TGCTCTAAAA	60
GGCGTGAATT	TGGAATTGAA	AAAAGGCGAT	ATTTTGGGCG	TGATAGGCTA	TTCAGGGGCG	120
GGGAAATCCA	CGCTCATTCT	CTTGATCAAT	TGTTTAGAGC	GCCCCAGTTC	TGGCGAAGTT	180
TTAGTCAATG	GGGTCAATCT	GTTAAACTTA	AAGCCTAAAG	AATTGCAAAA	AGCGCGCCAA	240
AAAATAGGCA	TGATTTTCCA	GCATTTCAAT	TTATTGAGCG	CTAAAAACGT	GTTTGAAAAC	300
GTCGCTTTCT	CTCTAGAAAT	CGCCCGATGG	GAAAAAATA	AGATTAAATC	AAGGGTGCAT	360
GAATTGTTGG	AATTAGTGGG	GTTAGAAGAT	AAAGTGCATT	TTTATCCTAA	ACAGCTCAGC	420
GGCGGGCAAA	AACAACGAGT	GGCGATCGCT	AGGAGTTTAG	CGAATTGCC	TAATTTGTTG	480
CTTTGCGATG	AAGCCACATC	CGCTTTGGAT	TCTAAAACCA	CGCATTCTAT	TTTAACGCTT	540
CTAAGCGGCA	TTCAAAAAA	GTTTGATTG	AGCATCGTTT	TCATCACACA	CCAGATTGAA	600
GTGGTTAAAG	AATTGTGCAA	TCAAATGTGT	GTGATCAGCA	GCGGCGAAAT	CGTAGAAAGA	660
GGCTCGGTGG	AAGAAATTTT	TGCTAACCTT	AAACATGCTG	TTACTAAAGA	ATTGCTTGCC	720
ATCAAAACG	AACATGCGGA	TCAAAAATCG	CAAGACATTT	ATCGCATCGT	GTTTTTAGGG	780
GAGCATTTAG	ACGAGCCGAT	CATTTCTAAW	TTTTGW			816

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

ATGGGGGCTT	TGATAGCCAT	GTTTTTTTTT	ATGCTCATTA	AAAAGACTAT	CGCTTATAAA	60
GAAGATAAAA	AGAGCGCGGC	TTTAAAGGTC	GTGCCTTATT	TGGTGGCGTT	GATGAGCTTA	120
GCCTTTAGCT	GGTATTTGAT	CGTGAAGGTT	TTAAAACGCC	TCTATGCGGT	GAGTTTTGAA	180
ATCCAGCTCG	CTTGCGGTTG	TGTCCTTGCG	CTTTTGATTT	TTATCCTTTT	TAAAAGATTT	240
GTGTTAAAAA	AAGCCCCGCA	ATTAGAAAAT	AGCCACGAAA	GCGTCAATGA	GCTTTTAAAT	300
GTCCCTTIGA	TTTTTGCC					318

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

128

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...471
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17

```

ATGATTAAAA GAATTGCTTG TATTTTAAGC TTGAGCGCGA GTTTAGCGTT AGCTGGCGAA      60
GTGAATGGGT TTTTCATGGG TGCGGGTTAT CAACAAGGTC GTTATGGCCC TTATAACAGC      120
AATTACTCTG ATTGGCGTCA TGGCAATGAC CTTTATGGTT TGAATTTCAA ATTAGGTTTT      180
GTAGGCTTTG CCAATAAATG GTTTGGGGCT AGGGTGTATG GCTTTTTAGA TTGGTTTAAC      240
ACTTCAGGGA CTGAACACAC CAAAACCAAT TTGCTCACCT ATGGCGGCGG TGGCGATTTG      300
ATTGTCGAATC TCATTCCTTT GGATAAATTC GCTCTAGGTC TCATTGGTGG CGTTCAATTA      360
GCCGGAAACA CTTGGATGTT CCCTTATGAT GTCAATCAAA CCAGATTCCA GTTCTTATGG      420
AATTTAGGCG GAAGAATGCG TGTGGGGAT RCAGTGCCTT TGAAGCGGGC G              471

```

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 834 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...834
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18

```

ATGTATCGCC ATGTGTTGAA AGATTTCTCC CTAGATTTTA GCAAAGAAAG CGTTCAAGAG      60
CTGTTTAACC AGCTGGCTAA AGACACTTTT TTATGCTTTT TGCCGTGTTTT AATCATTTTA      120
ATGGTGGTGG CGTTTTTGTC TAATGTCTTG CAATTGGGCT GGCTCTTTGC CCCTAAAGTC      180
ATTGAGCCTA AATTTTCTAA AATCAACCCT ATCAATGGCG TCAAAAACCT TTTTCTTTA      240
AAAAAGATCC TTGATGGGAG TTTGATCACT TTAAGGTTT TTTTAGCTTT TTTTCTGGG      300
TTTTTCATCT TTTCTTTATT TTTAGGGGAA TTAACCATG CGGCTCTTTT GAATTTGCAA      360
GGCCAGTTGT TGTGGTTTAA AAGCAAGGCG TTATGGCTCA TTTCTTCGCT TTTATTTTA      420
TTTTTGTCT TGGCTTTTGT GGATTTAATC ATCAAACGCC GCCAATACAC TAACCTTTA      480
AAAATGACTA AACAAGAAGT TAAGGACGAA TACAAACAGC AAGAAGGAAA CCCAGAAATC      540
AAAGCCAAAA TCCGCCAGAT GATGGTAAAA AACGCCACGA ATAAAATGAT GCAAGAAATC      600
CCCAAATCCA ATGTCGTGGT GACTAACCCT ACCCATTATG CCGTCGCTCT CAAATTTGAT      660
GAAGAACACC CTGTGCCTGT GGTAGTGGCT AAAGGCACGG ATTATTTAGC CATTAGGATT      720
AAGGGTATCG CCAGAGAGCA TGACATAGAA ATTATAGAAA ATAAAACGCT CGCTAGAGAG      780
CTTTATAGAG ACGTGAAATT GAACGCCACC ATACCAGAAG AATTGTTTGA GCGG              834

```

(2) INFORMATION FOR SEQ ID NO:19:

129

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...360
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19

ATGAATACAA	GSCCCTTAAT	CGCTACGCTT	TTGCAAGCGC	CTTTGCATGT	TTTAGGGATT	60
AGAGAGCCAG	TTTCTTTTCA	GCCTTTTAC	CCCAAAACAG	AAAAGCCTAA	TCGCCCTCAA	120
AAGTTCGCGC	ATGTTTCTAG	CATGCCCAGT	TTGGAATTTT	TAGAAAAATT	GGTGATCCGC	180
TACCTTTTAG	AAGACAGAAG	CCTATTGGAT	TTAGCGGTGG	GTTATATCCA	TAGTGGGGTA	240
TTCTTGCATA	AAAAACAAGA	ATTTGACGCT	TTATGTCAAG	AAAAATTGGA	CGACCTTAAA	300
TTAGTTGCGT	TATTATTAGA	TGCGAATTTA	CCCCTAAAAA	AAGGGGGTTT	TGAAAAGGAA	360

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 678 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...678
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20

ATGGGGCAGG	CATTTTTTAA	AAAAATTGTT	GGCTGTTTCT	GTCTTGTTTA	TTTATTTTAA	60
TCTAGCGCAA	TAGAAGCAGT	AGCACTTGAC	ATTAAGAATT	TTAATCGTGG	TAGGGTGAAA	120
GTGGTGAATA	AGAAGATTGC	TTATTGGGGA	GATGAAAAAC	CTATTACGAT	TTGGACTTCA	180
TTAGACAATG	TTACCGTGAT	CCAACCTGAA	AAAGATGAAA	CTATTTCTTA	CATCACAACA	240
GGTTTCAATA	AAGGTTGGAG	TATTGTGCCT	AATTCTAATC	ATATATTTCAT	TCAACCTAAA	300
TCGGTAAAAA	GTAATCTCAT	GTTTGAAAAA	GAAGCAGTGA	ATTTTGCCCT	AATGACAAGA	360
GATTACCAAG	AATTTTTTAA	GACAAAAAAA	CTTATCGTAG	ATGCGCCTGA	CCCTAAAGAA	420
TTAGAAGAAC	AAAAAAAAGC	TCTAGAAAAA	GAAAAAGAAG	CTAAAGAACA	GGCGCAAAG	480
GCACAAAAAG	ATAAAGAGA	AAAAGAAAAG	GAGGAGCGTG	CAAAAAATAG	AGCCAAATTA	540
GAAAATCTCA	CTAACGCTAT	GAGTAACCCA	CAAAATTTGA	GCAATAACAA	AAATCTTAGC	600
GAATTGATCA	AGCAACAGAG	AGAAAATGAA	TTAGACCAAA	TGGAACGAAC	TAGAGGACAT	660
GCAAGAGCAG	GCTCAAGC					678

130

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21

ATGAATACAG AAATTTTAAC CATCATGTTA GTTGTCTCCG TGCTTATGGG ATTGGTAGGC	60
TTAATAGCGT TTTTATGGGG GGTAAAAGC GGTCAGTTG ACGATGAAA ACGCATGCTT	120
GAAAGCGTGT TGTATGACGC GCGAGCGACT	150

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22

ATGTTTGTAG CGGCCGGGCT TGGGGCTTAT GCGATCGCGC TTTTCCACCT CTTTACGCAT	60
GCGTTCTTCA AATCCCTCCT TTTCTTAGGC TCAGGCAATG TCATGCATGC GATGGAAGAC	120
AATCTGGATA TTAATAAAT GGGCGCTTTA TACAAGCCTA TGAGGATCAC AGCTGTCTTT	180
ATGATTATAG GGTCAGTGGC TTTGTGTGGG ATCTACCCCT TTGCGGGCTA TTTCTCCAAA	240
GACAAGATT TAGAGGTCGC CTTTGGGATG CACCACCACA TTTTATGGTT TGTTCTTTTG	300
ATTGGGGCGA TCTTTACCGC TTTTATAGC TTCAGACTCA TCATGCTGCT GTTTTTTGCA	360
CCCAAACAAC ATGAAATCAA CCACCCCA	390

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs

131

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23

ATGTTTATAT	CTTCTTCTTA	CACGCTGAGT	TTTGTATGGC	TTTTTTTAAT	TTTCTTTTTT	60
TTCAAAAATA	AGCCATTGGG	TTTGAGGTTT	TCGCTCTCTT	TGATAAGCGT	GATTTTAAGC	120
AATATCGCTT	TGAAAGACTC	CCTATCGCTC	AATGAATTTT	TAAGCAGTTT	TACAGCCCCC	180
TTAAGCCCCC	TTAGCTGTCT	TTTGATCCTT	GCTTATGCAA	GCTTTTCTTG	CCATATACTC	240
AAAAAGCCCC	CTTTAGAAAC	CTTGCAATCT	TATAGCGTCA	TGCTGTTTTT	CAATCTGTTG	300
CTTTTGACAG	ATATTTTAGG	GTTTTTGCCT	TTTTCAATCT	ACCATCATTT	CATGGCTTCT	360
CTGATTTTTA	GCGCGCTTTT	TTGCAGCAGT	TTGTTTTTGA	GTAGCCCCCT	ATTAGGCGTG	420
ATCGCTTTAG	TGGCTTTATC	CAGTTCGCTT	TTGATGCGTT	CTAATTTTCA	AATCTTAGAT	480
TCTTTATTGG	ATTTCCTATT	ATTTCTTTTT	GTCTTTTTTA	AGACTTTATA	TCTTGCTAAA	540
AAAAGGTTA						549

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24

ATGCGCCTAG	ATTACGCCCT	ATTCAACCAG	CATTTAGCAA	ATAGCAGAGA	AAAAGCTAAA	60
GCGTTGGTTT	TAAAAAACA	GGTTTTAGTC	AATAAAATGG	TGGTTTCTAA	ACCCTCTTTT	120
ATCGTTAAAG	AGGGCGATCA	AATTGAAGTC	ATCGCTCCCA	ATCTATTCTG	TAGCAGGGCT	180
GGGGAAAAAT	TAGGGGCTTT	TTTAGAAGAT	CATTTTATAG	ATTTTAAAGA	AAAGGTTGTT	240
TTAGATGTGG	GAGCGAGTAA	GGGAGGCTTT	AGTCAAGTGG	CTCTTTTAAA	AGGGGCTAAA	300
AAGGTGCTTT	GCGTGGATGT	GGGGAAAATG	CAATTAGATG	AAAGTTTGAA	AAACGACCAA	360
CGCATAGAAT	GTTACGAAGA	ATGCGATATT	AGAGGGTTTA	AAACGCCAGA	AAAAATTGAT	420
TTAGCACTTT	GTGATGTGAG	CTTTATTTCT	TTATATTGTA	TTTTAGAAGC	GATTTTGCCT	480
TTAAGCGGTG	AATTTTAAAC	GCTTTTCAAA	CCGCAATTTG	AAGTGGGCAG	AACAATAAAA	540
CGCAATAAAA	AGGGGGTGGT	GATGGATAAA	GAAGCCATTT	TGAACGCTTT	AGAAAACCTT	600
AAAAACCATT	TAAAAACAAA	GGATTTTCAA	ATCTTAACGA	TCCAAGAAAG	CTTAGTGAAA	660

132

GGGAAAAACG GGAATGTTGA ATTTTATC CATTTCAGC GAGCC

705

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25

ATGAGCCTAC CACCGGTTTG CATTTTGAAA GATGTGAATC ACCTTTTACA AGTCTTRCAT	60
TCTTGGTGG CGTTAGGCAA TTCCATGCTA GTGATTGAGC ATAATTTAGA CATCATCAAA	120
AACGCTGACT ACATTATAGA CATGGGGCCT GATGGGGGGG ATAAGGGCGG GAAAGTCATT	180
GCGAGCGGCA CGCCTTTAGA AGTGCGCAA AATTGCGAAA AAACCCAAAG CTATACGGGA	240
AAATTTTATG CTTTGGAATT GAAA	264

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26

ATGCAAAATC GATCGCATGA AATACAAGGC GTATCACACA TTAAGAATAA TTATAAATTT	60
TTACACAAAG AGCTTGACAA TTATATCAGC AAAGGGTATC GCATTGAAGA GATTATGGC	120
GCGTTTTTGT GGCTCAAAAT CGTAGCCATA GGTITAGAGT TGGCGGAAGA CGATCCGCAA	180
GTGGTGTTTG AGAGCATCAA CGCTACAGGC GTGCAATTAA AAGGGCTGGA TCTCATCCGC	240
AACATTTTGA TGATGGGGGA AAATYCTGAC AACCAGAATC GTCTTTATAA TACTTATTGG	300
GTGCCTTTAG AAAATTGGCT TGGTGAAAAG GATTTGAATG ATTTCATCAA AACCTATTGG	360
AGAATCTATT TTGAGGATAG AGTTACAAGA GGGAGAGCGC GAAGTGATT ACGCGCTAAA	420
AGCCCCACCAC AGAGACAATT TCCC	444

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27

ATGGATACCA TAAAAAGCAT TCCCATAGA ACTTTTATTT TACTCTATAA AAGCTCACCA	60
AAATGTGTTG TGTGGCATC AATTACAGTG CTATTTGTCG GCATTCTTYC ATCTCTGAAT	120
ATTCTTGTTA TGATAAAATT GATTGATATT GTGGTGAATC TATTACAAAA GCATACGCAT	180
TTTGAATACA GCTTGCTGTT ACCAACTTTA CTACTATGGG GAGCCTTGCT GTTTTAAACG	240
CATGTGTTCT CAGGAAATTT TATCAAGCTT GCAAACCATT ATTGCCGAAC AATTTTCTAT	300
AAATATCATC ACTCAGCTTG C	321

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28

ATGATCTTTT ACACCACCAT TAAAGAGCCT TAAAAAACC TCCAATACCG CTATGCGCAA	60
TTTTTTGGCA AGATCAAGCC TTGTTCGTTT TTAGAGTCTC TAAAATCATG CTTTTTCAA	120
ACCTATTCTT TTTCTTTAAC GCGAAAACAA GATTTCAAAT CGCATTGCGC CCATTTCATT	180
GACAGCGCCC ATTCCAACGC CTTAGTGGGT AATTGTATC GAGCGTTATT CATAGGGGAT	240
AGCTTGAATA AAGACTTAAG AGACAGGGCT AACGCGCTAG GGATCAACCA CTTACTGGCC	300
ATTAGCGGGT TTCATTTAGG GATTTTGAGC GCGAGCGTGT ATTTTCTTTT CTCTCTTTT	360
TATACCCCTT TACAAAACG CTATTTCCCT TACAGGAACG CTTTTTWA	408

(2) INFORMATION FOR SEQ ID NO:29:

134

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 162 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29

ATGAATAAAC CATTTTAAAT CTTACTCATA GCCCTAATTG CCTTTAGCGG CTGTAACATG	60
AGAAAATACT TCAAACCCGC TAAACACCAA ATTAAAGCGA AGCGTATTTT CCTAACCATT	120
TGCAAGAAAG CATCGTTTCG TCTAATCGTT ATGGAGCCAT TT	162

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 375 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30

ATGGCGGCTT GGAACACTTT AGTAGAAAAA ATCATCGCTC CTAAACACAA GGTCAAAATT	60
GGTTTTGTGG GCAAGTATTT AAGCTTAAAA GAATCTTATA AATCCTTGAT TGAAGCCCTA	120
ATCCATGCGG GGGCGCATCT GGATACGCAA GTCAATATTG AATGGCTGGA TAGCGAGAAT	180
TTTAATGAAA AGACTGATTT AGAGGGCGTT GATGCGATTT TAGTGCCGGG GGGCTTTGGA	240
GAAAGGGGGA TTGAGGGCAA AATTGCGGCC ATTCAAAGGG CTAGGTTAGA AAAACTCCCC	300
TTTTTAGGGA TTTGTTTGGG CATGCAATTA GCGATCGTTG AATTTTGTCG CAAATGTTTT	360
AGGCTTGAAA GGGGC	375

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 747 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

135

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31

ATGACTAAAG CGTTGTGCC TTAAGTTTG TTAGTGAGCG CGATTTTATT AGCGTTTTTCG	60
CTCATCTTAA TCCCACTTC TAAGAGCGCT TATTACGGGT TTTTGCGTCA AAAAAAGAC	120
AAGATTGACA TTAACATCAG AGCGGGTGAA TTCGGGCAAA AATTAGGCGA TTGGCTCGTG	180
TATGTGGATA AGACTGAAAA CAATTCCTAT GATAATTTGG TGCTTTTTTC TAATAAAGT	240
CTCTCTCAAG AAAGCTTTAT TTTGGCTCAA AAAGGCAATA TCAACAATCA AAACGGCGTG	300
TTTGAATTGA ATTGTATAA CGGGCATGCG TATTTCACTC AAGGCGATAA AATGCGTAAG	360
GTTGATTTTG AAGAATTGCA TTTCGCAAC AAGCTCAAGT CTTTCAATTC TAATGATGCG	420
GCTTATTTGC AAGGCACGGA TTATTTGGGT TATTGGAAAA AAGCCTTTGG TAAAAACGT	480
AATAAAAATC AAAAAACGCC TTTTCTCAA GCGATCTTAG TTTCTTGTT CCCTTTAGCG	540
AGCGTGTTTT TAATCCCTT ATTTGGCATC GCCAACCCGC GATTCAAAAC GAATTGGAGT	600
TATTTCYAWG TCCTTGGAGC GGTGGGGTW TATTTTTTAA TGGTGCATGT GATTTCTACG	660
GATTTGTTTT TGATGACCTT TTTCTTCCC TTTATTTGGG CGTTTATTC TTATTTATTG	720
TTTAGAAAAT TCATTTTAAA GCGTTAT	747

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

ATGAGTAAGA GCGCGATTTT TGTCTTTCT GGCTTTTTAG CGTTCTTGCT CTATGCTTTG	60
TTATTATATG GTTTGTGTT AGAAAGGCAT AATAAAGAAG CAGAGAAAAT CCTTTTAGAT	120
TTAAATAAAA AGGACGAACA AGCCATTGAC TTGAATTTAG AAGATCTGCC AAGCGAGAAA	180
AAGAATGAAA AAATTRAAA AGTAACGGAA AAACAGGACG ATTTTTTAGA GCCTAAAAGA	240
AGAACCCAAA GAGGAGCC	258

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

136

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33

```

GTGATGGCTC AATCCTTGCT TGTTCATGCC TTTTGTGCCG CCTTGCTCGC CCTAGCCTTT      60
ATGATCAATC TTTACACCCT TTTTAAAGAA AAGAATTTCA TCCAATTGAA CCGGAAAATC      120
TATCTTGTCA TGCCAGCGAT TTATATTCTT TTAAGCATCG CTCTTTTGAG TGGGGTTTTT      180
ATTTGGGCGA TGCAACAATT TGAATTTTCT TTTAGCGCTG TTGTCATGCT TTTGGGGTTG      240
TTGTTGATGC TCATTGCAGA AATCAAACGC CATAAAAGCG TGAAATTCGC TATCACTAAA      300
AAAGAAAGGA TGAAAGCCTA TATCAAAAAA GCTAAAATCC TGTATTTTTT AGAAACGATT      360
CTTATCATCG TGTTAATGGG CATT                                     384

```

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34

```

GTGCGTAATG TGGTTTTATT CATTTTAACA GCGATCTTTT TAGCGTTCAT GCTTTTAGTG      60
AGTTATTGCA TGCCCCATTA TAGCGTGGCT GTCATTAGCG GGTGGAAGT CAAAGAATG      120
AATGAAAATG AAAACACGCC CAATAATAAG GAAGTAAAAA CCCTTGCTAG AGATGTCTAT      180
TTTGTGCAAA CTTACGACCC TAAGGATCAA AAAAGCGTGA CCGTCTATCG TAACGAAGAC      240
ACGCGCTTTG GCTTCCCTTT TTATTTTAAG TTTAATTCGG CTGATATTTC AGCTCTCGCC      300
AAAGTT                                     306

```

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid

137

- (C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35

ATGTTTAAAA AAATCATTTT TTGTGCGTT TTTTGTATAG GGGGATTGT CATTCCACCC	60
CTTGAAGCCA TGCCTATTTT GCGCAATAAA ACCCCCAAAA AAAATTACCA AGAAGCCCAT	120
GAAAAGCTCT ATAGAAGCAT CATTACCGC CAAAASSTCA CGCGTAAAAA AAGCGGGTGG	180
TATTTTTTAG GGGGGGTTGG CGCTGTAGAA GCCATTAAGG ACTATCAAGG CAAGGAAATG	240
AAAGATTGGA TGCCACGCTC AATT	264

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 384 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36

GTGCATTTTA CGTGATCTT TCTAACCTA TTAAATGGA TTTTGCCAGC CAAAAACAAG	60
CAGGCGTGCA AAAAGCCAC CAACCAGATC CATTCAAGGY YTGCAAAACA TCCAGCAAAA	120
TATCCCCCT CAAGTATTAA CCCCTCAATC CAAGCGGGTA TACAAGGGT GATGCAAGGT	180
TTTGGGGCTT TGAGCAGCAY YTTAGAAGYC CCCYTATTTG TTTTYAAGC AAAATGTGGG	240
TGGATTGGGG GCTTTGAGCA TTATTATCC CCTTTATATG GGTGGGGCAA GATTCACGAT	300
GGTGCGCATT GCGATTTGAT GCAAAAAGAC GCCAATGGAA GGGGTATCGG CTTGGAAAAA	360
GGTCTTCCAC CTTTCAAGGG GCTG	384

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

138

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...324
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37

ATGCAGAACT	TTTTCTCTCG	TTTAGAAGG	TGGGCGTTGC	CCTTTTATTT	TGTGAGCGCT	60
TTAGCAGCGA	TTGATATTGA	TGAAGTAACA	GAAGCTCAAG	CTAATAGCAT	TAAATTAAGC	120
GATCAGTTAG	TGAGCCTGAG	CGATAAGCTT	TTAGAAAAAG	CGGTGGATAG	GGGGCGCAAT	180
ACCGATCACT	TAAAGATCT	TAACGATTTC	CATGAAAAAA	TCAAACATTT	GCGCTTGATT	240
TTAGAGCCTA	AGCCTAAGGG	CAAAGAAGAT	AGTCCTAACT	TGGGAGGTAA	TAAGGATATG	300
AAAACGGTTG	AAATCGGAAG	CGGT				324

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...354
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38

GTGATTTTAG	CGTTCGCCTT	TGGCATGAGT	CTTCTTGGAT	TAGCGGGCAT	GTTTCATTGAT	60
ATTCTTTTTT	TATCCACAGG	CGTTCATATC	CCTAGAAAAG	AGGATATTTT	ATGGATTTCT	120
TTAATAGGGA	TTAGCGGGAC	TTTAGGGCAG	TATTTCTTAA	CCTATGCTTA	CATGAACGCT	180
CCTGCTGGGA	TCATCGCCCC	CATTGAATAC	ACCGCATTG	TTTGGGGGCT	ATTGTTTGGG	240
CTGTATTTAG	GCGATACATT	TTTGGATCTT	AAAAGCTCTT	TAGGGGTGGC	TTTGATCTTA	300
TGTTCAGGCT	TGCTCATTGC	CTTGCCCGCT	CTTTTAAAAG	AATTAAAAAA	AATT	354

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 162 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

139

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39

ATGATCTATT TAGGGAAGAA AAATTTTAAC GCCCTTTTGA AAGGGGCGTA TTTAATGGAT	60
GAGCATTTTA GAAACGCCCC TTTTGAAAGC AATTTACCCG TTTTAATGGG ATTAATCTGG	120
CGTGTGCTAT ATCTAACTTT TTTTCCAATC CAAAAGCCA CT	162

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 864 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40

ATGGCCGCCA AATCCAAAGC GYAAACGCTT AAAGTCTTTT CAAAATTTTT CAGCAATTC	60
AAAATCACTA AACTCAAAGA CAACCACGAA GAAGCCCACA AACTTTTTGG AGAAAATAGC	120
CGTAAAGCCC ATGACACTGA GATCATTTAC TCCACTTTGC AAGTGGTCCC CAGGTATTCA	180
ATAGAAACCG TGGGCTTTAG TTTGTTGATT TTAGCGGTCG CTTACATCTT ATTCAAATAC	240
GGCGAAGCTA GAATGGTACT CCCTACCATT TCTATGTATG CCCTAGCGCT TTATCGCATA	300
CTCCCTTCTG TAACTGGAGT GATCAGCTAT TATAATGAAA TCGCTTACAA CCAGCTTGCA	360
ACCAATGTTG TTTTAAAAG CCTTTCTAAG ACCATCGTTG AAGAGGATTT AGTCCCTTTA	420
GACTTTAATG AAAAAATCAC TCTCCAAAAC ATTTCATTCT CTTATAAGTC AAAACACCCG	480
GTTTTAAAAA ATTTCAACCT CACCATTCAA AAAGGTCAAA AAATCGCTCT CATAGGCCAT	540
AGCGGGTGCG GAAAATCCAC GCTGGCGGAT ATTATTATGG GGCTTACCTA CCCTAAAAGT	600
GGGGAAATTT TTATTGATAA CACCTTTTA ACCAGCGAAA ACAGGCGCTC ATGGCGTAAA	660
AAAATAGGCT ATATCCCCCA AAATATTTAC CTTTTTGATG GCACTGTGGG GGATAATATC	720
GCTTTTGGGA GTGCTATAGA TGAAAAACGC TTGATTAAGG TGTGCAAAAT GGCTCATATC	780
TATGATTTTT TATGCGAGCA TGAGGCGCTT AAAACCCAAG TGGCGGAAGG GGCCTAAGC	840
TTAGCGGCGG TCAAAAACAG CGCA	864

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

140

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...576
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41

ATGCTTGATA	TATGGATAGA	TATGATAATC	TGTATTTTTT	ATTGCTCTTT	TTTTACGACT	60
CCTTACATTG	TAGGCGATAT	TTTGCAATTG	AAATTTATCC	GTCAAAAAC	CTGCGAGAAG	120
CCTGTTTTAC	TCCCACAAAA	GGATTATGAA	GAAGCGGAA	ATTATGCTAT	TAGGAAAATG	180
CAATTATCCA	TTATTTCTCA	AATTTTAGAT	GGGTGATCT	TTGCTGGTTG	GGTCTTTTTT	240
GGTTTGACGC	ATTTAGAAGA	TCTCACGCAT	TATTTAAACC	TTCTGAAAC	GCTAGGTTAC	300
TTGGTGTTTG	CCTTGTTGTT	TTTAGCGATT	CAAAGCGTTT	TAGCTTTACC	CATTAGCTAC	360
TATACTACCA	TGCATTTGGA	TAAGGAATTT	GGCTTTTCTA	AGGTGAGTTT	ATCGTTGTTT	420
TTTAAGGATT	TTTTCAAAGG	ATTATTGCTC	ACTTTAGGCG	TGGGGTTGTT	GTTGATTTAC	480
ACTCTCATAA	TGATCATTTA	ACATGTGGAG	CATTGGGAGA	TCAGCTCGTT	TTTTGTCTGT	540
TTTGTTTTCA	TGATTTTGGC	TAATCTTTTT	TTACCC			576

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 504 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42

ATGCTAAAAA	AAATATTTTT	AACCAACAGC	TTAGGGATT	TATGCTCTAG	GATTTTTTGGC	60
TTTTTACGGG	ATTTAATGAT	GGCCAATATC	CTAGGGGCTG	GGGTGTATAG	CGATATTTTC	120
TTTGTTGGCT	TCAAATTGCC	TAATCTATTC	AGGCGTATTT	TTGCGGAGGG	CTCTTTTTCT	180
CAAAGCTTTT	TACCGAGCTT	CATACGGAAT	TCCATTAAAG	GGGGTTTTGC	GAGTTTGGTG	240
GGGCTTATTT	TTTGTTGGCG	TTTATTCATG	TGGTGCTTAT	TAGTAGCGCT	CAATCCCTTA	300
TGGCTAACCA	AACTCCTAGC	TTACGGCTTT	GATGAAGAAA	CGCTCAAACT	ATGCACCCCT	360
ATTGTAGCGA	TCAATTTTTG	GTATCTTTTA	TTGGTGTTTA	TCACCACTTT	TTTAGGCGCG	420
CTTTTACAAT	ACAAACACAG	CTTTTTTGCC	GCGCTTATGC	GCAAGCTTAC	TCAATTTATG	480
CATGATTTTA	GCCCTTTTGA	TTTC				504

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 459 base pairs

141

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43

ATGAATTTAG AAGTGGCTCT AAAGGCGTTT GAAACGCTAT TGCCATGCAA TAAACAAGAA	60
GTTTTAAAAA ACCTAAAGCC CTTAGATTTA ATCGGCCGTT GCGAGCTTTT AAGCCCTAAC	120
ATTTTAATAG ATGTGGGGCA TAACCCCAT AGCGCTAAAG CCTTAAAAGA AGAAATCAAA	180
CGCATCTTTA ACGCTCCAAT CGTTTTGATT TATAATTGCT ATCAAGATAA AGACGCTTTT	240
TTGGTGCTAG AAATTTTAAA GTCTGTGGTT AAAAAGGTTT TGATTTTGA ATTGCATAAT	300
GAAAGAATTA TCCAATTAGA AAAACTTAAA GGGATTTTAG AAACTTTAGG GTTAGAACAC	360
GCCTTGTTTG AAGAACTGAA AGAAAATGAA AATTATTTGG TGTATGGCTC ATTTCTGGTA	420
GCCAACGCTT TTTATGAACG CTATCCAAG AAGAGGGAT	459

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44

ATGGCTATCG GGTTCCTT AGTGTTGGG ATTTACTCA CCCTTTT TAG CCGTTCTTAT	60
TGCGTGAGT TTGGGGGCGT TTCAGGGTA TTATGGAGG CTAGTGGATT TAGTGGGGCA	120
AAGGTTGAGC GAAATTTGGA GCGCGATCCC CATGCTTTT TTA CTATTG TGATTTT	177

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

142

- (ii) MOLECULE TYPE: DNA (genomic).
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45

ATGAAGAAAA	AAGCAAAAGT	CTTTGGTGT	TGTTTTAAAA	TGATTCGTG	GTTGTATTTG	60
GCGGTCITTT	TTTTGTGAG	CGTATCAGAC	GCTAAAGAAA	TCGCTATGCA	ACGATTTGAC	120
AAACAAAACC	ATAAGATTTT	TGAAATCCTT	GCGGATAAAG	TGAGCGCCAA	AGACAATGTG	180
ATAACCGCCT	CAGGGAATGC	GATCCTATTG	AATTATGACG	TGTATATTCT	AGCGGRTAAG	240
GTGCGTTATG	ACACCAAGAC	TAAAGAAGCG	TTATTAGAAG	GCAATATTAA	GGTTTATAGG	300
GGCGAGGGCT	TGCTCGTTAA	AACCGATTAT	GTGAAATTGA	GTTTGAACGA	AAAATATGAG	360
ATCATTTTCC	CCTTTATGT	CCAAGACAGC	GTGAGCGGGA	TTTGGGTGAG	CGCGGATATT	420
GCTAGCGGGA	AGGATCAAAA	ATATAAGATT	AAAAACATGA	GCGCTTCAGG	GTGCAGCATT	480
GACAACCCCA	TTTGGCATGT	CAATGCGACT	TCAGGCTCAT	TTAACATGCA	AAAATCGCAT	540
TTGTCAATGT	GGAATCCTAA	GATTTATGTC	GCGGATATTC	CTGTATTGTA	TTTGCCCTAT	600
ATTTTCATGT	CCACGAGCAA	TAAAAGAACT	ACCGGGTTTT	TATACCCTGA	GTTTGGCACT	660
TCCMAC						666

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46

ATGCTGGATT	TTGATTTGGT	TCTTTTGGC	GCGACTGGG	ATTTAGCCAT	GCGAAAGCTC	60
TTTGTTCGC	TTTATGAAAT	TTATATTTCA	TTTATGGTTT	TAAAAACGAT	TCTAGGATTA	120
TCGCATCGG	GCGTAAGGAG	CTATCCAATG	AAGAGTTTT			159

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

143

- (ii) MOLECULE TYPE: DNA (genomic).
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47

ATGCAAGATT TACCCCATG CCCTAAACGC AACGACGCCT ACACCTACCA TGATGGCACG	60
CAGTTCGTTT GCTCTAGCTG TTTGTATGAA TGAATGGAA ATGAAATTAG TAATGAAGAA	120
TTGATCGTTA AAGATGGCCA TAATAATCTT TTACAAAATG GGGACTCGGT CATTCTCATT	180
AAAGATTTAA AGGTAAAGG CTCATCTTTG GTGCTTAAAA AAGGCACTAA AATCAAAAAT	240
ATCAAGCTTG TCAATAGCGA TCACAATGTG GATTGTAAAG TGAAGGGCA GAGCTTGTCT	300
TTAAAATCTG AATTCCTTAA AAAAGCT	327

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48

GTGGATGGGG CTATCATAAC AGGGAATTAT GCCTTGCAAG CAAAACTCAC CGGAGCCTTA	60
TTTTCAGAAG ATAAGGACTC GCCTTATGCT AATCTTGTAG CCTCTCGTGA GGATAATGCG	120
CAAGATGAAG CGATAAAGC GTTGATTGAA GCCTTACAGA GCGAAAAGAC CAGGAAATTC	180
ATTTTGGATA CCTATAAGGG GGCGATTATC CCGGCTTTT	219

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 711 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

144

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49

GTGTTTYCCA	TGCTGGTGTT	GGTGTGAGC	GATAATTTT	TAGGGCTTTT	CATTGGCTGG	60
GAAGGGGTGG	GGCTATGCTC	TTACTTGCTC	ATTGGCTTTT	GGTATCATAA	AAAAAGCGCG	120
AATAACGCTT	CTATTGAAGC	CTTTGTGATG	AATCGAATCA	CGGATTTAGG	CATGCTCATG	180
GGGATTATTT	TGATCTTTTG	GAATTTTGGC	ACCCTCCAGT	ATAAAGAAGT	CTTTAGCATG	240
CTCAATAACG	CCGATTATTC	CATGCTCTTT	TACATTAGCG	TGTTTCTTTT	TATTGGCGCT	300
ATGGGGAAGA	GTGCTCAATT	CCCTATGCAC	ACATGGTTAG	CCAACGCTAT	GGAGGGGCCT	360
ACCCCTGTAT	CCGCTCTCAT	CCATGCARCG	ACGATGGTAA	CCGCTGGGGT	GTATCTAATC	420
ATCAGAGCCA	ATCCTTTGTA	TAGTGCGGTG	TTTGAAGTGG	GTTATTTTAT	CGCATGCTTA	480
GGAGCGTTTG	TGGCTCTTTT	TGGAGCGAGC	ATGGCTTTAG	TCAATAAGGA	TTTAAACGC	540
ATCGTGGSYT	ATTCCACGCT	TTCTCAATTA	GGGCTATATG	TTTGTAGCGG	CCGGGCTTGG	600
GGCTTATGCG	ATCGCGCTTT	TCCACCTCTT	TACGCATGCG	TTCTTCAAT	CCCTCCTTTT	660
CTTAGGCTCA	GGCAATGTCA	TGCATGCGAT	GGAAGACAAT	CTGGATATTA	C	711

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50

ATGATGATAA	CCAAACAATC	GTATCAAAGA	TTGCTTTTAA	TGCGGGTTTT	TGTGTTTTTCG	60
CTTTCGGCGT	TTATTTTAA	CACCACGGAG	TTTGTCCTTG	TTGCACTTCT	GTCAGACATT	120
GCGAAAAGCT	TTGAAATGGA	GAGCGCAACA	GTGGGGCTTA	TGATCACTGC	TTATGCATGG	180
GTGGTGTCTC	TTGGCTCATT	GCCCTTGATG	CTGCTTAGCG	CTAAATTTGA	AAGGAAACGC	240
TTATTGCTTT	TTCTTTTCGC	TCCTTTTATT	TTTCAAGCATA	TCCTTTTCGC	T	291

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 840 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

145

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51

ATGAACTGA	GAGCAAGTGT	TTTAATCGGT	GTGGCAATTC	TGTGCTTAAT	TTTAAGTGGC	60
TGCAGTAACT	ATGCGAAAAA	AGTGGTGAAA	CAAAAGAACC	ATGTTTATAC	GCCTGTGTAT	120
AATGAAGTGA	TAGAGAAGTA	TAGTGAGATC	CCCTTAAATG	ACAAACTCAA	AGACACACCA	180
TTCATGGTGC	AAGTGAAGTT	GCCAAATTAC	AAGGACTATT	TGTTGGATAA	TAAACAAGTT	240
GTACTAACTT	TCAAACTTGT	TCACCATTCT	AAAAAGATTA	CGCTCATAGG	CGATGCCAAT	300
AAGATCCTCC	AATACAAGAA	TTACTTCCAA	GCTAACGGGG	CAAGATCTGA	CATTGATTTT	360
TACTTGCAAC	CCACTTTGAA	TCAAAAGGGT	GTGGTGATGA	TAGCGAGTAA	CTACAATGAT	420
AATCCCAACA	ACAAAGAAAA	ACCACAGACC	TTTGATGTGT	TGCAAGGAAG	TCAGCCAATG	480
CTAGGAGCTA	ACACAAAAAA	CTTGCAATGGC	TATGATGTGA	GTGGAGCAAA	CAACAAGCAA	540
GTGATCAATG	AAGTGGCAAG	AGAAAAAGCT	CAGCTAGAAA	AAATCAATCA	GTATTACAAG	600
ACTCTCTTGC	AAGACAAGGA	ACAAGAATAT	ACCACTAGGA	AAAATAACCA	ACGAGAAATT	660
TTAGAAACAT	TGAGTAATCG	TGCAGGTTAT	CAAATGAGGC	AGAATGTGAT	TAGTTCTGAG	720
ATTTTAAAGA	ATGGCAACTT	GAACATGCAA	GCCAAAGAAG	AAGAAGTTAG	GGAGAAGCTA	780
CAAGAAGAAA	GAGAGAATGA	ATACTTGCGC	AATCAAATCA	GAAGTTTGCT	CAGTGGAAG	840

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52

ATGTGGTTAG	ATCACATCGC	TAAAGAGATC	AGAAGTTTAG	TGGAACACGA	TATTGAAGTG	60
GGTATTGTGA	TTGGTGGAGG	CAATATCATT	AGGGGGGTTA	GCGCGGCTCT	AGGGGGGATC	120
ATTAGGCGCA	CCAGTGGGGA	TTATATGGGC	ATGTTAGCCA	CCGTGATTAW	GCGG	174

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

SUBSTITUTE SHEET (RULE 26)

146

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...372
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53

GTGCATAACT	TCCATTGGAA	TGTGAAAGGC	ACCGATTTTT	TCAATGTGCA	TAAAGCCACT	60
GAAGAAATTT	ATGAAGGGTT	TGCGGACATG	TTTGATGATC	TCGCTGAAAG	GATCGTTCAA	120
TTAGGACACC	ACCCCTAGT	CACTTTATCC	GAAGCGATCA	AACTCACTCG	TGTTAAAGAA	180
GAAACTAAAA	CGAGCTTCCA	CTCTAAAGAC	ATCTTTAAAG	AAATTCTAGA	GGACTACAAA	240
CACCTAGAAA	AAGAATTTAA	AGAGCTCTCT	AACACCGCCG	AAAAAGAAGG	CGATAAAGTT	300
ACCGTAACTT	ATGCGGACGA	TCAATTAGCC	AAGTTGCAAA	AATCCATTTG	GATGCTAGAA	360
GCCCATTTAG	CT					372

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...270
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54

ATGAATAAAA	CCATAAAAGC	CGCCGCCCTA	GCCTATAACA	TGGGGCAAGA	TCATGCCCCA	60
AAAGTGATCG	CAAGCGGGGT	GGCGGAAGTG	GCTAAAAGGA	TCATTCAAAA	AGCTAAGGAA	120
TACGATATAG	CGCTCTTTTC	TAACCCCATG	CTGGTGGATT	CGCTCTTAAA	GGTGGGAATTA	180
GACTGCCGCA	TACCTGAAGA	ATTGTATGAA	AGCGTGGTGC	AAGTGTTTTT	ATGGCTCAAC	240
AGCGTGGAAG	ATAACGCGCA	AATGTCCAAG				270

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 633 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

147

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55

ATGGGGAAAA	TTTCAGCGCA	TTTAGCCCAT	GAAATCAGAA	ACCCCGTAGG	CTCTATCTCT	60
CTTTTAGCTT	CGGTGTTATT	AAAGCATGCG	AACGAAAAAA	CTAAACCCAT	TGTTGTAGAA	120
TTGCAAAAAG	CTTTATGGCG	CGTAGAAAGG	ATCATTAAG	CCACCTTGCT	TTTTTCTAAA	180
GGCATTCAAG	CCAACGCAC	CAAGCAAAGT	TTGAAAACGC	TAGAGAGCGA	TCTCAAAGAA	240
GCCCTAAACT	GCTACACTTA	CTCTAAAGAC	ATTGATTTTC	TTTTTAATTT	TAGCGATGAA	300
GAAGGGTTTT	TTGACTTTGA	TTTAATGGGG	ATTGTGTTAC	AAAATTTCTT	GTATAACGCC	360
ATTGATGCGA	TTGAAGCCTT	AGAAGAGAGC	GAACAAGGTC	AGGTCAAAAT	TGAAGCGTTC	420
ATTCAAAATG	AATTTATTGT	CTTCACCATT	ATTGATAATG	GCAAGGAAGT	GGAAAATAAA	480
AGCGCTTTAT	TTGAGCCTTT	TGAAACCACT	AAATTAAAGG	GGAATGGCTT	AGGGTTAGCC	540
CTGTCTTTGC	AAGTCGTAA	AGCCCATGAA	GGGAGCATTG	CGCTATTAGA	AAATCAAGAA	600
AAAACCTTTG	AAATTAAGAT	TCTTAACGCT	TCT			633

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 636 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56

GTGTCAGAAT	TTATCAAGT	TTATGACCCT	TTGGGTAATA	TTTGGCTGAG	CGCTCTTGTC	60
GCCTTATTGC	CGATTTTGTT	ATTTTCTTA	TCTTTAATGG	TTTTTAAACT	CAAAGGTTAT	120
ACAGCGGCCT	TTTGTAGCGT	GGCCTTATCA	GCCATTATTG	CGGTTTGTAGT	GTATAAAATG	180
CCTGTAGCA	TGGTGGGTTT	AAGCTTCCTT	TATGGCTTTC	TTTATGGCCT	ATGGCTATTTC	240
GCTTGGATCA	TTATTGCCGC	GATTTTTTTA	TACAACTCA	GCGTTAAATC	CGGCTATTTT	300
GAAATCTTAA	AAGAAAGCGT	TCAGTCCATC	ACTTTAGATC	ACCGCATTTT	AGTGATTTTG	360
ATTGGCTTTT	GTTTTGGCTC	ATTTTATAGAA	GGGGCGATCG	GCTTTGGAGG	GCCTATTGCC	420
ATCACAGCGG	CGATTTTAGT	GGGGTTGGGG	TTAAGCCCTT	TGTATTCTGC	TGGGTTATGT	480
TTGATCGCTA	ACACCGCTCC	TGTGGCCTTT	GGCGCGGTGG	GTATCCCTAT	AAGCGCGATG	540
GCGAGCGCGG	TAGGGGTGCC	AGCGATCTTA	ATTTACGCCA	TGACGGGTAA	AATCCTCTTT	600
TTTGTGAGCT	TGTTAGTGCC	GTTTTTTATT	GTGTTT			636

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 546 base pairs

(B) TYPE: nucleic acid

148

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57

ATGGAAATTA AAATGGCTAA GGATTATGGT TTTTGTITTTG GCGTCAAAAG AGCGATACAA	60
ATCGCTGAAA AAAATCAAAA CAGCTTGATT TTTGGCTCGC TCATTCATAA CGCTAAAGAA	120
ATCAATCGTT TGGAAAAAAA TTTCAATGTG AAAATTGAAG AAGATCCTAA AAAAATCCCT	180
AAAAATAAGA GCGTGATCAT AAGAACCCAT GGCATTCTTA AACAGGATTT AGAATACTTG	240
AAAAATAAGG GGGTTAAAAT CACTGACGCG ACTTGCCCGT ATGTGATCAA ACCTCAGCAA	300
ATTGTGGAAT CCATGAGTAA AGAAGGGTAT CAAATCGTGC TTTTGGGGA CATTAAACCAC	360
CCTGAAGTCA AGGGCGTGAT CAGCTATGCC ACTAACCAGG CTTTAGTCGG CAATTCGTTA	420
GAAGAATTGC AAGAAAAAAA ATTGCAACGG AAAGTGGCTT TAGTCTCTCA AACCACCCAA	480
GCAAACCCCA AAACCTCTTGC AAATCGCTTC TTATTGGTG GARGRTGCAC TGAAGTGCCT	540
ATTTTT	546

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 672 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58

ATGGATCATG AGTTTTTGAT TACCATGCGT TTGAGCTTTT CTTTAGCTTT GATTACCACC	60
CTTATTTTAC TCCCTATAGG GATTTTTTTA GGCTATTTT TAAGCCTTAA ACGCAATCTT	120
TTAACGAGCT TAACAGAAAC GCTTGTGTAT ATGCCTTTAG TTTTACCCCC AAGCGTGCTA	180
GGGTTTTATC TTCTTTTAAT CTTTTGCGCT TCTTCTTTTT TGGGAGCGTT TTTACAAGAT	240
GTGTTAAATG TGAAACTCGT TTTTAGTTTC CAAGGGCTTA TCTTAGGGAG CGTGATTTTT	300
TCCTTGCCCT TTATGGTAAG CCCTATTAAA AGCGCGTTAA TTTCCCTTGC CACTTCTTTA	360
AAAGAAGCCA GTTATAGCTT GGGTAAAGGG GAATACTACA CCCTTTTTTT TGTCTACTC	420
CCTAACATCA AACCAGTGT GTTGATGGCT ATCATTACAA CTTTATGCA CACTATAGGT	480
GAATTTGGCG TGGTGATGAT GCTTGGGGGT GATATATTAG GGGAAACAAG AGTGGCTAGC	540
ATTACGATCT TTAACGAAGC TGAAGCACTC AATTATTCTA AAGCCCATCA ATACGCCTTA	600
ACGCTCACGC TTATTAGTTT TAGCCTCTTG TTTGTTACCC TATTTTTTAA TAAAAACAA	660
AGCTCGTTTT TA	672

SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59

ATGCATCCTA TAATGTTTGC CTATATCGCT AACGCGCTCG CTCAAGCTAG AAAGATCAAC	60
GGAACACTTT GCATGGCGTT TCAAAAAATA TCTCAAGTCA AAGAATTAGG CATTGATAAA	120
GCAAAGAGTT TGATAGGCAA CCTTCTCAA GTGATTATCT ACCCCACAAA AGATACTGAT	180
GAATTAATAG AATGTGGCGT CCCATTAAGC GATAGTGAAA TCAATTTCTT ACACAACACG	240
GACATGAGAG CCAGACAAGT GCTAGTAAAA AATATCGTTA CAAACGCTTC AGCTTTTATT	300
GAAATTGATT TAAAAAGAT TTGCAAGAAC TACTTTATAT TCTTGATAGC AATGCTGGTA	360
ATAGAAAAAT CCTCAATGAT CTTAAAAAAG CAAACCAAGA AACTTATAAG GAAGAGTATT	420

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60

ATGTGCCTGA CAGCGGGCTT GATGCGTTGG CTCAAATCGG TAAAGCCTGA ACGAATCTTG	60
CATTCTGTGG TGCAATTTGT GGATATTGCC GGATTGATTA AGGGGGCGAG CAAGGGGGAG	120
GGTTTAGGCA ATCAGTTTTT AGCCAATATC AAGGAATGCG AACTGATCTT GCAAGTGGTG	180
CGCTGTTTTG AAGATGACAA TYATCACGCA TGTGAACGA	219

(2) INFORMATION FOR SEQ ID NO:61:

150

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61

ATGCATGTTG CTTGCTTTTT GGCTTTAGGG GATAACCTCA TCACGCTTAG CCTTTTAAAA	60
GAAATCGCTT CCAAACAGCA ACAGTCCCTT AAAATCCTAG GCACTCATTT GACTTTAAAA	120
ATCGCCAAGC TTTTAGAATG CGAAAAACAT TTGAAATCA TTCCTGTTTT TGAAAATATC	180
CCTGCTTTTT ATGACCTTAA AAAACAAGGC GTTTTTGGG CGATGAAGGA TTTTATATGG	240
TTATTAAAGC AATTAAAAA CATCAATCA AACGTT	276

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62

ATGAAAAAGA AGCCATTGAT GTGGCGTATC TGTGCGTTAA GGAGACTTCT TCTAGGGTTC	60
AAGAGAGAGA GAGAGTTATT AAGCTTCGCT AAACATTGGA ATATCCCAAC GATGTGCGTT	120
TTACACACA CTCAAGCCGA AGCCGGCGAT GCGTTTGTC AAGAACTAA AGGGATCATA	180
GACGAAGAAT GGGGGTTTAA AGGTTTTGTC AGAGCCTATG TGAGGGTCAA TTCCGTTGCC	240
TTTTCATTTA GGGGGTTGAA AGTCCCTGTT GAAGGTTTAG AAGAATTGGT AGATGAAACG	300
AAAAATGCC TTTCAGACGC TGAAAAAAT AAGAAAAGGC ATTTCTTGAG TATTCAAAGA	360
GTTAAGATTC AAGAAAGAAA ACAGGCTATG ATAGAGGAAT GTAAAACCAT TATCCATGTT	420
GCATCAGGCG CTGCAGGAGT TGCTGGGCTT ATCCCCATAC CTTTTCAGCA TCGGCTCGCT	480
ATCGCACCCA TTCAAGCAGG GATGATCTAT AAAATGAATG ACGCTTTTGG AATGGATTG	540
GATAAATCTG TGGCGCGAG TTTGGTCGCA GGATTGTTAG GCGTAAACTG TCGCGCAAGT	600
GGGGAGGACT CTCGT	615

(2) INFORMATION FOR SEQ ID NO:63:

151

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63

GTGCTTGGCG	TGTTAAATTT	AAGGGGCAAT	GTCTTCCCTT	TGATCAGTTT	GCGTTTAAAG	60
TTTGGCTTGA	AAGCCGAAAA	ACAAAACAAA	GACACTCGTT	ATTGGTGGT	ACGCCATAAC	120
GAT						123

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64

GTGAAAAGCG	TTTTTAGCGA	AGAAAAAGAA	ACGCCTGTTA	CTAAAGAAAA	CGGCTCTTAT	60
TTGATCGCTT	ATGACCCCTT	AGATGGGAGT	TCAGTGATGG	AGGCGAATTT	CTTAGTAGGC	120
ACGATTATAG	GGGTTTATGA	AAAGGATTAT	AAGCGCAGAA	ATTTAGTTGC	AAGCCTTTAT	180
GTGGTTTTTG	GGCATAAAAT	AGAATTGGTG	GTGGCTTTAG	AAGAAGTTTA	TCGTTACGCT	240
TTTTATCAAA	ACAAGTTTCA	TTTTATAGAA	ACCATCGTTT	TAGAAAATAA	GGGTAAATC	300
ATCGCTAGCG	GAGGCAATCA	AAAGGATTTT	TCYTTGGGCT	TAAAAAAGGC	TTTAGAAGGG	360
TTTTTTGCAG	AAAATTACCG	CTTGCGATAC	TCAGGATCTA	TGGTGGCTGA	TGTCCATCAT	420
GTGTGGTTA	AAAAGGGCGG	AATGTTTTC	TACCCGCAAA	AGAAATTGCG	AAAGCTTTTT	480
GAAGTCTTTC	CTTTAGCCTT	GATGGTTGAA	AAAGCTAAAG	GGGAAGCGTT	TTATTTTGAT	540
AAGGGGGTTA	AAAAGCGTTT	GCTAGATCAA	AGCGTAGAAA	GCTACCATGA	AAAAAGCGAA	600
TGCTATTTAG	CCAGCCCGCA	TGAAGCTCAG	ATTTTAGAAA	AACATTTTAA	GGGAGAA	657

(2) INFORMATION FOR SEQ ID NO:65:

152

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 564 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...564
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65

ATGAAAAGCA TTGGAGAAGT GATGGCGATA GGGGGCAATT TCTTAGAAGC CTTACAAAAA	60
GCGTTATGCT CTTTGGAAAA CAATTGGCTA GGGTTTGAAT CGTTAAGCAA AGATTTAGAG	120
GCGATAAAAA AGGAAATCCG CCGGCCCAAT CCCAAACGCT TGCTCTATAT TGCTGATGCG	180
TTCAGGTTGG GCGTTTCTGT GGATGAAGTG TTTGAATTAT GCCAGATTGA CAGGTGGTTT	240
TTATCTCAA TTCAAAAACT AGTCAAAGCA GAAGAGGGCA TCAATTCTAG CGTTTTAACG	300
GACGCCAAAA AATTGAGAGG GCTTAAAAAT TTAGGCTTTA GCGATGCCAG GATTGCCACT	360
AAAATCAAAG AAAATGAAAA TTTAGAGGTC AGCCCTTTTG AAGTGGGAAT AGCTAGATCT	420
AATTTACAAA TCGCGCCCCA TTTTGAAGAA GTGACACTT GCGCGGCGGA GTTTTTATCG	480
CTCAGCCTTA TTTGTATTCC ACCTATGCCC CTAACCCTTT GCCCCTATT GGAAACAAAC	540
AAGAAAAACA AGAAAAGAAA ATCC	564

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 693 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...693
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66

ATGTTTGGGA ATAAGCAGTT ACAGCTTCAA ATCAGTCAAA AAGATTCTGA GATTGCGGAG	60
TTAAAAAAG AAGTCAATCT CTATCAAAGC CTTTTAAATT TGTGCTTGCA TGAGGGTTTT	120
GTAGGTATTA AAAACAATAA AGTCGTTTTT AAAAGCGGGA ATCTTGCAAG CTTAAACAAT	180
TTAGAAGAAC AAAGCGTTCA TTTTAAAGAA AACGCAGAAA GCGTTAATTT ACAAGGGGTT	240
TCTTATTCTT TGAAAAGCCA AAATATTGAC GCGGTGCAGT ATTTTTCATT GGCTAAAAAA	300
ACAGGGGGTG TGGGGGAATA CCATAAAAT GATTTGTTTA AGACTTTTGT CACGAGCTTA	360
AAAGAGGGCT TAGAGAACGC GCAAGAAAGC ATGCAGTATT TCCATCAAGA AACAGGCTTG	420
CTCTTGAATG CCGCTAAAAA TGGCGAAGAG CATTCTAATG AAGGATTAAT AACCGTTAAT	480
AAAACGGGTC AAGACATTGA ATCGCTTTAT GAAAAGATGC AAAACGCCAC TTCGTTAGCG	540

153

GACTCCCTCA ACCAACGGAG CAATGAAATC ACTCAAGTCA TTTCTTTGAT TGATGATATT	600
GCAGAGCAAA CCAATCTCTT AGCCCTAAAC GCCGCTATTG AGGCCGCACG AGCGGTGAAC	660
ATGGCAGAGG GTTTCGGTG GTGGCTGATG AGG	693

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67

ATGTGGATTA TGTCTTCACT TTCTAGTTCA TTCTTTCATT CGCTCTTCTT CATCAAATCA	60
AACCCTGGCC AACTCTTAAA AGGTTGGGGT TCAAAAATCT TTTTCATAAA TAGAAAGTTT	120
GTTTTAGCAC AGTATAATCC TAGCGTTTCA ATTTTATTTT TACTCAATAG GGTGTTTGTT	180
GTTCGCGTT	189

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68

GTGGGCGCTA ACCCTGTGCC GCATGCGCAA ATCTTGCAAT CAGTTGTGGA TGATTTGAAA	60
GAGAAAGGGA TCAAATTAGT GATCGTGTCT TTTACGGATT ATGTGTTGCC TAATTTAGCG	120
CTCAATGACG GCTCTTTAGA CGCGAATTAC TTCCAGCACC GCCCTTATTT GGATCGGTTT	180
AATTTGGACA GAAAAATGCA CCTTGTGGT TTGGCCAATA TCCATGTGGA GCCTTTAAGA	240
TTTTATTCTC AAAAAATCAC AGACATTAAA AACCTTAAAA AAGGCTCAGT GATTGCTGTG	300
CCAAATGATC CGGCCAATCA AGGCAGGGCG TTGATTTTAC TCCATAAACA AGGCCTTATC	360
GCTCTCAAAG ACCCAAGCAA TCTATACGCT ACGGAGTTTG ATATTGTCAA AAATCCTTAC	420
AACATCAAAA TCAAACCCCT AGAAGCTGCG GTTATTGCC	459

SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69

ATGGGGCTTG TTGCGAGCGG CATTACGAT GAAGAGCTTT TAAAATGGCT TCAGGCTTTT	60
GGGTAAAAA TGGGTCTTTG TTTTCAAGTG CTAGATGATA TTATAGACGT TACACAAGAT	120
GAAAAAGAAA GCGGTAAAC CACGCATTTA GACAGCGCTA AAAACAGCTT TGTGAATTTA	180
TTGGGGCTAA AAAAGGCAGC GGTACGCCC AAACCTT	216

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70

ATGGGGTTTA ACCGCTTGGT GGATAGAGAC ATTGATAAGG ATAACCCAAG GACGAAAAAC	60
CGCCCGAGCG TGGATGGTAG GATCAGCGTT AAAGGCATGG TCATTTTATG CGTTTCAAAC	120
GCTCTTTTGT TCGTGGGAGT GAGTTATTTT ATCAACCTT TAGCTTTCAA GCTTTCGTTA	180
CCTTTTTTAA TCATTTTAGG GGGTTATTCG TATTTCAAGC GCTTTTCTTC TTGGCGCAT	240
TTTGTCGTGG GTTTGGCTTT GGGTTTAGCC CCCATTGCAG GAAGCGTGGC GGTTTTAGGG	300
GATATTCCTT TATGGAATGT CTTTTTGGCY TTAGGGGTGA TGTGTGGGT GGCTGGGTTT	360
GATTTGCTCT ATTCTTTACA GGATATGGAG TTTGATAAAG AAAGGGGCTT GTTTTCCATT	420
CCTAGCCAAT TAGGGGAAAA ATGGTGCTTG AATCTTTCAA GGCTCTCGCA CCTTGTGGCA	480
CTGATCTGCT GGCTTTGTTT TGTGAAATGC TATCATGGGG GGCTTTTTCG GTATTTGGGC	540
TTAGGGGTTT CAGCCTTGAT CTTACTCTAT GAGCAGATTT TAGTGGCCAG AGATTATAAA	600
AACATTCCTA AAAGCCTTTT TTGTGAG	627

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71

GTGGAGCAAA ATAAAATCAT TAAACTCTTC ACTGTGGCGA CTATGGCGAT GATGCCCCC	60
ACATTGATTG GCACGATTWA TGGCATGAAT TTAAATTCA TGCCGGAGTT AGAATGGCAA	120
TACGGGTATC TTTTTCGCT GATTGTCATG GCGATTCTA CGATTTTGCC GGTGATTAT	180
TTCAAAAAGA AAGGGTTGGT TGTAGCCTTT CATGGAATTT TTATCCTCAC TCTTAGACGC	240
TCTTTCTACA CCGCATGGCA TAGTCTCCTT GGCTACGCCA CGCTT	285

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72

ATGTTTCGATT CAATCGTTTA TTTTTCAT AAGAGCGGGT TTGTTACCAC GCTTGTTTTA	60
GTTTGGATT CGCTTTATTT GGTGATGACT TTATGGGTCT TTTTGTATAA AAGCATTTGA	120
TTAAAGATTG AACTCAGGCG CGAGATGCAA TCTTTGTCTA ACATTCTTAA TGGAGCGCAA	180
GACGCTCCAG AGCATTTTAT GTTTAATAAA AAAAGAAATG ATGAGACCAA AAGGTATTCT	240
AATGAATTGT TGCAGGSCCTT GGAAACACCA GGTCTT	276

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

156

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73

ATGGCGATGC	TYTATTGCAT	GCGGTTATTG	ATGCCGATTT	TAGGAGCGAT	TAAAGGGGGG	60
GATATTGGCG	AATGGTTCCC	TGATAATGAC	CCCAAATACA	AAAACGCCTC	TTCTAAAGAG	120
CTTTTAAAAA	TCGTGTTGGA	TTTTTCTCAA	AGCATTGGGT	TTGAATTGCT	TGAAATGGGA	180
GCGACCATCT	TTAGCGAAAT	CCCTAAAATC	ACTCCTTACA	AACCGGCGAT	TTTAGAGAAT	240
TTGAGCCAAC	TTTTGGGTTT	AGAAAAATCT	CAAATCAGCT	TGAAAGCCAC	TACAATGGAA	300
AAAATGGGGT	TCATTGGCAA	ACAAGAAGGG	CTGTTAGTCC	AAGCGCATGT	GAGCATGCGT	360
TATAAACAAA	AACCTT					375

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...3534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74

ATGATACCAA	ATTTAGATAT	AGAAGGAGAA	ACAATGACTA	ACGAAGCCAT	TAACCAACAA	60
CCACAAACCG	AAGCGGCTTT	TAACCCGCAG	CAATTTATCA	ATAATCTTCA	AGTGGCTTTT	120
ATTAAAGTTG	ATAATGTTGT	CGCTTCATTT	GATCCTAATC	AAAAACCAAT	CGTTGATAAG	180
AATGATAGGG	ATAATAGGCA	AGCTTTTGAG	AAAATCTCGC	AGCTAAGGGA	GGAATTCGCT	240
AATAAAGCGA	TCAAAAATCC	TACCAAAAAG	AATCAGTATT	TTTCAAGCTT	TATCAGTAAG	300
AGCAATGATT	TAATCGACAA	AGACAATCTC	ATTGATACAG	GTTCTTCCAT	AAAGAGCTTT	360
CAGAAATTTG	GGACTCAGCG	TTACCAAATT	TTTATGAATT	GGGTGTCCCA	TCAAAACGAT	420
CCGTCTAAAA	TCAACACCCA	AAAAATCCGA	GGTTTTATGG	AAAATATCAT	ACAACCCCTT	480
ATCTCTGATG	ATAAAGAGAA	AGCGGAGTTT	TTGAGGTCTG	CCAAACAAGC	TTTTGCAGGA	540
ATTATCATAG	GAAACCAAAT	CCGATCGGAT	CAAAAAATCA	TGGGCGTGTT	TGATGAATCT	600
TTGAAAGAGA	GGCAAGAAGC	AGAAAAAAT	GGAGAGCCTA	ATGGAGATCC	TACTGGTGGG	660
GATTGGCTTG	ATATTTTTTT	ATCATTTGTG	TTTAACAAAA	AACAATCTTC	CGATCTCAAA	720
GAAACGCTCA	ATCAAGAACC	AGTTCCTCAT	GTCCAACCA	ATGTAGCCAC	TACCACCACT	780

SUBSTITUTE SHEET (RULE 26)

157

GACATACAAA	GCTTACCGCC	TGAAGCTAGG	GATTTGCTTG	ATGAAAGGGG	TAATTTTTCT	840
AAATTCACCTC	TTGGCGATAT	GAACATGTTA	GATGTTGAGG	GAGTCGCTGA	CATTGATCCT	900
AATTACAAGT	TCAACCAATT	ATTGATCCAC	AATAACGCTC	TGCTTCTGT	GTTAATGGGG	960
AGTCATAATG	GCATAGAACC	TGAAAAAGTT	TCATTGTTGT	ATGGAAACAA	TGGTGGTCCT	1020
GAAGCTAGGC	ATGATTGGAA	CGCCACCGTT	GGTTATAAAA	ACCAACGAGG	CGACAATGTG	1080
GCTACACTCA	TTAATGTGCA	TATGAAAAAT	GGCAGTGGGT	TAGTCATAGC	AGGTGGTGAG	1140
AAAGGGATTA	ACAACCCTAG	TTTTTATCTC	TACAAAGAAG	ACCAACTCAC	AGGCTCACAA	1200
CGAGCATTGA	GTCAAGAAGA	GATCCAAAAC	AAAGTGGATT	TCATGGAATT	TCTTGCACAA	1260
AATAATGCTA	AATTAGACAA	CTTGAGCAAG	AAAGAGAAAG	AAAAATTCCA	AAATGAGATT	1320
GAAGATTTTC	AAAAAGACTC	TAAGGCTTAT	TTAGACGCCC	TAGGGAATGA	TCACATTGCT	1380
TTTGTTTCTA	AAAAAGACAA	AAAACATTTA	GCTTTAGTTG	CTGAGTTTGG	TAATGGGGAA	1440
TTGAGCTACA	CTCTCAAAGA	TTATGGGAAA	AAAGCAGATA	AAGCTTTAGA	TAGGGAGGCA	1500
AAAACCACTC	TTCAAGGTAG	CCTAAAACAT	GATGGCGTGA	TGTTTGTGTA	TTATTCTAAT	1560
TTCAAAATACA	CCAACGCCCTC	CAAGAGTCCT	GATAAGGGTG	TGGGTGCTAC	GAATGGCGTT	1620
TCCCATTTAG	AAGCAGGCTT	TAGCAAGGTA	GCTGTCTTTA	ATTTGCCTAA	TTTAAATAAT	1680
CTCGCTATCA	CTAGTGTCTG	AAGGCAGGAT	TTAGAGGATA	AACATAATCGC	TAAAGGATTG	1740
TCCCCACAAG	AAGCTAATAA	GCTTGTCAAA	GATTTTTTGA	GCAGCAACAA	AGAATTGGTT	1800
GGAAAGCTT	TAAACTTCAA	TAAAGCTGTA	GCTGAAGCTA	AAAACACAGG	CAACTATGAC	1860
GAGGTGAAC	AAGCTCAGAA	AGATCTTGAA	AAATCTCTAA	AGAAACGAGA	GCGTTTGGAG	1920
AAAGATGTAG	CGAAAATTT	GGAGAGCAAA	ACGGGCAACA	AAAATAAAAT	GGAAGCAAAA	1980
TCTCAAGCTA	ACAGCCAAAA	AGATGAGATT	TTTGCCTTGA	TCAATAAAGA	GGCTAATAGG	2040
GATGCAAGAG	CAATCGCTTA	CGCTCAGAA	CTTAAAGGCA	TCAAAGGGA	ATTGTCTGAT	2100
AACTTGAAA	ATATCAACAA	GGATTTGAAA	GACTTTAGTA	AATCTTTTGA	TGAATTCAAA	2160
AATGGCAAAA	ATAAGGATTT	CAGCAAGGCA	GAAGAAACAC	TAAAGCCCT	TAAAGGCTCG	2220
GTGAAAGATT	TAGGTATCAA	TCCAGAATGG	ATTTCAAAAG	TTGAAAACCT	TAATGCAGCT	2280
TTGAATGAAT	TCAAAAATGG	CAAAAATAAG	GATTTCAAGCA	AGGTAACGCA	AGCAAAAAGC	2340
GACCTTGAAA	ATTCATTAA	AGATGTGATC	ATCAATCAAA	AGATAACGGA	TAAAGTTGAT	2400
AATCTCAATC	AAGCGGTATC	AGTGGCTAAA	GCAACGGGTG	ATTTCAGTGG	GGTAGAGCAA	2460
GCGTTAGCCG	ATCTCAAAA	TTTCTCAAAG	GAGCAATTGG	CTCAACAAGC	TCAAAAAAAT	2520
GAAGATTTCA	ATACTGGAAA	AAATTTGCA	CTATACCAAT	CCGTAAAGAA	TGGTGTAAC	2580
GGAAACCTAG	TCGGTAATGG	GTTATCTAAA	GCAGAAGCCA	CAACTCTTTC	TAAAAACTTT	2640
TCGGACATCA	AGAAAGAGTT	GAATGCAAAA	CTTGGAATTT	TCAATAACAA	TAACAATAAT	2700
GGACTCGAAA	ACAGCACAGA	ACCCATTAT	ACTCAAGTTG	CTAAAAAGGT	AAAAGCAAAA	2760
ATTGACCGAC	TCGATCAAA	AGCAAGTGGT	TTGGGTGATG	TAGGGCAAGC	AGCGAGCTTC	2820
CTTTTGAAAA	GGCATGATAA	AGTTGATGAT	CTCAGTAAGG	TAGGGCTTTC	AGCTAACCAT	2880
GAACCCATTT	ACGCTACGAT	TGATGATCTC	GGCGGACCTT	TCCCTTTGAA	AAGGCATGAT	2940
AAAGTTGATG	ATCTCAGTAA	GGTAGGGCTT	TCAAGGGAGC	AAAAATTGAC	TCAGAAAATT	3000
GACAATCTCA	ACCAGGCGGT	ATCAGAAGCT	AAAGCAAGTC	ATTTTGACAA	CCTAGATCAA	3060
ATGATAGACA	AGCTCAAAGA	TTCTACAAA	AAGAAATGTTG	TGAATCTATA	TGTTGAAAGT	3120
GCAAAAAAAG	GGCTACTAG	TTTGTACGG	AAATTGGACA	ATTACGCTAC	TAACAGCCAC	3180
ACACGCATTA	ATAGCAATGT	CAAAAATGGA	ACAATCAATG	AAAAAGCGAC	CGGCATGCTA	3240
ACGCAAAAAA	ATTCTGAGTG	GCTCAAGCTC	GTGAATGATA	AGATAGTTGC	GCATAATGTG	3300
GGAGTGCTC	CTTTGTACGC	GTATGATAAA	ATTGGATTCA	ACCAAAAGAA	TATGAAAGAT	3360
TATTCTGATT	CGTTCAAGTT	TTCCACCAGG	TTGAGCAATG	CCGTAAAAGA	CATTAGTCT	3420
GGCTTTGTGC	ATTTTTTAAC	CAATATATTT	TCTATGGGAT	CTTACAGCTT	GATGAAAGCA	3480
AGTGTGGAAC	ATGGAGTCAA	AAATACTAAT	ACAAAAGGTG	GTTTCAAAA	ATCT	3534

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

158

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75

```

ATGAAAGCGT TGAAGACTTT TTTAAAAAAA TCCCTTATTC TGTTACTAGC AATTGCCTTA      60
AACCACTTAA ACGCTGTGGC TATGATTGTG GATAATCCTA CGCAGAACGC TTGGAATGGT      120
GCTAAAAGAG CATGGGATGA AAGCAAGTGG GCTAAACATT TAGCCACTAT TACTGAAAGG      180
ATCAAGCTCG CTCAAGACAC ATTAGATAGG GCTAATCAGA CGCTTAATTC CATCAACAAA      240
GTGAATGATG TTTTGAACAA AACCAATCAA TTCTAACAG GCAGTATTTT AAGCATCCCC      300
AATCCCATGC AGTATGTAGA AAAAATCCAA AGTTTGGCCA AGCAAGTTCA AGCCAATACT      360
GAAAGGATCA AAGAAAATGC ACAAACATAT GATATACGCA ATCAAATTGC AGCCAAACGC      420
ATCTCTGAAA AATGCCCTGA ACTCAATTGG GATGTCAGTC AAGACGCGAG CCCTACAGAG      480
AAAAACTTAC ACCAATTTTT CACGAGCAAG GGGAAAGAAA GCGCTAACAC AAAGGCTCTA      540
AAGGATTTTG CTAACGCCAT AGGTAACACT CAAATCAGCA CGGCGAACGA TTTAGGAGCT      600
GGACTTAGAG GCAGAGCCTT ATTAGAATAC ATTTGCATT CAAAAAGGCAA TTTAGAAGCG      660
GCTAAAAAAA TCCAATTATT AGACAGCCAA ATGACTTTAG CTCTACTCAA TAACGACTAT      720
ACGGCTTATG AAAAAGCTTAG AGCTGAAAAA GAAGAATTAA AAAGACAAAT CGCTTCAAAT      780
GTGTATGCGA AAGTCAACA GCTTGTGTGA GCTTCCCAAG ATAGAGCGTT TAGTCAAATG      840
GATAATGAGT TGGGCGTTAA AACTTTTGGG TTCAACGATG AGAATGTTAA AAAAGGTTAT      900
TGCAAGAAAG AAAACAGAAA TGGCAAAAGC GAGTGCATCC CTAACATGCT CAATGTTAAT      960
CGCTTAAAG CGCAATTTGA TGAGCTTAAT TTAGATTATA GTAGGGATAT TGCTGGTAAA      1020
AAAGGTGAAG CAGCCGCTAA AGTGTTCAT GACTACAAAC ACCGATTCCA ACAATTAAGC      1080
GTAGAACTG CTTTAGAAAT CGCTCAAAAT TTAAGTTTAA TGAATAAGAC GCTAGGTTTA      1140
ATGGTGCAAA TGCAAAAGCTA TGCAATTCAAG CAACAAATGG GCTATTTTGA AGATATTATT      1200
CCTGCTGACG CCCTAAAAGA TGACAAAGAG CATCAAGAAA ATCTTGAACA AAAACAACAA      1260
GAAATAGAGA AAGTCTATAG GGCTAAATTA GACGCTTATG GTTTCCTTAA TGGTAGTGTA      1320
GGAAAGGCAA GTGCGTGAA TTCAAATAGT AATAATGAAG CCCCAGCTC TGATAATATC      1380
CAGTCGTTA ATCCGTAT

```

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76

```

GTGATGGATG CAGAAAATGG GGAATTGCTC GTTGCAGGAA GTTACCCTGA ATACAATTTC      60
AACGATTTTG TAGGCGGGAT CAGTCAAGAC AAATGGCAAA AACTCCAAGA TGATATTAT      120
AACCCTTTAT TAAACCGCTT CGCAATGCCT TGTATCCGCC GGGATCTGTG GTTAAATGG      180
CGGTGGGGT

```

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 base pairs

159

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77

```

ATGAATTTTT TTGACACCCT TATGGGTATG TTTGTTGAGC CATCTCAAAA AGTAGCCAAA    60
AGTCTTGCTG AACATGTGGG TAGCTTTTTT CATGCACAAC TCATTTTAAA CACAATTATT    120
ACTATTTTAT TTATGATATG GCGGTATAAG CGTGTGAAAG AGGGCGATAT GTTTGAGTTT    180
AAAACCGCTA TGGGTGTGGT TGTATTTATA GCGTTTGTAG GATTTATCAA TTGGGGGATT    240
AAAAATCCTA ATGATTTTAA CACTTATTTT ATCAATACGA TATTCTACCC ATCTGAAAAA    300
CTAGCCATAC TTATCGCTCA AAGCCTAAAT GATGGCTTAG AAATCCCCAC TAACACTAAT    360
TTAAGTCCTA GTGAAATTTT TAGCATAGGA AATTTAGCCT CAAGTGCCTA TGCAATGATA    420
GTTAATCTGT GGGATAATGC TTTGATGGT ATTAACATGT TTAATTGGCT CACAATGATA    480
CCTAAAATAA TTATGTTTTT TTTAGTGATT TTAGGGGAAT TATTGTTTTT AGGCTTATTG    540
CTTATTATTG TGTATTAGT TACAGCAGAA ATTTTATGT GGTTCAGCATT AGGTTTAATT    600
GTATTGCCTT TAGGTTTAAT CCCCCAAACC AAAGGCATGT TATTTAGCTA TCTTAAAAAG    660
CTCATTTCCT TTAATCTTTA TAAACCTTGT ATGATGTTAG TAGCTTTTTT TAATTATGGA    720
ATAATCTATA AAGTCAATAC TTTAATCCCC ACTAAACACG AAGTCACACA AGGCTTTTAT    780
GGCAATGCGG ATAAATGGC AAATGAGGGA AAAATTATTG ATGTCCTTGG CAATGTCTTA    840
GAAGGAGATT GGAATCTTTA TATAGCCCAT AGTTCTATTG TAGGCTTTTT AACCATTATT    900
GTTTTAGGTT CTGTGATTG TTTCTTTCTA GTCAAACGAG TGCCTGATTT TATCAATAAT    960
ATCTTTGGCA CAAGTGGAGG CGTGGGGGCA GTAACAGAAA TGATGCAAAA AATTGGCATG   1020
ACAATAGGCG GAGCTGTATT TGGGGGTAGT GCAGTTATGG TTGCTAATCA AGTTAAGCAA   1080
GCCTATCAGA GTGCTGGGGG CGGACTAGCA GGAATTCAG CTGGAGCTAA AGCTTTTGGG   1140
CTTGGAGCAA TCACTGGAGG GCAAGTGCT ATGGCAAACC ACAGGAGTGT TAAAGCTGGG   1200
GTGAAACACT TTGTAGCAAG TGTAAAAGT GGCTTTGGAT TTGATAATGA TAAAAATAAT   1260
AAA

```

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78

SUBSTITUTE SHEET (RULE 26)

160

ATGGATGAAC CAGAAACCAG TTTAGAGCAA AACGCTCTTA TAAGACTATC AAATCTCATA	60
AGCTTGCGCA ACACCCAACA ACTTACAAGT ATCATCGCCA CTCATGATCC TATTGTCTTA	120
GATAGTTGCG AATGGGTATT GCTCCTTAAG AATGGCAACA TTGCTCAATA CAAACCTTTA	180
AATTCTATAT TAAAACTGT AGCTAAACT TTTAACTTTA AAGAAAAACC AACCACAAAA	240
GACTTATTAG CGTTACTAAA GGATATT	267

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79

GTGAAAACCT TAGGATTGTC TTCGCTTGGT GGGACTTTAG AATTTTACGA TTTTATCATC	60
TTTGTATTTT TTACAAGTAT CATTGCCAAA CACTTTTTC CAAACACGCT TAGCCCTATC	120
TGGTCTGAAA TCAACACTTA TGGGATCTTT GCTGCAGGTT ATCTGGCGCG CCCGCTTGGT	180
GGCATTAGTA TGGCCCACTT TGGGGATAAA TTCGGTCGTA AAAACATGTT CATGCTCTCT	240
ATTTTATTAA TGGTAATCCC AACCTTTGCG CTAGCTTTGA TGCCAACTTT TAATGATTG	300
GTGGGTTTTG GCGTGGATAG CATGGGGCTT ACCCCTAAAA ACGCTCATTA TCTTGGTTAC	360
ATAGCTCCTG TTTTTTTRGT RCTTGTTAGG ATTTGTCAAG GCGTCGCTGT GGGTGGTGAA	420
TTGCCTGGCG CTGCGGTTTT TGTCCATGAA CATGCCCCAC AAGGACAAAA AAACACTTAT	480
ATCGGTTTTT TAACCGCTTC CGTAGTTTCT GGGATTTTGC TTGGGAGTTT GGTTTATATC	540
GGGATTTACA TGGTTTTTGA CAAGCCTGTT GTTGAAGATT GGGCTTGGCG GGTTCGCTTT	600
GGGCTTGGAG GAATTTTTTG TATCATTTCT GTGTATTTGA GCGGCTTTTT AGAAGAACT	660
CCCGTTTTTC AGCAAATGAA GCAGGGACGA TGCCTTAGTC AAATCCCCGC T	711

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1413

SUBSTITUTE SHEET (RULE 26)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80

ATGCGCAAAT	TTTTGGATGG	GGCAAAAAGT	GAGGTTTTAA	AATACGATGT	GATTTCTTTT	60
GATATTTTTG	ATACCCCTCT	TCTAAGACCT	TTCATTAAAC	CCACAGATTT	ATTTTGTAT	120
ATTGAGACTA	AATACAATAT	TAAAGGTTTT	CATCAAGCAA	GGATCCTGGC	AGAAATGCAA	180
TCCAGAAAAT	TAAGTAAAAG	ACAAGACATT	ACTCTAGATG	AAATTTATCA	TCAAATCCCA	240
AAAGAGTTTC	ATTCATATAA	GGGAGTAGAA	ATCGCTACTG	AAAAAGAGGT	GCTTGTTCCTA	300
AACCTGGAGA	TGTTAGAACT	CTATCGTTTC	GCTAAAGAGA	ACAATAAGAG	AGTGATTATT	360
GTATCAGATA	TGTATTTACC	TTTAGAGGTT	CTTGAAGATA	TTTTAATTTT	TAAGGGTTTT	420
GATGGTTATA	CAAATTTCTA	TCTTAGTAAC	CATATAATGC	TCACTAAACA	TTCAAAGGAT	480
TTGTTTAAAGC	ATGTTTAAAA	ACAAGAAAAT	ATTACTAATA	CGCAGATATT	GCATATCGGT	540
GATAATCTCT	GGGCAGATGA	CGCTATGCCT	AAAAGTTTAG	GCATAGCAAC	GCTATTTAGA	600
AAAAGCGTGT	TGAAACAATT	AGAAGAAGTT	TTTCCTAAAT	ACAAAACATT	TAATCCAACC	660
AGTGTTGCGC	AAAGTTTTAT	TTTAGGATCT	TTATGCGTTT	TTTATAAAAA	TTATATTCAT	720
AAACATGAAA	AAATTTGATTA	TTGGTTTCTT	TTAGGAGCGA	TGCAGGCAGG	AATTGCAGCC	780
GTTGCTTATT	GCCAGTTTAT	CTATAAGGAG	ATTACACAAA	GAAATATTGA	TACTTTAGTG	840
TTTGTGCGC	GAGATGGTTA	TTTATTGCAA	AAAATTTTAA	ATATTTTATA	TCCAAATTCA	900
TATAAAACTA	CTTATGCTCA	TGCTCCCAGA	ATTTTAAAAA	AAGCGGTATT	TTTAGAAGTC	960
GTAGAGGGCG	AGAGTTTGGG	AATTTTGCCT	ATTTTGAAG	GCGAAGAAGA	AGTTAAAAAG	1020
AAGCAAATCA	CCACCAACCA	ACAGGCGTAT	GTATATCTCT	ATAGCAATTT	TGAACATTGC	1080
CGCCATTTAG	CGTTAAATAT	TTTAGATAAT	TACAGAAAAT	ACTTGTTTTC	ATCAAATTTA	1140
GAAGGAAATA	TCGCTATTGT	AGATACGATT	ACTTTAGGCT	ATCTTTCGCA	AGGGTTAATC	1200
CAAAAAGCTT	TAAATAAAGA	AGTTTTTGGG	TGCTATGTGG	ATCTCCTAAG	AAATTTTAAAT	1260
TATGATTGCG	TGAGTTTCTT	ACCTTTTTC	CACCTTAAAC	CCGTTTATTT	TCATAATTGG	1320
GATTTTATGG	AGTTTTTGCT	AACAAGCCCT	GAATACCCTA	TTTTAAATGT	AGAAAATGGC	1380
GTCCAATCT	TATCAAAAAG	ACGTTTCATC	TTG			1413

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81

GTGTTGAAAT	TCTTTGAAGA	TTCCAAACAG	CTTAGCACGC	CTATGGGAAA	GAGCGCGGTG	60
GGGATTTTGA	TTTTCCAAGA	TATTGCAGCC	ATTCCCATGC	TTTTAATTTT	GACGATTCTA	120
GGCAGTAAGG	ATTCTCATGT	CAATTTGCTC	ATTCTTAAAA	CCCTTATTTC	AGCGGGGATT	180
ATTTTAATTC	TTTTATTATT	GCCTGGAAAA	AAAGGGGCTA	ATCTCATCTT	AGAGCAAGCG	240
AAAGACACGC	GCTTGCCTGA	AATCTTTATA	GGCAGCGATT	TTAGTGATTG	TTTGCAGCGC	300
GGCGGGGTG	AGCCATTTTT	TTGGGTTTTT	TATGTCTTTG	GGGCGTTTCA	TTGTGGGCAT	360
GGCGATTTT						369

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs

162

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82

ATGATTITAG CCCTTTTGAT TTCTAAAGAA AAAACGCATT TAGAAGCGTT GTATTATTTG	60
AGCTATGGCG TGCTTTTAGG GGGCGTGGCT CAAATCTTAT TACACTTTTA TCCTTTAGTA	120
AAATTAGGCT TATGGGATTT ATTATTTAAA GGGTTGTTGG GTTTTAAGAC TAAAAATACA	180
AACAAAAAAG AATATCGTTT GAATAGGGCT AAAAAGGATC TAAAAGCGTT TTCAAGCAA	240
TTCTTCCCA GCGTCTTAGG CAATTCTAGC GCTCAGATCG CTTCTTTTTT AGACACCACA	300
ATCGCTTCTT TTCTGGCGAG CGGGAGCGTG TCTTATTGT ATTACGCCAA TAGAGTCTTC	360
CAGCTCCCTT TAGCCTTATT CGCTATCGCT ATCTCCACAG CTCTTTTCCC TAGCATTGCG	420
ATCGCGCTTA AAAACAACCA GCAGGATTTA ATCTTACAAC GCTTGCAAAA GGCGTGGTTT	480
TTTTTGGTGG GGGTTTGCT TCTTGCAGC ATTGGGGGGA TAATGTTAAG CAAAGAAATC	540
ACCGAACTTT TATTGAAAG GGGGCAATTT AGCCCTAAAG ACACCCTAAT CACTTCGCAA	600
GTCTTTTCGC TCTATCTTTT AGGCTTGCTC CCTTTTGGGC TAACCAAACCT CTTTCTTTA	660
TGGCTTTATG CGAAATTAGA GCAAAAAAAA GCGGCTAAAA TCTCTTAAT TTCGCTTTT	720
TTAGGTTTAG CGGCTTCTTT GAGTTTAATG CCTTTGTTAG GGGTTTGGG TTTGCGT	777

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83

GTGCTAAAAT ACCCTACRRT GTTCATGTGT GCGGATGCGG TCATTATCAG TAAGGCGGAC	60
ATGATTGAAG TGTTTAATTT TAGGGTTTCT CAAGTCAAAG AAGACATGCA AAAATTAAAG	120
CCTGAAGCGC CCATTTTTTT AATGAGCTCC AAAGACCCTA AAAGCTTGGA AGATTTTAA	180
AATTTCTTTT TAGAAAAAAA GCGTGAAAT TACCAATCCA CGCATTGCTT T	231

(2) INFORMATION FOR SEQ ID NO:84:

163

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 540 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...540
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84

ATGCTGCTTT	GCGCGGAAG	GAATGAGACT	TTAAAAAAG	CGGTGCCTAT	TGGTGTGGGC	60
TTGATAGAGA	GCGCGATCAA	TTTAACGAGA	ATGTGCCTTA	AAAACCTGA	TACAGAAAGC	120
CTTATTTT	TAGGGAGCGC	GGGGAGTTAT	AGCCCAGAAA	CGGAGATTTT	GAGCGTGT	180
GAAAGCATTG	AAGGCTATCA	AATTGAAGAG	AGTTT	TAGCC	ATTTAAACAG	240
TTGGATAATT	TCATTACAT	AGAACTAAA	GAGCAGGCTC	TTTTTGAAAG	GGTGCCTGTG	300
AATAGCAGTA	ACTACATCCA	CACCAGCGAA	ATGTTTGCTA	AAAAAATGGT	TCAAAGGGC	360
GTTTTATTAG	AAAACATGGA	GTTTTTTAGC	GTCTTAAGCG	TGGCTAAAAT	TTTTTCTTTA	420
AAGGCTAAAG	GGATTTTTTG	CGTGAGCAAT	CATGTAGGGC	TTAACGCGCA	TAAGGAATTT	480
AAAGAAACC	ACGCCAAAGT	CAACAGATT	CTAGAAAACA	TCATTGATAG	TTTGATAGTT	540

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 639 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...639
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85

GTGTATGAAG	AAAGGATCAC	TCTGGCTTCT	CAAGGGATCC	CTAAAACGAG	TAAAGTGGGC	60
TTTGAAATCT	TTGACACTAA	AGACTTTGGG	GCGACTGATT	TTGATCAAAA	CATCAAACCTC	120
ATTCGCGCCA	TTGAGGGGGA	ATTGTCGCGC	ACGATTGAAA	GTTTAAACCC	CATTCTTAA	180
GCCAAATGTG	ATATTGCAAT	CCCTAAAGAC	AGCGTGT	TTG	TGGCTAAAGA	240
AGCGCTTCAG	TGATGCTCAA	GCTTAAGCCT	GACATGAAGC	TTTCACCCAC	TCAAATTTTA	300
GGGATTAAAA	ATTTAATCGC	TGCAGCTGTG	CCTAAACTCA	CGATAGAAAA	CGTGAAATC	360
GTGAATGAAA	ATGGCGAATC	AATAGGCGAG	GGCGATATAC	TAGAAACTC	CAAAGAATTA	420
GCCTTAGAGC	AATTGCGCTA	CAAACAAAAT	TTTGAAAAACA	TTTAGAAAA	TAAGATCGTC	480
AATATCTTAG	CCCCTATTGT	GGGGRGTAAA	AACAARGTRG	TCRCAARRGT	CAATRCGGAG	540
TTTRATTTCA	RCCAAAAGAA	AAGCACCAAA	GAGACTTTTG	ATCCCAATAA	TGTCGGTAAG	600

164

GAGCGAGCAA AATTTAGAAG AAAAAAAGA AGGCGCTCC

639

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86

GTGATAARGA AAGGCTATAT AAGAGGAGAT CTTATGCGTA TAGTTAGAAA TTTATTTCTT	60
GTATCGTTTG TGGCGTATAG TAGTGCGTTC GCAGCGGATT TAGAAACCGG AACCAAAAAC	120
GACAAAAAGA GCGGTAAAAA ATTTTACAAA CTCCATAAAA ACCATGGCTC AGAAACCGAG	180
ACTAAAAACG ATAAAAAGCT TTATGATTTC ACTAAAAATA GCGGATTAGA AGGCGTGGAT	240
TTAGAAAAAA GCCCTAACCT TAAAAGCCAT AAAAAAGCG ATAAAAAGTT TTATAACAA	300
CTCGCTAAAA ACAATATCGC TGAAGGGGTG AGCATGCCGA TTGTGAATTT CAATAAGCC	360
CTATCTTTTG GGCCTTATTT TGAAAGGACT AAAAGCAAAA AAACCCAATA CATGGACGGC	420
GGGTGATGA TGCACATCCG TTTT	444

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87

GTGATGATCG ATCCCCAAAT GGTGGAATTT AGCATTTATG CGGACATCCC TCATTTACTC	60
ACGCCCATTA TCACTGACCC TAAAAAGCT ATCGGGGCTT TGCAAGCGT GGCTAAAGAA	120
ATGGAGCGCC GATACTCTTT AATGAGCGAA TACAAGGTTA AAACCATGTA TTCTTATAAT	180
GAACAAGCCC AAAGTAACGR CGTTGAAGCG TTCCCTATT TGATTGTGGT GATTGATGAA	240
TTAGCGGATT TGATGATGAC AGGGGGCAA GAAGCGGAGT TTCCTATCGC TAGAATCGCT	300
CAAATGGGGC GAGCGAGCGG CTGACACCTC ATTGTGGCGA CCCAACGCCC GAGCGTGGAT	360

165

GTCGTAACCG	GCTTGATTAA	AACCAACTTG	CCTTCAAGGG	TGAGTTTGTAG	GGTAGGCACT	420
AAGATTGATT	CTAAAGTGAT	TTTAGACACC	GATGGGGCGC	AAAGCTTACT	AGGAAGGGGC	480
GATATGCTCT	TTACCCCCCC	AGGAACAAAC	GGGTTAGTGC	GCTTGCAATG	CCCCTTTGCC	540
ACTGAAGATG	AAATCAAAAA	AATCGTGGAT	TTTATTAAAG	CCCAAAAAGA	GGTGAATAC	600
GATAAAGATT	TCTTGCTAGA	AGAATCGCGC	ATGCCTTTAG	ACACCCCTAA	CTATCAAGGC	660
GATGACATTC	TAGAAAGGGC	TAAAGCGGTG	ATTTTAGAAA	AAAAGATCAC	TTCTACGAGC	720
TTTTTACAAC	GCCAATTAAA	AATCGGCTAC	AACCAAGCCG	CCACCATTAC	TGACGAATTA	780
GAAGCTCAAG	GCTTTCATC	CCCAAGAAAC	GCCAAAGGCA	ACAGAGAGAT	TTTGCAAAAT	840
TTT						843

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88

ATGAATTTTT	TTAAAAATCCT	TTAATGGAG	TTAAGAGCCA	TTGTTTCTCA	TAAGGGCGTT	60
TTATTGATCC	TTATAGGCGC	TCCTTTAATC	TATGGCTTGT	TATACCCCTT	GCCTTATTTG	120
AAAGACATCG	TAACGCAGCA	AAAAATCGCC	CTTGTAGATG	AAGACAATTC	CTTCCTTTCT	180
AGGCAATTAG	CTTCATGGT	GCAAAGCTCC	AACGAGTTAG	AAATCGCTTT	CTTAGCCCC	240
TCTATGCTGG	AAGCCAAAAA	GCTTTTAAAA	GAAGAAAAAA	TTTATGGGAT	CTTACACATT	300
CCCTCTCATT	TTGAAGCCAA	TATTTATAAA	CAAAGTGCCT	GTAACGATAG	ATTTTATGTC	360
GAACGCCAAT	TACTTTTTGA	TTTATGGTGC	GTTAGCGAAT	GCGGTGGTGG	GGAGCATCAA	420
CGCCTTAAAC	GA					432

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...219

166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89

GTGGGGGGCT TAGCCATGCT GGGCTTTTTT TATAATATTG AAAAAATTC GCTCGCCACA	60
GCGACGGCTT TCTCGCAATG CGCGCCTAWT TATACGGTGC TCCTTCCCC TTGCTTTTG	120
AAAGAAAAGC TCAAAAGAAG CGCGTTAATT TCCGCATGCA TCGGGCTAGT GGGGGTGGTG	180
TTGATTCAG ATCCTAGCGT GGAAAATGTA GGACCTAGT	219

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 933 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90

GTGTGCTGGA CGGATTGAT TCAAGGGCTT TTGATGATGA GCGCTTTAAT CGTGGTGCCG	60
ATTGTTATGA TAATCCATCT TGGAGGGGATT GGAGAGGGGA TTAAATCAT TAGAGAGATC	120
AAGCCTGAAA ACCTWTCTTT CTSGCAAGGC TCTAGCGTAG TCGCTATTAT TTCAAGCCTT	180
GCTTGGGGGT TAGGCTATTT TGGGCAACCC CATATTTTAG TCGGCTTCAT GTCTATCCGC	240
TCCATTAGAG ATGTGCCTAA AGCGACCACT ATTGGGATT CTTGGATGGT TATTTCTTTA	300
ATTGGGGCAT GCGTTATGGG GCTTTTAGGC GTTGCTTATG TACATAAATY TGACTTGAGT	360
TTAGAAGACC CTGAAAAGAT TTTCAATTGTA ATGAGTCAAT TGCTCTTTAA CCCTTGGATC	420
ACAGGCATTT TATTGAGCGC GATTTTAGCG GCGGTGATGA GCACGGCCAG TTCGCAACTG	480
CTTGTAAGCT CTTCTACCAT TGCTGAAGAT TTCTATGCCA CGATTTTCAA TAAAAACGCC	540
CCCCAAAAAT TAGTGATGAC GATTTCTAGG CTTTCGGTTT TAGGGGTGGC TTGCATCGCT	600
TTTTTCATTT CAACGGATAA AAACGCTAGC ATCCTCAGCA TCGTGAGTTA CGCATGGGCT	660
GGCTTTGGCG CGAGTTTGG CTCTGTGATT TTGTTTTTAC TTTTITGGTC AAGAATGACG	720
CGCATTTGGC CGATTGCTGG CATGCTCTCT GGGGCTAGCA CGGTGATTTT ATACGATAAA	780
TTTGGCAAAA GCTTTTGGGA TATTTATGAA ATCGTTCCGG GCTTTATTGT AGCGAGCGTA	840
GCTATTGTTG CGTTTAGTTT GTTTTCTAGC GTGCGATCAG GCACTAAAGA GGCCTTTGAA	900
ACCATGCTTA AAGAAATTGA GAGCTTAAAG CAT	933

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

167

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91

GTGGGGCTTT TTATCGTTTT GTTTTTAATT ATAATGAAGC ACCAAACCTC CCCCTATGCT	60
TTCACGCATA ATCAAGCCCT TGTCACCTAA ACCCCCCCTT ATTTACAGCA ACTCACTATC	120
CCTAAACCAA ATGACGCTTT AAGCGCGCAT GCGAGCTCTT TAATCAGCTT GCCTAACGAC	180
AATCTTTTGA GCGCTTATTT TAGCGGCACT AAAGAAGGGG CAAGGGATGT GAAAATCAGC	240
GCGAATCTTT TTGACAGCAA GACTAATCGC TGGAGCGAAG CCTTCATTCT TTTAACCAA	300
GAAGAGCTTT CTCATCATTG GCATGAATAC ATCAAAAAA TTAGG	345

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92

ATGCTTGCTAG GGCCAACAGG CGTGGGGAAA ACGACGACTT TGGCTAAATT AGCCGCACGC	60
TATTCTAGAA TGCTGGCTAA AAAATACAAG GTGGGCATTA TCACTTTAGA CAATTATCGC	120
ATTGGGGCTT TGGAGCAATT GAGTTGGTAT GCTAATAAAA TGAAAATGAG TATAGAAGCG	180
GTGATTGACG CTAAGGATTT TGCTAAAGAA ATTGAAGCTT TGGAACTACTG CGATTTTATT	240
TTAGTGGATA CGACAGGGCA TTCGCAATAC GATAAGGAAA AAATTGCCGG TTTGAAAGAG	300
TTTATAGATG GGGGTTATAA TATGATGTA TCCTTAGTGC TTTGCGTTAC CACTAAGTAT	360
GAAGACATGA AAGATATTTA TGATTCTTTT GGGGTGTTAG GGATTGACAC TTTAATCTTT	420
ACGAAATTAG ATGAGAGTAG GGGGTTAGGG AATTTGTTTT CTTTAGTGCA TGAAAGCCAA	480
AAGCCTATCA GTTATCTTTC TGTCGGCCAA GAAGTGCCTA TGGATTTGAA AGTGGCTACT	540
AATGAGTATT TAGTGGATTG CATGCTAGAT GGCTTTAGTA ACCCTAATAA GGAACAAGCA	600

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

168

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93

GTGGGAGGAG	CGAGCTTTAT	TTCTGGGGGC	AATGGCACGC	TTTATGGCTT	GAATGTGGGC	60
TATGACCGAT	TGGTTAAAG	CGTGATCCTT	GGGGGTTATG	TGGCTTATGG	CTATAGCGGT	120
TTTAACGGGA	ACATCATGCA	TTCTTTGGCT	AATAATGTGG	ATGTGGGGAT	GTATGCGAGG	180
GCTTTTTTGA	AAAGAAACGA	ATTCACTTTG	AGCGCGAATG	AAACTTATGG	AGGCAATGCG	240
AGTCATATCA	ATTCTTCTAA	TTCTTGCTC	TCTGTGTTGA	ACCAACGCTA	CAACTACAAC	300
ACCTGGACAA	CGAGCGTGAA	TGGGAATTAC	GGCTATGATT	TCATGTTCAA	ACAAAAAGC	360
GTGGTGCTAA	AACCTCAAGT	GGGCTTGAGC	TATCATTTCA	TAGGCTTGAG	CGGGATGAAA	420
GGTAAATGC	AAAATCCAGC	TTACCAACAA	TTCTGTCATG	ATTCAAACCC	TTCTAACGAA	480
TCGGTTTTTA	CGCTCAACAT	GGGGTTAGAG	AGCCGTAAAT	ATTTTGGTAA	AAATTCCTAT	540
TATTTTGTA	CGGCGAGGTT	GGGTAGGGAT	CTTTTGATCA	AAGCTAAAGG	CGACAATGTG	600
GTGCGTTTTG	TGGGTGAAAA	CACTTTATTG	TACCGCAAGG	GGGAAATTTT	TAACACTTTT	660
GCGAGCGTGA	TCACAGGAGG	CGAAATGCAT	TTGTGGCGTT	TGATGTATGT	GAATGCGGGG	720
GTGGGGCTTA	AAATGGGCTT	GCAATACCAA	GATCTTAATA	TCACTGGGAA	TGTGGGCATG	780
CGAGTGGCGT	TT					792

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1017 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94

ATGGACGGCT	ATGGGTTTAA	AATGCAAGAC	TTGGGCCAAA	AAACTCAAGT	TATCCAACAC	60
ATCTTTGCCG	GGGATGATGT	GAGCGCTTTA	GAAGTCAAAG	AAAATGAATG	CGTTAAAATC	120
RTGACTGGAG	CGATGGTGCC	AAAGGGAATA	GAAACGATTG	TTCCCATAGA	ATGCATGCTA	180
GAGAGTCATA	AAGATTTTCG	CCTAGCTCCT	AAAGATTTTA	AAATTCACGC	TAATATCCGT	240
CAAAAGGGCG	AGAACGCTTC	TTTAAACAGC	GTTTTAGTCC	CTAAAAATAC	CCGTTTGAAT	300
TATGGCCATA	TCGCGCTCAT	TGCCTCTCAA	GGGTTCAAAG	AAATCAAAGC	GTTTAGAAAA	360
TTAAAAATCG	CTCTCTTTAG	TAGCGGCGAT	GAATTAGTGC	CTTTAGGGCA	AAACGCCCTA	420
GAGTGCCAGG	TTTATGATGT	TAATTCAGTG	GGTGTTTTTA	ACATGCTTAA	AAACTACAAC	480
ACGCATTTTC	TAGGGGTTTT	AAAAGATGAT	AAAAATTAC	AGCTTAAAT	ACTTGAATTG	540
CAAGGCTATG	ATGTCATCCT	TTCAAGTGCG	GGGGTGAGCG	TAGGGGATAA	AGACTTTTTT	600
AAAGACGCTT	TGAAAGAAAG	AAACGCCCTT	TTTTATTACG	AAAAAGTCAA	TCTCAAACCT	660
GGAAAGCCGG	TAACTTTAGC	CCAACCTAAT	CAAAGCATTA	TTATAGGCTT	ACCGGGTAAT	720
CCTTTAAGTT	GCTTACTGGT	TTTACGAGTT	TTGATTCTAC	CCTTATTGGA	GCGCTTATCC	780
TTAAATAAAG	ATTTTAAATT	AAAACCTTTT	AAGGCTCAAA	TCAATGCCCC	TTTAAAGCTT	840
AATAACAAAC	GGACGCATTT	AATCTTAGGC	AACCTATTCAA	ACCACCAATT	CATTCCTTAC	900
AACAACCGCT	ATGAATCAGG	AGCGATTCAA	GCCCTTGCGC	AAGTGGATTG	TATCRCTTTA	960
ATTGATGAAG	GAGTGGGATT	GTTTCAGGGC	GAAATTGAAA	TTTTAAGGTT	TGAAAAAT	1017

SUBSTITUTE SHEET (RULE 26)

169

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95

ATGCCATACG CCTTAAGAAA AAGATTTTTC AAACGCCTTT TATTGTTTTT TTTAATTGTT	60
TGTATGATAA ATTTGCATGC CAAAAGCTAT CTGTTTCTC CTTTGCCCC AGCGCACCAG	120
CAATCATTAA AGACAGAGCC TTGCTCTTG GAGTGCTTGA AAGACTTGAT GCTGCAAAAT	180
CAATCTTTT CTTTTGTATC CCAATACGAT GATAACAACC AAGATGAGAG CCTTAAAACT	240
TATTACAAGG ACATCTTAAA CAACTCAAC CCCGTATTCA TCGCTTCTCA AACTCCAGCT	300
AAAGAAAGCT ATGAGCCTAA GATTGAATTA GCGATTTTAC TGCCTAAAAA GGTGGTGGGC	360
CGTTATGCGA TTTTAGTGAT GAACACCCTT TTAGCGTATT TTGAACACCA GAAACAACGA	420
TTTCAATATC CAAGTCTT	438

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96

ATGCCTATTA ACCCTCTCTA TCTTTTCCCC AATCTTTTTA CCGCTAGCAG TATTTTTTTA	60
GGCATGATGA GTATTTTTTA CGCTTCCAGT TACCAATTG TCATGGCGTG TTGGTTAGTG	120
GTGGCGAGTC TTATTTTAGA TGGGCTTGAT GGGCGTGTCC CAAGGCTTAC CAAACACCAC	180

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

170

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...699

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97

ATGCTTTTCAG	CCTTGCTTTC	TAAATGGGG	ACTTACGCCT	TATTACGCTT	CTTGCTCCCG	60
CTTTTTCCCTG	AACTTTCAGA	AAATTATTTA	ACCCCATAG	CCATTGTGGC	GCTGTGCATG	120
ATCATTTATG	GAGGTTTTCT	AGCCTACGCT	CAAAAAGATT	TAAAAACCCT	CATCGCTTAT	180
AGCTCTTTCT	CGCACATGGG	AGTCGTGGTG	CTTGGGGTTT	TTTCTTTCAA	TGTTGAAGGG	240
GTTTCAGGGG	CGGTGTTTAT	GATGTTTGCG	CATGGCGTTA	TCGTCATGGG	ATTATTTTTA	300
CTCGCTGGTA	TCTTGGAAGA	ACGCGCCAGC	AGTTTAGAAA	TCGCTCGCTT	TGGATCGATC	360
GCTAAAGCG	CTCCTGTTTT	TGCAGCCTTT	TTTATGATCG	TTTTAATGGC	GAATGTGGGC	420
ATGCCTTTAA	GCATTGTTTT	TGTGGGAGAG	TTTTTGARCT	TGTTAGGGTT	TTTTGCCACT	480
TACCCTCTTT	TGGCTATCAT	TGCCGGGACA	AGCCTCATTC	TATCAGCGGT	TTACATRCTC	540
ACTTCATATA	AAGATGTGTT	CTTTGGCAAC	TTAAAAACCG	GGAACAACCA	AATCAGCGTG	600
TTTGAAGATT	TAAACGCTCG	TGAGGTAGGG	GTTTAAAGCG	TGATTTTAGC	CTTTGATCTT	660
AATTTTAGGG	ATTTATYCYA	AAGCGCTTTT	AAAACCGAT			699

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...96

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98

GTGGAATTGA	TTAGCAATAA	CCCTAACGCC	AGCCAACAAT	CTATCGTTAT	TCCTTTGGAG	60
ACTTTTGCCT	TGGCGCGAGC	GTTAAAGGGA	ATCTTT			96

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs

171

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99

ATGAAAATTT TTGGGACTGA TGGCGTGAGG GGTAAAGCAG GGGTGAAACT CACCCCCATG	60
TTTGTGATGC GTTTAGGCAT TGCTGCCGGA TTGTATTTTA AAAAACATTC TCAAACGAAT	120
AAAATTCTAA TCGGTAAGA CACCAGAAAG AGCGGCTATA TGGTAGAAAA CGCTTTAGTG	180
AGCGCTCTCA CTTCCATAGG CTATAATGTG ATCCAAATAG GGCCTATGCC TACCCCTGCG	240
ATCGCTTTTT TAACCGAAGA CATGCGCTGT GATGCGGGCA TTATGATAAG CGCGAGCCAC	300
AACCCTTTTG AAGACAATGG CATCAAGTTT TTCAATTCCT ATGTTTATAA ACTCAAAGAA	360
GAAGAAGAAA GAGCGATTGA AGAAATCTTT CATGATGAAG AATTACTGCA TTCTAGCTAT	420
AAAGTGGGCG AGAGCGTCGG TAGCGCTAAA AGGATAGACG ATGTGATAGG GCCGCTATAT	480
CGCGCATTTG AAGCACTCTY TYCCCAAACA TTT	513

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100

GTGCGAGCCG TGTTTGTCTT TGGTTTGAAG GCGGCGTTTT GTATAGGGAT TTTTCTAT	60
GGCGCTTATT ATTTCTAGA TGAGTTTTTA ATCAAGCTC	99

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

172

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...210
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101

GTGAGGAGCG GTAAAAGATT AGGCTATACC AATCAAGTGA TCACCGATAT TGTCAATATC	60
GGTATTGGGG GGTCAGATTT AGGCGCTTTA ATGGTTTGCA CCGCCCTAAA ACGCTACGGC	120
CACCCAAGAT TARRAATGCA TTTTGTGTCT AATGTGGAAT GGCACGCAGA TTTTAGACGT	180
TTTGGAAGAAA ATCAACCCGG CCAGCGCGCT	210

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...390
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102

ATGAATCTTG TCTTTTGTG GCGCCCTCTA GGAGGGGCTA TAGGGAGCTC GTTAAGGTAT	60
TTTGTGGGCA AAATGATGCC CAGTAAATTT TTAATGTTTG AAAGTTTCCC TTTAGGGACT	120
TTTAGCGTGA ATCTCATAGG GTGTTTTATC ATCGGCTTTA TGGGGCATTG GCGCCGCTAAA	180
AAAGTTTITG GTGATGATTT TGGGATTTTC TTTGTAACCG GAGTTTTAGG GGGTTTTACG	240
ACCTTTTCTT CTTATGGGTT AGACACTTTA AAACCTCTGC AAAAATCCCA ATACCTTGAA	300
GCCATTCTT ATGTCTTAGG CACTAACCTT TTAGGGCTTA TTGGGGTAGC TATCGGTTGG	360
TTTTTGGCTA AGAATTTTGT AGCGGTTAAT	390

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

173

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103

ATGTTGAAA	AACTGATTGA	AAGAGTGTG	TTTGCCACTC	GTGGTTGCT	AGCCCCTTA	60
TGCATTGCCA	TGTCGTTAGT	GTGGTGGTT	TTAGGCTATG	TGTTTCATGAA	AGAGTTGTGG	120
CACATGCTCA	GCCATTTARA	CACCATTAGT	GAAACGGATT	TGGTTTTATC	AGCCTTAGGT	180
TTAGTGATT	TGTTGGTTCA	TGGCCGGCT	TGTTTGATG	GTGCTGCTCG	CCAGTTA	237

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104

ATGCACTATC	AATTACAAG	TTTCAATATA	ATACAAGATC	TTTTTATAAC	TTGTCATGTG	60
TTAAGGATCA	AAATGCGCGT	GTTTGTITGC	TTTTTAGGGG	TTTTTGTATC	TAACGGCTTG	120
GCTCGTTTTG	GCTATGTGGT	TTTAATCCCC	CTACTCATTT	TATCAGGGAG	TTTAACCCCA	180
CACCAAAGCT	TCCAACCTGG	TATTGCGGTG	CTAATGGGCT	ATGTTTTTGG	GAGCTTTTAA	240
ATCCAATTTT	TAAGCCCGTT	AATGTCATTA	SAAAGCATCG	CTAAAATCAG	TTTTAAATTA	300
ACACTT						306

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

174

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105

GTGGATATGA AAGACGCTGT AGGGACTTAT AAACATYCA GGGCT

45

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3081 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...3081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106

GTGTGTTTAG	ACCATCAGGT	TGGAGCAGGC	AAGACTTTGT	GCGCTATAGC	CAGCTGCATG	60
GAACAAAAAC	GCATGGGATT	AGTGAATAAA	ACGCTCATTG	CCGTGCCTAA	CCATTTAACC	120
AAGCAATGGG	GCGATGAATT	TTATAAGGCT	TACCCTAACG	CTAATGTGTT	AGTTGTTGAT	180
AGCAAGGACA	CCACTGAAAA	AGAAAGAGAA	CTTTTATTCA	ATCAAATCGC	TAACAACAAT	240
TATGACGCTG	TGGTTATCGC	GCACACCCAT	TTGGAAATTAT	TGTCTAACCC	TAGAGGAATC	300
ATAGAAGAAT	TGAAAGAAGA	AGAGCTAGTG	AATGCTGAAA	AAAACCTTGA	AAGGCAAGAA	360
TTAGCTTATA	AAAATAACCC	TAGAGAAACT	AAAAAACCCA	ATGAAAGAGC	CTTTAAAAAC	420
AAGTTGGATA	AAATCCGTGC	TAAATACGAT	GCGATTTTAG	AAAAACAAGG	CTCTCATATT	480
GATATTAGTC	AAATGGGGAT	TGACAATTG	ATTGTGGATG	AAGCCCACTT	ATTCAAAAAT	540
CTAGCCTTTG	AAACTTCTAT	GGAAAAAATT	GCAGGACTTG	GTAACCAACA	AGGCTCTAAT	600
CGCGCTAGAG	ATTTGTTTAT	TAAAACGCGC	TACTTGCATC	AAAACGATAA	GAAAATCATG	660
TTTTTAACCG	GCACGCCTAT	AGCTAATTCC	TTGAGTGAAA	TGTATCACTT	GCAACGCTAT	720
TTAACCCTTG	ATGTGTTAAA	AGAAAGAGGG	TTAGAATTCT	TTGATGATTG	GGCTAAGACT	780
TATGGGGAAG	TGGTGAATGA	TTTGAATTA	GACACTTCCG	CTCAAAGTTA	TAAAATGGTT	840
AATCGCTTTT	CTAAATTTAG	CGATGTGCAA	GGCTTAAGCA	CCATGTATAG	AGCTTTTGCG	900
GATATTGTCT	CTAATGATGA	TATTTTAAAG	CATAACCCCC	ACTTTGTGCC	TAAAGTGTAT	960
GGGGATAAAC	CTATCAATGT	GGTGGTGAAA	AGAAGCGAAG	AAGTGGCTCA	ATTCATTGGA	1020
GTGGCTTTAG	AAAATGGAAA	ATATAATGAA	GGCTCTATCA	TTGATAGGAT	GCAAAAATGC	1080
GAGGGCAAGA	AAAGCCAAAA	AGGGCAAGAC	AATATCCCTT	CTTGCACCAC	AGACGCTAGA	1140
AAAGTGGCTT	TGGATTACCG	CTTGATTGAC	CCTAACGCTA	AAGTAGAAAA	AGAATTTTCT	1200
AAAAGCTATG	CTATGGCAAA	AAATATCTAT	GAGAATTATT	TAGAAACTCA	TGCCACTAAA	1260
GGCACACAAC	TTGGTTTCAT	AGGGCTATCC	ACACCCAAAA	CCCATAGCCA	AAAAGTCAGT	1320
TTAGAAGCGC	TAGATAACGC	TCACGAAACT	GAAAAATAAA	ATCCCCTAGA	TAAAGCTCAA	1380
GAACCTTTAG	AAAGCTTGTC	TAGTTATGAT	GAAAAGGGCA	ATCTTATCGC	TCCTAGCAAG	1440
AAAGAATTAG	ATGAACGAGCT	CAAGAGAGAA	GAAGCTAAAA	GCGTCAATTT	AGATGAAGAG	1500
ATAGCTAAAG	GCTGTTTCGTT	TGATGTTTAT	AGCGATGTTT	TAAGGCATTT	AGTCCAAATG	1560
GGTATCCAC	AAAATGAAAT	CGCTTTCATC	CATGACGCTA	AAACCGAAGA	GCAAAAAGCAG	1620
GATTTGTTTA	AAAAGCTCAA	TCGTGGCGGA	GTCAGGGTAT	TATTGGGCAG	TCCTGCTAAA	1680
ATGGGCGTAG	GCACTAATGT	GCAAGAAAGA	TTAGTCGCTA	TGCATGAATT	AGATTGCCCA	1740
TGGAGACCTG	ATGAATTGTT	GCAAAATGGAA	GGGCGTGGGA	TAAGGCAAGG	CAATATTTTA	1800
CACCAAAATG	ATCCTGAAAA	CTTTAGAATG	AAAATCTATC	GTTACGCCAC	TGAAAAGACT	1860
TACGATAGCC	GTATGTGGCA	AATCATAGAA	ACTAAATCTA	AAGGCATAGA	GCAATTTAGA	1920
AACGCGCACA	AATTAGGCTT	GAATGAATTA	GAAGACTTTA	ATATGGGTAG	CTCTAATGCC	1980

175

AGCGAGATGA	AAGCAGAAGC	GACAGGCAAT	CCCTTGATTA	TTGAAGAAGT	CAAATTGAGA	2040
GCGGAGATTA	AAAGCGAAGA	ATCAAAATAC	AAAGCCTTCA	ATAAAGAGCA	TTACTTCAAT	2100
GAAGAAAGCT	TAAAAAACAA	CGCTTCTAAA	TTGGATTATC	TAAAACAGGA	ATTGAAAGAT	2160
TTAGAAACGC	TTCAAAGATC	CGTAATAATC	CCCACTCATA	CAGAGATCAA	GCTCTATGAT	2220
TTGAAAAATG	AAGAAAGTAA	GGATTATGAG	CTTATCAAAG	TTAAAGAGGT	AGAGCCTTTA	2280
AAAGAAAACG	CCTCTATGAG	TGAAGAATTA	ACGCACAAGA	AACTCAAAGA	ACAAAACAAG	2340
CAAATAGCCG	AACAAAATAA	AGAAAAGCTA	GACGCTATTA	AAAAGCAATT	TGCAAGCAAT	2400
TTGAACACCT	TGTTTGTGAA	TGAAGAAGAA	GATTATAAGC	TTTTAGAATA	CAAGGGCTTT	2460
GTGGTGAATG	CTTATAAAAC	TAAGTATCAA	GTGGAGTTTA	GTTTAAGCCC	TAAAGACAAT	2520
CCCAATATTG	CCTATAGCCC	TAGCAATATG	GTTTATAAAA	ACGATACTAT	CAACATGTTT	2580
AGCTCTTATA	ATTTCTGCGC	TGAGATCAAG	TTTGATGGGT	TTTTAAAAAG	GTTTGATAAC	2640
GCTATCATA	AACTCCCTGA	AAAAATCAAG	GAATTAGAAA	ACTCCATTGA	AATCACGAAA	2700
AAAAATATCG	CTAAATACAC	AAGATTAGTG	GAGCAAAAAC	CTTCTTACCC	ACGACTAGAA	2760
TACCTGCAAG	CTTTAAAATG	GGATCATAAA	ACTCTAATAG	ATGATTTAGC	TAAAATGAGC	2820
AAAGACAGAA	ATTATAAGCC	TGCGTTCAAC	CCTAAATCTA	AAGAAGTCTT	AAAGAATTTG	2880
AACGCTGAAA	AAAGAGCGAG	TTTAGAGAAT	GAGAGGGGAG	AGCAAGGGGT	TAAGGGGAAC	2940
ACAAAGAGTG	ATGATGAAAT	AGAGCCAGCT	ACAGAACAAG	TGATTGAAAA	AGAAATAGAA	3000
AAAGGAGATG	AAATCGCTAA	TAATGTTGAT	TACTACGAGA	ACGAACAAGA	AGTGGAAATT	3060
ACTAAATCAA	TGGGTAGAAG	A				3081

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107

ATGGCCGAAG	AAGAAAAGAC	CGAACTCCCT	AGCGCGAAAA	AAATCCAAAA	AGCCAGAGAA	60
GAAGGCAATG	TGCCTAAAAG	CATGGAAGTG	GTGGGGGTTT	TTAGGGTTAT	TGGCTGGGCT	120
AATGAGTATT	TTTGTTTTTT	TTATATGGTG	GGTGGGATGG	CTTTAGCGAG	ATGTATCGCC	180
ATGTGT						186

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

176

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108

```

ATGAAAACAC TCGTGAAAAA TACCATATAT TCTTTTTTGC TATTGTCTGT TTTGATGGCA      60
GAAGATATAA CAAGCGGCTT AAAGCAACTG GATAACACCT ACCAAGAGAC CAACCAACAA      120
GTGCTCAAAA ACCTAGATGA GATTTTTTCA ACCACTAGCC CTAGCGCTAA TAATAAAATA      180
GGTCAAGAAG ATGCTCTAAA CATCAAAAAA GCGGCCATTG CTTTGAGAGG AGATTAGCG      240
TTATTGAAAG CCAATTTTGA AGCGAATGAG TTATTTTTCA TCTCAGAAGA TGTGATTTTT      300
AAGACTTATA TGTCTAGCCC TGAACTTTTA TTAACCTATA TGAAAATCAA TCCCTTAGAC      360
CAAAAGACTG CTGAGCAACA ATGCGGAATA TCCGATAAAG TTTTAGTTCT TTATTGTGAG      420
GGGAAGCTGA AAATCGAGCA AGAAAAACAA AATATAAGAG AGCGTTTAGA AACTTCTCTA      480
AAGGCATATC AGAGCAACAT TGGAGGTACA GCTTCCTTAA TCACTGCTTC ACAGACGCTT      540
GTAGAAAGCC TAAAAAATAA AAATTCATC AAAGGAATCA AAAAGCTTAT GTTAGCTCAC      600
AACAAGGTCT TTTTAAATTA TTTAGAGGAG TTGGACGCAT TAGAAAGATC CCTAGAACAA      660
AGTAAGCGAC AATACCTACA AGAAAGGCAA TCAAGTAAGA TCATTGTTAA A              711

```

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109

```

GTGAGCGAAA AAGACAGGGC GTTCTTTTGA GCGAGCTTGT CTTGCGTGGA TTATGTTGTG      60
GTGTTTGGAG AAGACACGCC CATAAAATTG ATTCAAGCCC TAAAGCCTGA TATTTTAGTC      120
AAGGGAGCGG ACTACCTCAA TAAAGAAGTC ATAGGGAGCG AGTTGGCTAA AGAAACCCGT      180
TTGATAGAAT TTGAAGAAGG TTATTCCACA AGCGCTATCA TAGAAAAAAT TAAAAGGACA      240
CATAATGAT

```

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

177

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110

GTGTATGACA AATCCTTGTG TAAGACCATG GCGCTAGCGT TGAAGGCTTT AGGCGTTAAA	60
AGGGCGATGG TGGTTAATGG AGGGGGGACA GGTGAAATCG TGTTCATGA CATTACGCAT	120
GCGTGCGAAT TGAAAAATAA CGAAATTTTA GAGTATGATT TGAGCGCTAA AGATTTTGRT	180
TTRCCCCCCT CA	192

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 684 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111

ATGCTAGTAG AAATAGAGAA TTTGACTAAA ACTTATGGGA GTTTAAAAGC GCTAGACAAT	60
ATCAGTTTGA AACTACCCAA ACAGCAATTT ATAGGCCTTT TAGGGCCTAA TGGGGCGGGT	120
AAAACCACTC TGTAAAAAT TTTAGCCGGA TTGAATTTGA ACTATCAAGG GGAAGTGAAA	180
ATTTAAACC AAAAGATTGG TATAGAGACT AAAAAAGCG TGGCGTTTTT AAGCGATGGC	240
GATTTTTTAG ATCCTAAAT AACGCCTTTA AAAGCGATCG CTTTTTATAA GGATTTTTTT	300
AGCGATTTTG ATGAATCAA AGCCCTAAAT TTGTTAAAAC GCTTCAGCGT GCCTTTAAAA	360
AGAGAGTTCA AAGCCCTTC AAAAGGCATG AGGGAAAAAT TGCAGCTGAT TTTAACCCTA	420
TCACGAAACG CTTCTTTGTA TCTTTTGTAT GAGCCGGTGG CTGGGATTGA CCCTATTGCA	480
AGAGAAGAGA TTTTGTAGTT AATCGCTAAG GAGTTAGCC AAAACGCAAG CTTGCTAGTC	540
TCTACGCATT TGGTGGTGGG TGTGGAAAAG TATTTAGACA GCGCGATTTT TTTAAAAGAA	600
GCTAAAGTGG TGGCTTTTGG GGATGTGGGG GAATTAATAA AAGGGTATAG CAGTTTGGAG	660
GCAGCGTATA AAGAAAGGTT GAAA	684

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

178

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...819
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112

ATGAACAAGC	TTTTTTTAGC	TTTTATTGTT	GGGGGAATGC	TTTAAAGTGC	TGATGCTTTA	60
AACGATAAGA	TTGAGAATTT	AATGGGGGAG	CGATCCTACC	ACATGAACAA	GCTTTTTTTA	120
GAGCGTTTGT	TTAAAAATCG	TAAGGATTTT	TATGAAATGG	GGCGTTTGGA	TTCCTTAAAA	180
CTACTCAACA	CTCTCAAAGA	AAACGGGCTT	TTATCGTTTA	ATTTTGACAA	ACCAAGCGTG	240
TTAAAAATCA	CTTTCAGGC	TTCAAGTAAT	CCCCTAGCGT	TTGCCAAAAG	CATCAACAAT	300
TCTTTGAATA	TGATGGGGTA	TTCGTATGTT	TTGCCTATTA	GAATGCAAAG	CTCTTCAGGC	360
GAGAATGTTT	TTTCATACGA	GCTTAAAACG	GAATACGTTT	TAGACCCTAA	CATTTTGATA	420
GAGACGATGA	AAAGGCATGG	TTTTGATTTT	ATGGATATTA	GACGGGTGTC	TTTAAAGGAG	480
TGGGAATACG	ACTTTGCCTT	ACAAAAGATC	AAGCTCCCTA	ACGCGAGAGC	CTTAGTTTTG	540
AGTAGCGATC	CTGTGGAGTT	TAAGGAAGCG	AGCGGGAAAT	ATTGGCTGAG	CGTGAATCAA	600
AACGCGTATT	TAAAAATAAG	CTCCAATAAC	CCTTTGTGGC	AACCCAAAAT	CATTTTTTAT	660
GATGAAAAC	TAAAGATCAT	TCAAATCATT	GCTAAAGAAA	ACAGACAACA	AGAAATCGCT	720
CTTAACCTGC	TTGATGGCGT	GCGTTTATC	CATATCACTG	ACGCAAAAAA	CCCTATCATT	780
TTAAAAAATG	GGATTAGCGT	GGTTTTTGAT	GCGATGCCT			819

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...45
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113

GTGTCTCGCC CGTTCAAAAC GATCAAAAAA CCCCCACAAC CCCCT

45

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

179

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114

ATGATCGCTG TATTACCGCC CTTGTTTTCT ATGGGGAGCT TTGATGAGTG GATTTATAGG	60
GGGCTTGTGG CTTTAATGGT GAGCTGTCCT TGC GCGTTAG TGATTTCTGT GCCTTTAGGG	120
TATTTTGGAG GCGTGGGAGC GCGAGCCGA AAGGGGATTT TAATGAAAGG AGTGCATGTT	180
TTAGAGGGTG CTTACCCAAA C	201

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 969 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115

GTGCAACACT TCAATTTCTT CTATAAGAT TCTTTATTTT CTATCGCTTT ATTCACTTTC	60
ATTATCGCTC TTGTGATTTT ATTAGAACAG GCTAGAGCGT ATTTACCCCG AAAGAGAAAC	120
AAAAAATTTT TGCAAAAATT CGCCCAAAAT CAAAACGCCT ATGCGAGCAG CGAGAATTTA	180
GACGAGCTTT TAAAGCATGC TAAAATTTCC AGTTTGATGT TTTTAGCTAG GCGGTATTCT	240
AAAGCGGATG TGGAAATGAG CATTGAAATC TTTAAAGGGC TTTTGAATCG CCCCTTAAAA	300
GATGAAGAAA AAATCGCTGT TTTAGATTTA TTGGCTAAAA ATTATTTTAG CGTGGGGTAT	360
TTGCAGAAAA CAAAGACAC CGTGAAAGAA ATTTTGCGCT TTTCCCAAG GAATGTGGAA	420
GCGTTGTTGA AGCTTTTGCA TCGGTATGAA TTAGAAAAAG ATTATTCAA GGCTTTAGAA	480
ACTTTGGAAT GTTTGGAAGA ATTAGAGGTG CCTAAAATTG AAACGATTAA AAATTACCTC	540
TATTTAATGC ATTTAATAGA GAATAAGGAA GATGCGGCTA AAATCTTGCA GTTTTCAAAA	600
GCGTCGTTAG ATTTGAAAAA AATCGCTCTG AATCACTTAA AATCGCATGA TGAAAATCTT	660
TTTTGGCAAG AAATTGATAC AACC GAACGG CTAGAAAATG TGATCGATCT TTTATGGGAT	720
ATGAATATCC CTGCTTTTAT TTTAGAAAAA CATGCCCTTT TGCAGGACAT CGCGCGATCT	780
CAAGGGTTGC TTTTGGATCA CAAACCTTGC CAAATTTTGG AATTAGAGGT TTTACGCGCT	840
CTATTGCATA GCCCTATAAA AGCGAGTCTG ACTTTTGAAT ACCGCTGCAA GCATTGCAAA	900
CAAATCTTTC CTTTGAAG CCATAGGTGT CCTGTGTGTT ACCAGTTAGC GTTTATGGAT	960
ATGGTGGCT	969

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

180

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...30
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116

ATGGAACACC TTACAAGGGG AATTAAGCAC

30

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 153 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...153
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117

GTGGTTATCT TAGGCTCRCA TGGCAAGGAA GAGTATTACG CTAGCAAGAT TGCAGCCCCC
ATTTTAAAG AAATACCGA AATTTAGTG CGTTACAATT ACCTATCGCC CTCTATTGCG
ATTCAAAACG CTTTGAAAA AAACCGCTTA AAA

60
120
153

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

181

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118

ATGAAAAAGG TTATTGTGGC TTTAGGCGTT TTGGCGTTTCG CAAATGTTTT AATGGCAACC	60
GATGTTAAGG CTCTTGTAAG AGGTTGTGCC GCTTGCCATG GGGTTAAGTT TGAAAAGAAA	120
GCTTTAGGTA AAAGCAAAAT CGTTAACATG ATGAGCGAAA AAGAGATTGA AGAGGATCTT	180
ATGGCTTTTA AAAGCGGTGC CAACAAGAAAT CCTGTCATGA CCCGCAAGCT AAAAAAT	237

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119

ATGGGGATTG CAACCACTCT CATCAGTGAG GTTTCTAAGT TTTATTACGC TTTAAATAC	60
CATGCGAAAT TTATGAGCTT GGGGGAGCTT GGGTGCTATG CGAGCCATTA TTCGTTGTGG	120
CAAAAATGCA TAGAGCTCAA TGAAGCGATC TGTATTTTAG AAGACGATAT AACCTTGAAA	180
GAGGATTTTA AAGAGGGCTT GGATTTTITA GAAAAACACA TCCAAGAGTT AGGCTATGCG	240
CGTTTGATGC ATTTATTGTA TGATGCCAGC GTGAAAAGTG AGCCT	285

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120

182

ATGCACCTTA	AAAGTGGGGC	TGTTTTATC	TCTGATGCGC	ATTTTTTGCC	CAAAAGCCCT	60
CATTTAATCC	ATACGCTTAA	AGAACTTTTA	AGCGCCAAAC	CCCCGCAAGT	CTTTTTCATG	120
GGCGATATTT	TCCATGTTCT	TGTGGGCTAT	TTACCCCTAG	ATAAAGAGCA	GCAAAAAATC	180
ATTGATTTAA	TCCATGCGTT	GAGCGAAATT	TCACAAGTCT	TTTACTTTGA	AGGCAACCAT	240
GATTTTTCCA	TGCGTTTTGT	ATTCAATTCC	AAAGTAATGG	TTTTTGAGCG	CCAAAACCAA	300
CCCGCATTAT	TCCAGTATGA	TAACAAACGC	TTTTTGCTAG	CCCATGGGGA	TTTATTCATC	360
ACTAAAGCGT	ATGAATTTTA	CATCACGCAG	CTCACTTCCA	CTTGGGCTAG	ATTTTTTTTA	420
ACTTTTTTAA	ATTTATTAAG	TTTTAAAACC	TTATACCCTT	TT		462

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121

GTGCAACCGA	TGAAATCTAA	AAAACCTTTAT	TTAGCTTTAA	TCATAGGGGT	TTTATTAGCG	60
TTTTTAACCC	TATCTTCATG	GCTAGGTAAT	AGCGGTTTAG	TGGGGCGTTT	TGGGGTGTGG	120
TTTGCCGCAA	TCAATAAAAA	ATATTTTGGG	TATCTTTCAT	TGATTAATTT	ACCCTATTTG	180
GCGTGCGTTT	TATTCCTTTT	ATACAGGGCT	AAAAACCCTT	TTACAGAAAT	CGTTTTAGAA	240
AAAACCTTAG	GGCATCTATT	AGGCATTTTA	TCTTTACTCT	TTTTGCAATC	TAGCCTGTTG	300
AATCAAGGGG	AAATCGGCAA	CAGCGCGCGT	TTGTTTTTAC	ACCCTTTTAT	AGGGGACTTT	360
GGGCTTTATG	TGCTGATAAT	GCTTATGGTA	GTTATCTCTT	ATTTAATTTT	ATTCAAACCTG	420
CCCCCTAAAA	GCGTTTTTTA	CCCTTATATG	AACAAAACAC	AAAGCCTTTT	AAAAGAGATT	480
TACAAACAAT	GCTTGCAGGC	CTTTAGCCCT	AATTTTAGCC	TGAAAAAAGA	GGGTTTTGAA	540
AACACCCCAT	CAGATTCTCA	AAAAAAGAA	ACCAACAACG	ACAAAGAAAA	AGAAAACCTC	600
AAAGAAAACC	CTATTGATGA	AAACCACAAC	ACCCCTAACG	AAGAATCGTT	TTAGCGATC	660
CCTACCCCTT	ATAACACGAC	CTTAAATAAT	TCAGAGCCGC	AAGAAGGCTT	AGTCCAAATT	720
TCCCCACACC	CCCTACCCA	TTACACCAT	TACCCTAAAA	GAAACCGATT	TGATGATTTG	780
ACTAACCCCA	CTTTAAAAGA	ACCTAAGCAA	GAAACCAAAG	AAAGAGAACC	CACGCTAAAA	840
AAAGAAACGC	CCACCACACT	CAAACCTATC	ATGCCCATAT	CCGCATCCAC	ACAGAAAATC	900
ATGACAAAAC	RGAAAACCAC	AAAACCCCTA	ACCACCCCA			939

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 957 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

183

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122

GTGATGTTAA	GTAGAGACAT	TGTCCAATAT	TCCAAGATCC	GCACCGAGTT	ATACGCCTAC	60
CTCACTTATT	TGTTTTTCGA	CAATATCCGC	AACCACCTTC	CTGAAATCAC	TTTGGATTAT	120
TTAAACAGGC	AAATCAGTAA	GATGCAAGCT	GAAATCAAAA	TGGCAAAAAG	TTTTTTTGTT	180
TTAGACGCTA	AGGGCATGCT	CATGCTTAAG	CCAAGCCAAT	TTAAAGAGCA	GGGGCATAAG	240
GAAGGGCTAT	TAGAGCATGA	TTTAACAGAA	GGGATTGAAT	TAGAATCGCA	TGTCAGTTTT	300
AGCGATAAGT	ATTATTTTTA	TCAAGCCGTG	AATGAAAAGC	GTTGCATTTT	AACCGACCCC	360
TATCCTTCTA	AAAAAGGGAA	CCATTGGGTA	GTGAGCGCGT	CTTACCCGGT	GTATGATCAA	420
AATAACGATC	TAGCGTTTGT	GGTGTGCTTG	CAAATCCCTT	TGAGGGTGGC	GATTGAAATC	480
AGCTCGCCTT	CAAAGTATTT	TAAACTTTT	AGCGAAGGGA	GCATGGTCAT	GTATTTTATG	540
ATTTCATCA	TGCTCACTTT	AGTGTGCTG	CTTTTATTCG	TGAAATGCAT	TTCTAGCTTT	600
TGGACAGCGA	TCGTGCATTT	TAGCAGTTTT	GACATTAAAG	AAGTGTTCCT	CCCCATTGTG	660
CTTTTAACCC	TAGCTTTAGC	CACCTTIGAT	TTGGTCAAGG	CGATTTTTGA	AGAAGAAGTG	720
TTGGGTAAAA	ATAGCGGGGA	CAACCACCAT	GCGATCCACC	GCACCATGAT	CAGGTTTTTA	780
GGCTCTATCA	TTATCGCATT	AGCCATTGAA	GCGTTAATGC	TCGTGTTTAA	ATTACAGCGT	840
AGCGAGCCGG	ATAAAATCAC	TTATGCGGTG	TATTTGGCTA	TCGGCGTGCG	GGTGCTTTTG	900
ATCAGTTTGG	CGATTTATGT	TAAATTCGCT	TATAGCGTGT	TGCCCCAACG	AGAACGC	957

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123

ATGCTTATAC	ATGAAAAAAT	CAAAAGCCGC	TTTTCTAGGA	ATTGGTCTTT	AAGGAATAGG	60
GGCAGGCATT	TTGCATCTTC	AAGCGTGTAT	TTTTTCTCAC	TTCTTGTCAT	TACAGCGGTT	120
AATAGAAGTA	GTGCAGTTGC	TTGGTTATTG	ATGCCTGAAC	ATTTGATTGG	GTGGTTTTTG	180
ATTTCTTTTA	GTGGGGAATT	TGTAGCAGAC	ATGGCGTTTG	GCAAAAAAAG	TAAGATTTTT	240
AAAACCCGCT	TTGGAATTTC	TATTGTGAGC	GGCGTTTCAC	TATTGCTTGG	CGCTTACCAG	300
CGCTTTTATT	TTTTGTATGG	TTTGGCTTAA	TTAATTGGTG	GGCTGTCTTT	TTTA	354

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

184

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124

ATGTTTAAAA GCAGATTAAA TTCATGGATT TTATTAGGGA TTTTAGGGGT TTTAGTGGTG	60
GTTTTTTGGG ATGTCATAAA ATACAAAATA GAAGATTTCG AACATGATCA TTATCTATCA	120
CAAGTGAAG AAAGGGAAGA ATATTATAAA AACCACATAG AAGAAGCTTT GAAAAAGGAT	180
AGCGAATGCT TTGAAAAAGG AGGCGATAAA GTGGATTGCT CGGCTGCTAT GAGAATAGCT	240
GCTGGTGAAA GAAATAGAAG AATGTTAGAG ATTAAA	276

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 414 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125

ATGGTATTTT GGGGCGCTGT TTTCTTTTGA TGGGATCGAA CGGCATGGAA GCGCTTAATG	60
GTGTTTTTGA ACAGCTTGAW TTYCATGCTT GCGGCCTTGA GTTTGGGGTC GTTTTTAGGG	120
GCGATGGATCA AAAATGAAGC CCACACCACT CAAATCGTTT TGATTTCCTC TTTGCCCTTG	180
ATTTTTATGA TGGGTTTTGT GTGGCCTTTT GAATCCTTGC CCTCTTATTT GCAAGTCTTC	240
GTTCAAATAG TGCCTGCTTA TCATGGGATC AGTTTGCTCG GCGGATTGAA TCAAATGCAT	300
GCGGAATTTA TAGATGTTTC TATCCATTTT TACGCGCTTA TTGCGATTTT TATCGTGAGT	360
TTTATAGGGT GCGTGTTCAA ACTCAGCTCT TAAAGAAAG CTTGTGAAAA CGCT	414

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 762 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

185

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126

ATGCATGAGC	AAGGTTCTAT	AAGCTTTTCTA	GGCGRACAGG	GAGCTAAAAG	ATTATTATAC	60
ATACTCTACA	AGCTCGCAIT	TAATGCTAAG	TCTAATAAGA	TGCCCCTAGA	TAGACATTAC	120
GCCAAAATGT	TTTTGCAAGT	TGTAGCAAGA	ACTCTAATAA	AGAATGTCAA	TATATTAGAA	180
GAGCAAGGTT	TTATTGAAGT	CATTAAAGGA	AAACAAAGAT	ACTTGTATGT	GTATCTTAAA	240
GATTACAGAG	AATTAGAATG	CTTAGTGAAG	AGCAAGATGG	CTAAGTATGT	GATGTATTTA	300
AGACAATTCT	TTGATTATTT	GGATAGAAAA	AGGCGTTATG	GCTTTGATTT	TACGCTTAAA	360
AACCTAGCCT	TTGCTAAGAC	CAAAGAAAGC	TTACCCAGAC	ATTTAAACGA	TAAAGACTTA	420
AAGAGTTTTT	TAAAAACACT	CTTAGACTAT	AAGCCAGCTA	CAAGCTTTGA	AAAACGCAAT	480
AAGTGATTTC	TACTTATTGT	AATACTTGGG	GGACTTAGAA	AATGCGAAGT	GTTAAACATA	540
GAATTAAAAC	ACATTCAAGT	AGAAGAGCAA	AACACTCTCA	TTTTAATTCA	AGGTAAAGGT	600
AGAAAAGAGA	GAAAAGCCTA	TATTA AAAAG	AGTTTGTTAG	AACCAAGCTT	GAATGCTTGG	660
ATTAGTGATG	ATTACAGACT	AAAATATTTT	AATGGAGCAT	ATCTCTTTAA	AAAGGATAAG	720
CAAAAATCAC	AAAATTCTTT	AACGCTTTAT	AATTTATCCC	CT		762

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127

GTGGTCTTTA	AAATTTTAAG	TTTATGGTTA	GGGGTGTTTT	GTTTCCTTAG	GGCTACGCAT	60
TTTACTTTAG	GCGAAGAACC	CAAATATAAA	GACAATTTCA	CGCATTTTGA	ATACGCTAAC	120
CCTAACGCTA	GAAAAGGCGG	TGTTTTGAGA	AATGACGCTA	TAGGGACTTT	TGATAGCCTT	180
AACCCTTTTG	CGCTTAAAGG	CACTAAAGCC	GAAAGGCTTG	ATCTCATTTA	TGACACTTTA	240
ATGGTGCAAA	GCTTAGACGA	ACCTTTTGCA	GAATACCCCT	TAATCGCTAA	AGACGCCGAA	300
GTGGCTAAGG	ATAACAGCTA	TGTGATTTTT	ACCCTAGATA	AAAGAGCGAG	ATTACAGCAAT	360
AACGCTCCCA	TTTTAGCGAG	CGATGTGAAG	TTTAGCTTTG	ATACGATAAT	GAAATTAGGA	420
TCGCCCTTTT	ATAGGCAGTA	TTACCAAGAT	GTTAAAAAGG	CGGTTATCTT	AGACAAGCAC	480
CATGTTAAAT	TCATTTYCAA	AACCACTGAA	AATAAAGAAT	TGCCCTCAT	TTTAGGGCAG	540
TTGCAGATCT	TTTCC					555

(2) INFORMATION FOR SEQ ID NO:128:

SUBSTITUTE SHEET (RULE 26)

186

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...198
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128

GTGGCCATGA TAGATTGCGC GATTATTGGA GGTGGTCCTG CAGGTTTGAG TGCGGGGGCTT	60
TATGCCACTA GAGGCGGTGT TAAAAACGCC GTTTTATTTG AAAAAAGGAAT GCCTGGGGGG	120
CAAATCACTG GCAGTAGTGA GATTGAAAAT TATCCGGGCG TTAAGGAAGT GGTGAGCCGA	180
TTGGATTTC A TGCAACCA	198

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 546 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...546
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129

GTGGGGAAAA GCTTGAGATA CAGCTTGAAT TTAGATCTCA ATCAAAAAGC CGATTGTGTTT	60
TTCAACCGAAT TAGAGCCAAC AGGTCTCAGG CTCTCCCCCA TCATGAAACG CTTTACTATC	120
AAAGGCGAAT TTGATTCAGG GCTAAAATCC TATGACATGA GCTACATGTA TGCGAGCCTT	180
CAAGCTATAA GCGCGATCAG GAGATTACCC TTAGGGCTTT ATGATGGGGT GCATGTCTAT	240
TCTAAAACGC CCATGAAGGA TATTGAAAAA TTACGCAACG CTTTAAAAAC AATCAACCAC	300
CATGGCATAG GCATTGAAGG GTGGTGGCAA CAAAACGGGA ATTTTTCCTC GGCGATGGAA	360
TTGGAAAAAA GAGCGTTATT CATGTGCTC ATGCTCATTA TTTAATGGC GTCTTTGAAT	420
ATCATCAGCT CGCTTTTAAT GGTGGTGATG AACAGGCGTA AAGAAATCGC CCTACTCTTT	480
AGCATGGGGA GCAGTCAAAA AGAAATCCAA AAAACCTTTT TTTATTTGGG TAATATCATT	540
AGTTTA	546

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:

187

- (A) LENGTH: 741 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130

```

ATGAAAAAAA CTTTTTTGAT CGCTTTAGCG CTTACGGCTT CTCTTATAGG CGCTGAAAAC      60
ACCAAATGGG ATTATAAAAA TAAAGAAAAT GGCCCGCACC GCTGGGACAA ATTGCACAAA      120
GATTTTGAAG TGTGCAAAAG CGGTAAAAGC CAATCGCCCA TCAACATTGA GCATTACTAC      180
CACACGCAAG ATAAAGCCGA TTTGCAATTC AAATACGCCG CTTCTAAACC TAAAGCGGTC      240
TTTTTCACCC ACCATACTTT AAAGGCTTCG TTTGAGCCGA CTAACCACAT CAATTATAGA      300
GGGCATGACT ATGTGTTGGA TAATGTGCAT TTCCACGCCC CTATGGAGTT TTTAATCAAT      360
AATAAAACCA GGCCTTTGAG CGCGCATTTT GTGCATAAAG ACGCTAAAGG GCGTTTGTG      420
GTGTTAGCGA TTGGTTTTGA AGAAGGGAAA GAAAACCCCA ACCTTGATCC TATTTTAGAA      480
GGCATTCAAA AGAAACAAAA TCTTAAAGAG GTGGCTTTAG ACGCTTTCTT GCCTAAAAGC      540
ATCAATTACT ACCATTTTAA CGGCTCTCTC ACCGCTCCTC CTGCACAGA GGGGGTGGCA      600
TGGTTTGTC TAGAAGAAC TTTGGAAGTT TCTGCCAAC AATTGGCTGA AATCAAAAAA      660
CGCATGAAAA ATTCGCCCAA CCAACGCCCC GTCCAGCCTG ACTACAACAC CGTGATCATT      720
AAAAGCTCGG CTGAGACCCG C

```

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131

```

ATGAAAATTT CTTTATTGGG GCATGGAAAA ACCACTCTAG CCCTAGGGCG TTTTTTTAAA      60
AAAAACCATA ATGAAGTCAA ATTTTTTGAT GATAAATTCC CTGCATTTT TAAGGATAGC      120
GAGGGTTTTT TTTGCTACCC TAGTAAGGAT TTTAACCTTA ATGATTCCCA ACTAGAAATC      180
GTCAGCCCTG GCATTAGTTT CACGCACCCT TTAGTCATGA AAGCCAAGCA TTTAATGAGC      240
GAATACGATT ATATTGATAG TTTGTTTGAT CATTCTTTCA CGCCTACGAT GATAAGTATT      300
ACGGGCACTA ACGGGGAAAAC CACCACGACC GAAATGCTCA CCACACTTTT AGAAGATTTT      360
AAGGCTGTGA GTGGGGGGAA TATCGGCACG CCCTTGATTG AATTGTTTGA AAAACGATCG      420

```

188

CCCTTGTTGGG	TGCTAGAAAC	AAGCTCCTTT	TCTTTGCATT	ACACTAATAA	GGCTTACCCT	480
TTAATCTACT	TGCTCATCAA	TGTGGAAGCC	GATCATTGA	CTTGGCATTG	CAATTTTGAA	540
AATTATTGA	ACGCTAAACT	CAAGGTTTTA	ACATTGATGC	CTAAACTTC	GCTCGCTATC	600
CTCCCTTTAA	AATTCAAAGA	ACACCCTATT	GTTCAAACT	CGCAAGCGCA	AAAAATCTTT	660
TTTGACAAAA	GCGAAGAGGT	TTTAGAGTGT	TTAAAAATCC	CTTCTAACGC	CCTTTTTTTTT	720
AAGGGAGCGT	TTTTATTAGA	CGCGGCTTTA	GCCCTTTTAG	TTTATGAGCA	ATTTTTAAAA	780
ATAAAGAATT	TAAAATGGCA	AGATTATAGA	GAAAACGCCC	TTAAAAGACT	GAACGCTTTT	840
AAAATCGGCT	CGCATAAAAT	GGAAGAATTT	AGGGATAAAC	AAGGGCGTTT	GTGGGTAGAT	900
GACAGCAAAG	CCACGAATAT	TGATGCCACC	TTACAAGCCC	TAAAAACCTT	TAAAAACCAA	960
AAAATCCATT	TGATTTTAGG	GGGCGATATT	AAAGGGGTCA	ATTTAACCCC	CCTTTTTGAA	1020
GAGTTTAAAA	ACTATAAAAT	AAGCCTTTAT	GCCATAGGAT	CAAGCGCTTC	TATCATACAA	1080
GCCTTAGCGT	TAGAATTTAA	TGTTTCTTGT	CAGGTTTGGT	TGAAGTTAGA	AAAAGCGGTT	1140
CAAGAAATTA	AAAGCGTTTT	ATTACAAAAT	GAAGTCGCTT	TGCTTTCACC	TAGCGCGGCC	1200
AGTTTGGATC	AATTTTCTTC	GTATAAGAA	AGGGGTGAAA	AATTCAAAGC	GTTTGTTTTA	1260
AAAGAT						1266

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132

ATGAAAGAAA	TCATTGTCGC	CCTTGTTGGGC	CAGCCTAATG	TGGGGAAATC	GTCCTTAATC	60
AACGCTTTGA	GTAACSCCCA	TTTAAAGTG	GGGAATTTTA	CCGRGGTTAC	CGTGGATAAA	120
ATGGAAGTGA	GTTTGATCCA	WAAAGATCAT	CAARTSWYTM	TC		162

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...333

189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133

GTGCATCGTT	TTTCTAGAAA	CCCATGCGCA	TCTTGCAATC	GCGCTCGCTC	TTGTTGAGA	60
CTATCTCGCT	CATTAGTGAG	CGCGGTAAC	TGGTGGTTGA	GCTTGTCGTT	TTGCGGTGGTT	120
AGTGCTTTAT	TTTCTTTAGT	CAGCTCGGTG	ATTTTATGGG	TTAGCTCGGT	GTTTTCTCTT	180
TTTAGCCTTT	CTTTTCTGT	TGTCAATTCT	CTTTTTCTT	CAGTCAGCCG	ATCTCTGGCT	240
GCTAATAAGC	GTGTGTTTTC	TTTAGCTAAA	ATGTCTTTTT	CCGTTTTCAG	TTCTGCTTTT	300
TCTTTAGTGA	GCTTGTTATT	GTTTTGCCAT	AAT			333

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134

ATGCAAAAAA	TGGGCGTTGT	CTCTTATTCC	GTGTTTCAAG	CGTTTGAAAA	GGCTTTGAGT	60
CGGTTTAAAG	AGGGCGTTGT	TTTGATTGTG	GATTCTTTAA	GGCGTTTGAT	TATGGGGAGC	120
GCTTCAGTTA	AAGAATTGAG	TGGGGTAATA	GGCATTGTGG	GGCGGTTAAG	CCATGCCAAT	180
AGCGTGAGCA	TGCTTTTGT	GTTTGGGGCG	TTTTTATCTA	TCAATCTAGG	GATTTTAAAT	240
TTATTACCCA	TTCCAGCCTT	AGATGGGGCG	CAAATGCTAG	GGGTCGTTTT	TAAAAATATT	300
TTTCATATCG	CTTTGCCAAC	GCCCATACAA	AATGCGTTGT	GGCTAGTGGG	GGTGGGGTTT	360
TTGGTTTTTG	TCATGTTTTT	AGGGCTTTTT	AATGACATTA	CTCGTTTGCT	A	411

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135

SUBSTITUTE SHEET (RULE 26)

190

GTGATGGCTT TGGTGAATAT TAGTGTGGTA GTTCCTGAGG GGGAACTTTA TACAGGAGAG	60
GTTAAAAGCG TTGTGTGGCC AGGAGTGGAA GGGGAATTTG GGGTGCTTTA TGGGCATAGC	120
AACATGATCA CCTTGCTTCA GCGGGAGTG GTTGAGATTG AAACCGAAAA CCAAAAAGAG	180
CACATTGCTA TCAATTGGGG TTATGCAGAA GTTACTAATG AACGGGTGGA TATTTAGCC	240
GATGGAGCGG TCTTTATTAA AAAAGGATCA GATGACAGAG ATGATGCTAT CTCTAGGGCT	300
AAAAAGCTTT TAGAGGACGC AAGCTCTGAC AGGTTAGCGG TCTCTAGCGT GCTGGCTAAG	360
ATTGAGTCTC TT	372

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136

ATGTATTCCT TGCTCTTAGA TTGAATAAA AAGACCGCTC TTTTAGGCAC AAGAGGGTTT	60
TTTATCGACG ACAAACACAT CAAAGAAAAG GGCTTGACCA CGCCCACTCT TTTAGAGCTT	120
TATAGCGATT TGAAGAAGC GATTCGTTTA AAATGCGAAT ACTTCATTAT GGAGGTGAGC	180
TCCCATGCGA TTGTCCAAAA CGCATCGCTG GGCTTGATT CGCTCTTAA ATTCTACCA	240
ATATCACAAG CGATCATT	258

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137

ATGAAAACGA ACTTTTATAA AATTAAATTA CTATTGCTT GGTGTCTTAT CATTGGCATG	60
TTTAACGCTC CGCTTAACGC TGACCAAAAC ACGGATATAA AGATATTAG TCCTGAAGAT	120

191

ATGGCGCTAA ATAGCGTGGG GCTTGTCTTCT AGAGATCAGC TAAAAATAGA GATCCCTAAA	180
GAAACCCTAG AGCAAAAAGT GACCATACTC AATGACTATA ATGATAAGAA TGTTAATATC	240
AAGTTTGACG ACATAAGTTT AGGGAGTTTC CAACCTAATG ATAATCTAGG TATCAATGCC	300
ATGTGGGGCA TTCAAAATCT TCTM	324

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138

ATGATTGATA SCCTTGATGG GGCAAAAGAT GCACAATTGA TAAAAAAGC TTACGCGTTT	60
TTGTGTTTAG GAGGCGATGG CACGATTTTA GGGGCTTTAA GAATGACGCA TGCTCACAAT	120
AAGCCATGCT TTGGGGTGAG GATTGGGAAT TTAGGGTTTT TGAGCGCGGT TGAATTGAAC	180
GGGTTGAAAG ATTTCTTACA AGATCTCAAG CAAAACAGGA TCAAAITAGA AGAGCATTTG	240
GCTTTGGAGG GCCGTATTGG AAACACTTCT TTTTATGCGA TCAATGAAAT CGTGATCGCT	300
AAAAAAAAG CTTTAGGGGT TTTAGACATC AAAGCGTGCG CGGGCCATAC GCCCTTTAAC	360
ACTTATAAAG GCGATGGGCT TATCATTGCC ACGCCCCTAG GCTCAACCGC TTATAATTTG	420
AGCGCTCATG GGCCCATTTG GCATGCTTTA AGCCAAAGCT ATATTTTAAC GCCCTTGTC	480
GATTTTTCTT TAACGCAACG CCCTTTAGTG TTAGGGGGCG AATTTTGCTT GAGTTTTTGC	540
GCTCATGAAG ACGCTCTTGT GGTATTGAT GGGCAAGCCA CCTACGATT AAAAGCCAAC	600
CAACCCCTAT ACATTCAAAA AAGCCCCACG ACCACCAAGC TCTTACAAAA AAATTCAAGG	660
GATTATTTTA AAGTGCTTAA AGAAAAGCTG TTATGGGGGG AAAGCCCTAA CAAAAAAGA	720

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139

192

ATGATAGTGG	GTTTGATAGG	GGTTGTGGAA	AAAATCTCTG	CTTTAGAAGC	GCATATAGAA	60
GTGCAAGGGG	TTGTTTATGG	GGTGCAAGTT	TCTATGCGAA	CGGCTGCTTT	GCTCCAAACG	120
GGCCAAAAAG	CGCGTTTGAA	AATCTTACAA	GTGATTAAAG	AAGATGCGCA	TCTTTTATAC	180
GGGTTTTTAG	AAGAGAGCGA	AAAAATTCTC	TTTGAAAGGC	TTTTGAAAAT	CAATGGGGTA	240
GGGGGGCGTA	TCGCTTTAGC	CATTCCTTCA	AGCTTTTCGC	CGAATGAATT	TGAAAACATT	300
ATCGCTACTA	AAGAAGTCAA	AAGACTCCAG	CAAGTCCCAG	GCATAGGGAA	AAAGCTCGCC	360
GATAAGATCA	TGGTGGATTT	GATTGGCTTT	TTCATTCAAG	ATGAAAACAG	ACCCGCGCGC	420
AATGAAGTCT	TTTTCAGCCCT	AGAGAGTTTG	GGCTTTAAAA	GCGCTGAAAT	CAATCCAGTT	480
TTAAAAACCC	TAAAACCCCA	TCTCAGCATA	GAGGCAGCGA	TTAAAGAAGC	CTTACAGCAA	540
CTGCGCTCT						549

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140

GTGGGGGTTT	TGTTGCGTT	GTTTTCTTT	TATGCGAAAA	ATAACCTTTT	GGAAAACACC	60
CAAAATACGCA	TGCAATACAC	CGCTGATGCG	ATCGCTAAAA	GCCTTTTAGA	ATTAAATAAT	120
GCCTCTTCTT	TAGAGCCTTT	AAAAATCTTA	GAAGAACGAT	TCAAAAACAC	CCCCTTTGTT	180
TTGTTGGACG	CAGACAACAG	AGTCAAGTTT	TCTAATATCG	GGGTGTTTGT	GGCCTCTTTT	240
AAAAATGACG	CCTTAATCAA	AACCCCTTAT	TTTGCGCTTA	AAAAACAGGG	CTTTTACCTC	300
ACAGACAGCG	CCCCAACTAA	CCGCTTAGGG	GTTTCTAAAA	TCATTATTGC	AGAAGAAGAA	360
ATTCAAAAAA	TCTTTATCCC	CCTTTATAAA	ATGATAGGCT	ATGTGTTTTT	GGGCGCGAGT	420
TTGTTTGTGC	CGCTAATAGC	CATGTGGCTT	TATAAAATCC	CA		462

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141

GTGGTAATAA	TGATTTTAGT	CTGCTTTTFA	GCTTGCTCGC	AAGAGAGCTT	TATCAAAATG	60
CAAAAAAAG	CCCAAGAGCA	AGAAAATGAC	GGCTCTAAAC	GCCCCAGCTA	TGTGGATTCC	120
GATTATGAAG	TCTTTAGCGA	AACGATTTT	TTACAAAACA	TGGTGTATCA	GCCTATAGAG	180
GAAAGAAACG	CTTTTTTCCA	ACTGACTAAA	GATGAAGACA	ATTCTTTTAA	CCCTGAAAAT	240
TCCGTGATTT	TACTGAATGA	GCCAAGCGAT	AATAGTGAAA	AAAACCTACT	CTCATACCCA	300
AACGATCCCA	ATAACAATGA	AGACAACGCT	AATAATAGTC	AAAAAAATCC	GTTCTTTTAC	360
AAGCCCAAAA	GAAAAACAAA	AAACCCAAAA	CTCATTGAAT	ATTCCCAACA	AGATTTCTAC	420
CCCCTAAAAA	ATGGGGATAT	TATCATGAGT	AAAGAAGGGG	ATCAATGGTT	GATAGAAATC	480
CAATCCAAAG	CCTTGAAGCG	TTTTTTAAAA	GATCAAAACG	ATAAAGATCG	CCAGATCCAA	540
ACTTTCACCT	TTAATGACAC	TAAAACGCAA	ATCGCGCAAA	TTAAGGGCAA	AATTTCTTCG	600
TATGTTTATA	CCACCAATAA	CGGTAGCTTG	AGTTTAAGGC	CYTTTTATGA	ATCGTTTTTG	660
TTAGAAAAAA	AGAGCGATAA	TGTTTATACG	ATAGAGAATA	AGGCTTTAGA	TACTATGGAG	720
ATTTCAAAGT	GTCAAATGGT	GTTAAAAAAG	CATTCAACCG	ATAAATTAGA	CAGCCAGCAT	780
AAAGCCATCA	GTATTGATTT	GGATTTTAAA	AAAGAGCGCT	TTAAGAGCGA	TACGGAACCT	840
TTTTTAGAAT	GTCTTAAGGA	AAGT				864

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142

ATGGCCGCTC	CACTACTTGC	TCTGCCCTTT	CTTTCTAACC	CTTTAGTGCT	TGGTGCTTTA	60
GCTGTCATAG	GAGTGGGTGC	TTACTTGTAT	CCCAATAAGC	AAGATTCTTT	AGTTGTGCAA	120
GCAGATGGGC	TTTATAGTGA	AATCTTGGG	TTTTTCATTT	CGTTTTCTAG	CAAGATCTTG	180
AAAGGAATTG	GTGAGCCTTT	AGCCAATGTT	ATCCAACCTT	TGGTATGGT	TTTAGGAATG	240
CTTTTAATCC	TTTTGTATTC	CTTTAAACGC	TATCAAAACA	ATGATTTTAT	TGAAATCAAA	300
ACCTTTTTTA	TGCTTTTTGT	GTTTGTAGGA	TACCTTTCTT	TGTACCATTA	TGCTTTTAAA	360
TCTGATGGTT	CTAGTAGCGG	TAATGGTCGC	TCCAGTTTTG	CCTTTCAAAA	TCATGTAACA	420
GAAATTTTTG	ACACGCCTGC	TAAGTGTGTA	AATGCTGGGA	TTTCTAATGT	GGTTAAGGAA	480
TATCAAACAA	ATAGTGCAAG	AGAACACAAG	AATATAGACA	CGCACCACAG	TATCACTAAC	540
GCTAATATTT	CATTCCATGT	CAGACAAATT	TTAAGGAGTT	TGAATAAACT	ATATGAAGAC	600
TTCAAATTA	ATAATGGACT	ATCGCTAAAA	ACCCTTATTG	CAGCTGTTTT	GTTATTAGTT	660
ATTTTAGGAT	TAGAATTGTT	TTTATGTTC	AAAGTTTTCT	GTTATGTTTT	TATGACTTAT	720
TTAGAAAAAA	TTATTTACTT	GTCTTTGGTT	ATTTTCATGC	TACTGCTAGG	GTTTTTTCAG	780
CAGACTAGAG	GTTTTTTAGT	GTCTTATGTG	AAAAAAATTA	TTTCATTGAC	TTTTTACATG	840
CCTTTGTTGT	TGCTATTAGT	GTTATCAAC	TCTTTTGCAT	TACAATACGC	AATCAAAGTG	900
GGAGGGAGCA	ATGAAATAGT	GGCTAAATTT	GGCATTATTG	TAGCAATAGG	AATTCACCTG	960
ACATTTATTC	AAAAAGTCCC	CGAAATGATT	AACGCTATCT	TTGGCACACA	AGGTGGTCTA	1020
ACGGATGCTA	AAAGCTTCAT	ATATCAAGGT	GTGCAATGG	CTAGTGCTGG	AGCTGGAGCC	1080
ATAGCTGGAA	GTCTTAAGAG	TGTGGGTCGT	TCAGCATTTG	GTAGAACGCT	AGAAGCTTAT	1140
AAAGACGCAA	AATCTACGAT	AAACAGCACT	ACGGCTAACA	TGAGAGACAT	GCCAGGACAT	1200
CCTGGTGTTA	GAGTGGGTGT	GGAGACGATT	GAACCTCCCA	AGTCTCATAG	AGCTAGCAAA	1260

194

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143

GTGTTAAAAT	TTCAAAAATT	ACCCTTATTG	TTTGTTCCTA	TTCTTTATAA	TCAAAGCCCT	60
TTATTGGCTT	TTGATTATAA	GTTTAGTGGG	GTAGCGGAAT	CTGTTTCTAA	AGTGGGGTTT	120
AACCATTCCA	AACTCAATTC	CAAAGAAGGG	ATTTTCCCTA	CAGCCACCTT	TGTAACCGCC	180
ACGATCAAGC	TTCAAGTGRA	TTYCAAATCT	GCTCCC			216

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144

ATGGGTAATC	ATTTTCTAA	ATTAGGATTT	GTTTTAGCGG	CTTTAGGGAG	CGCGATAGGT	60
TTAGGGCATA	TCTGGCGCTT	CCCCTATATG	ACTGGGGTGA	GTGGTGGGG	TGCTTTTGT	120
TTATTGTTTT	TATTTTATC	CTTAAGCGTT	GGTGGCGCGA	TGTTTATCGC	TGAAATGCTA	180
TTAGGACAAA	GCACGCAAAA	AAATGTAACA	GAAGCTTTTA	AAGAGCTTGA	CATTAACCCT	240
AAAAAACGCT	GGAAATACGC	AGGGATCATG	CTTATTTCTG	GACCTTTAAT	ACTGACTTTT	300
TATGGCACTA	TTTTAGGTTG	GGTGCTTTAT	TATTTGGTGA	GTATTAGTTT	TAATTTGCCT	360
AGCAGTATCC	AAGAAATCTGA	ACAAATTTT	ACTCAAACCT	TGCAGTCTAT	AGGGTTACAA	420
TCCATAGGGC	TTTTTAGCGT	TTTATTCATA	ACCGGATGGA	TTGTTTCTAG	GGGGATTAAA	480
GAAGGCATG	AAAAACTCAA	TTTGGTTTTA	ATGCCCTTAC	TCTTTGCCAC	TTTTTTTGGT	540
TTGCTTTTTT	ATGCCGATGAG	CATGGATTCT	TTTTCTAAAG	CTTTCCATTT	CATGTTGATT	600
TCAAGCCAAA	AGATT					615

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145

ATGGA AAAAG	TTTGC GTGAG	CGCAT GGGGG	TTGCCTAAGA	TTTTAGAAGA	AAGATTAAAA	60
GAAAAATATG	GCGATGATG	GGAAAAACAT	GTTAAGGCTA	AAGCAATAAA	CGAAGAAGAG	120
CTTGAAGAAC	AAGTCAAAGC	TAAAGCCAAA	GAGCAACAAA	AGACACAAAG	AGAAAAAACA	180
CTCAATGGAT	TTTTAAAAAA	AGTTGGTTTA	AAAAAGCGTG	ATATGTTACA	AAGCACTATG	240
TTATTTGATG	AAGTCAAAGA	AGCTGATGTG	CTTTTCAAG	CAGAGCGTAA	AATTGGCGAT	300
TGGATTTTTA	GCAGTGCGGT	GTTCTTTTTT	GCTCTAGCCC	TTATAGAAGC	CATTATTATT	360
GTATGCTTAT	TGCCGTTAAA	AGAAAAAGTG	CCTTATTTAG	TAACCTTTTC	AAACGCTACA	420
CAAAATTTTG	CCATAGTCCA	AAGAGCAGAC	AAGAGCATCC	GTGCTAATCA	AGCGCTTG TG	480
AGACAATTGG	TAGCGTCTTA	TGTTAATAAT	AGAGAAAATA	TTTCAAGTAT	AAAAGAGCAA	540
AACGAAATAG	CCCACGAAAC	CATTAGGTTG	CAAAGCGCAT	TTGAAGTGTG	GGATTTTTTT	600
GAAAAACTGG	TTTCTTATGA	GCATAGCATT	TACACTAATA	TAAATCTAAC	ACGAAAAATT	660
AGCATTATCA	ATATCGCTTT	AATCAGTAAA	ACCCAAGCCA	ATATTGAAAT	ATCCGCACAA	720
CTTTTTTATA	AAGAAAAGTT	AGAAAGCGAA	AAGCGTTATA	GAATAATTAT	GACCTTTGAA	780
TTTGAACCTA	TTGAAATGTA	TACAAAATCT	GTTCCCCTAA	ACCCTACAGG	CTTTATTGTT	840
ACAGGTTATG	ATGTAAGTGA	AATTGCGATT	TTAAAAGATT	TAGATGAGAA	AAATAAAGTC	900
AAAGATGATG	GTGTGAAATC	TAGGATTATC	CATGTCGAGA	AAAAAGACCC	TCATATGAGC	960
CAGTATAAAG	ATGTTAAGGA	GCAA				984

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...228

196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146

ATGCTGCATA AGGCTAAGGT GGGCATCGTG TTTCAGGCGC TTTTAGGGAT TTTTGCCTG	60
TTTTTATTGT TGTTTTACTT GAGCGCGTTT TTAATGGTGG CTTTAAAGA CACTAAACGC	120
ATGTTTATAA GCGTTTTAAT AGGGAGCGTG GTGTTCCCTT GGAGCGATCT ATTGGTCTTT	180
GTAGGGTTTA AAAATATCAG CTTTGTTTTG GATATTGGTT ATGAAATC	228

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147

ATGCCGTTTT TGA AAAA CTG GATCTGGAGT TTAAAGATGG CTTTGAGCGC GATTAGTGGG	60
GCTAGTGGGG TGGGGAAAAG CGTCCTTATT GCGAGCCTTT TAGGGGCGTT TGGGCTTAAA	120
GAGAGCAACG CTTCAAACAT TGAAGTGGA TTGATCGCGC CTTTTTTAGA CACGGAAGAA	180
TACGGCATT TTAGAGAAGA TGAGCATGAA CCCTTAGTTA TTAGCGTGAT TAAAAAGAA	240
AAAACACGCT ATTTTTTAAA CCAAACAAGC CTATCTAAAA ACACGCTCAA AGCGTTATTA	300
AAGGGGCTTA TTAAACGCTT ATCTAACGAC AGATTGAGCC AGAATGAACT CAACGATATT	360
TTAATGCTCT CCTTATTAGA TGGCTATATC CAAAATAAAA ATARGCGTTT AGCCCCCTTT	420

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 924 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148

ATGCCACAAA ACCAGCTTGT GATCACCATC ATTGATGAAT CAGGCTCTAA GCAACTCAAA	60
TTTTCTAAAA ATTTAAAACG CAACCTCATC ATTCTGTG TCATTCTTTT ATTGATCGTG	120

197

GGGCTTGGCG	TGGGGTTTTT	AAAATTTTTT	ATCGCTAAAA	TGGATACGAT	GACAAGCGAG	180
AGGAATGCGG	TTTTAAGGGA	TTTAGGGGT	TTGTATCAAA	AAAATTACGC	CCTAGCGAAA	240
GAGATTAAAA	ACAAGCGAGA	AGAGCTTTTT	ATTGTGGGGC	AAAAGATCCG	TGGGCTAGAA	300
TCCTTGATTG	AAATCAAAAA	GGGGGCTAAT	GGGGGAGGGC	ATCTCTATGA	TGAAGTGGAT	360
TTAGAAAATT	TGAGCTTAAA	TCAAAAACAT	TTAGCACTCA	TGCTCATTCC	TAATGGCATG	420
CCCCTAAAAA	CTTATAGCGC	TATCAAACCC	ACTAAAGAAA	GGAACCAACC	CATTAAAAAG	480
ATTAAGGGCG	TTGAATCCGG	GATCGATTTT	ATCGCGCCAT	TGAACACGCC	TGTGTATGCG	540
AGCGCTGATG	GGATTGTGGA	TTTTGTGAAG	ACTCGTTCTA	ATCGGGGGTA	TGGGAAC TTG	600
GTGCGCATTG	AACATGCGTT	TGGTTTCAGC	TCCATT TATA	CGCACTTAGA	TCATGTCAAT	660
GTGCAGCCTA	AAAGCTTCAT	CCAAAAAGGG	CAGTTGATTG	GCTATAGCGG	GAAGAGCGGT	720
AATAGCGGCG	GCGAAAAATT	GCATTATGAA	GTGCGTTTTT	TGGGTAAAAAT	TTTAGACGCA	780
GAATAATTCC	TAGCATGGGA	TTTGATCAT	TTTCAAAGCG	CTTTAGAAGA	AAATAAATTT	840
ATTGAATGGA	AGAATCTGTT	TTGGGTTTTA	GAAGACATCG	TCCAGCTCCA	AGAGCATGTG	900
GATAAGACA	CCTTAAAGG	TCAG				924

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149

ATGATCACTG	GCTCTCACAA	CCCCAAAGAA	TACAACGGCT	TTAAATCAC	GCTCAATCAA	60
AACCCGTTTT	ATGGCAAGGA	CATTCAAGCT	TTAAAAACA	CGCTTTTAAA	CGCAAAGCAT	120
GAAATAAAGC	CCCTAAAGA	AACGCCAGAG	AAAGTCAATG	CCCTAGAAGC	GTATCATCGC	180
TATTTGATCA	AGGATTTTAA	GCATTTAAAA	AATCTTAAAT	ACAAAAATCGC	CCTGGATTTT	240
GGTAATGGCG	TGGGGGCGTT	AGGATTAGAG	CCGATTTTAA	AGGCTTTAAA	CATTGATTTT	300
AGCAGCCCTT	ATAGCGATCC	TGATGGGGAT	TTTCCTAACC	ACCACCCAGA	CCCTAGCGAA	360
GCGAAAAACT	TAAAAGACTT	AGAAAAACAC	ATGCGAGAAA	ACGCTATTTT	AATAGGCTTT	420
GCTTTTGATG	GCGATGCGGA	TAGGATTGCG	ATGCTAAGCT	CTCATCATAT	CTATGCGGGC	480
GATGAATTAG	CGATTTTATT	CGCTAAACGC	TTCATGCTC	AAGGCATCAC	CCCTTTTGTG	540
ATCGGCGAAG	TCAAATGCTC	TCAAGTGATG	TATAACGCAA	TCAATACTTT	TGGTAAGACG	600
CTCATGTATA	AAACCGGGCA	TAGCAATTTA	AAAATCAAGC	TCAAAGAAAC	TAATGCGCAT	660
TTTGCGGCTG	AAATGAGCGG	GCATATCTTT	TTTAAAGAAC	GCTATTTTGG	CTATGATGAC	720
GCTCTTTACG	CATGTTTAA	GGCTTTGGAG	TTATTGCTTG	AACAAAGTCC	AAGCGACTTG	780
GAAAACACCA	TTAAAAACCT	CCCCTATTCC	TACACCACGC	CTGAAGAAAA	AATCGCCGTG	840
AGCGAAGAAG	AAAAATTTGA	AATCATTCGC	AACTTACAAG	AAGCGCTTAA	AAACCCGCCA	900
AGCCATTTC	CTACAATCAA	AGAAATCATC	AGCATTGATG	GCGTGAGAGT	GGTTTTTGAA	960
CATGGCTTTG	GGCTTATTCG	CGCAAGCAAC	ACCCACCCCC	TATTTAGTCA	GCCGCTT	1017

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...621
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150

ATGTCCAAGA	ACCTTCAAAA	GAAGAATCCA	AAGAAGAGTT	TYCCACAAGC	CCAGAAAGCC	60
ATAAGGGAGA	TGAAATGTT	TGAAACCATT	GCYTTTATT	TCTTTCGAT	CCTTACTTTA	120
AGCATGGCGT	TAGTGGTGAT	CACAACCACA	AATATCCTCT	ATGCCATTAC	CGCTCTCGCT	180
AGTAGCATGG	TTTTTATTTT	TGCTTTTTTC	TTTTTACTGG	ACGCTGAGTT	TTTGGGCGTG	240
GTGCAATCA	CGGTGTATGT	GGGTGCGGTC	ATTGTGATGT	ATGCGTTTGG	CATGATGTTT	300
TTCAACTCCG	CTGCAGAAGT	AGTTGAACGC	AAGCAAAGCC	CTAAAATCTT	GTGCGTTCTT	360
TCATTTGGCG	TGGCGCTGTT	GCTCACCTTG	ATTTTAAGCG	CTCCTAGCAT	TGSSGAAAAC	420
CTTTCTAAGC	AAGTCAATTC	CAACGCTATT	GATGCGCAAA	TYCCYAACAT	TAAAGCGATT	480
GGTTATGTGC	TTTTCACCAA	TTACCTCAT	CCCTTTGAAG	CGGCGGCTTT	AATGCTTTTA	540
GTCGCTATGG	TTGGAGGCAT	CGCTACAGGG	ATTCAAAAAA	TCCATGGGAA	AAATCACACG	600
CAATTATATA	AGGAATCTCT	A				621

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 753 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151

ATGGGTGCAA	TTTTATCTAT	TTTAAACTT	GAAATCAAAT	CTTATCTCAC	CAATACAAGC	60
GCGCTATTTT	GGACTTTTAT	TTATCCTATT	TTAATGCTCC	TATTACTAAT	TTTTGTTTTT	120
TCAAAAAATA	CCACTGAAAT	TTTTTACTTT	AATAACATTA	TAGGTCTAAT	GGGACTTCTT	180
ATTATTTCCTA	GCGCGATCTT	TGGTCTCACA	CAAGCTATAA	CAAGCTCTAG	ATCGCATAAT	240
ATATTCTTAT	TCTACATGCT	ATCACCAGCA	ACTTTCAAAC	AAATAACTCT	AGCATTAATC	300
GCTTCAAGAC	TAATCGTTGT	AATCCTATAT	GCTTTTATCT	TTATTGTTCT	CTCTTTTTAT	360
GCGCTCAATA	TCATCACTAT	TCCTAATTTT	AAAGCGCTTA	TTTTGGGGTT	TATTAGCATT	420
TTTTCAAGCG	CATTGTTTTG	TTTTTGCTTG	GCAATTTTTG	TAGCTAGAAT	TTTTCAAAAC	480
GAACAAAGCA	TCTTAGGATT	TTGTAATATC	ATCAATCTCT	ATGCGCTAAT	GTCTTGTAAT	540
GTTTTTGTTT	CTTTAGAATA	CCTACCTAAT	ATTGGTCAAT	TATTTATCAA	AACATCTATT	600
TTTTACTACC	TTAATCAACT	TCTAATCAAA	GCTTTTCAAG	GGATTGATAC	TATACTGGTT	660
TTAGCAACTT	CAACATTTT	CATTATTGGT	GGCATTATTT	TATTTTACT	AAGCGCTAAT	720
CGCATGTTAC	TAACACCAA	AGAACGCATG	CGT			753

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152

ATGGCAGGCA CACAAGCTAT ATATGAATCA TCTTCGCGAG GATTCTTATC GCAAGTCTCC	60
TCAATCATCT CAAGCACAAG TGGTGTGCGA GGGCCATTTG CAGGAATAGT AGCGGGCGCT	120
ATGACAGCAG CGATTATTCC TATTGTTGTG GGATTACTA ATCCGCAAAT GACCGYTATY	180
ATTRACCCAA TAYAATCAAA GCATCGC	207

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153

GTGAGCCGTA TTTTAGGCTT GAGCGATGAT TTAGCGATGA CTTTATGCGC TGAATCCATC	60
CGCATTCAAG CCCCTATCAA AGGTAAAGAT GTCGTTGGTA TTGAAATCCC TAACAGCCAA	120
AGCCAAATTA TTTATTTAAG AGAAATTTTA GAAAGCGAAT TGTTCAAAA ATCCAGCTCG	180
CCTCTAACCC TAGCTTTAGG CAAAGACATT GTGGGTAACC CTTTCATCAC GGATTTAAAA	240
AAGCTCCCCC ACTTGCTCAT CGCCGGCAGC ACAGGGAGCG GTAAGAGCGT GGGCGTGAAT	300
CGGATGATTT TATCCTTACT TTATAAAAAA CCCCCC	336

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

200

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154

ATGGATGAAA GSCTCGTTTA TGGGGTGATT TGCATGCCCA GTCAGGTTTT TGCCAACACC	60
GGCACTAACG TGAGCATCAT CTTTTTTCAA AAAACGCCAA GCGCAAAGGA AGTGATCTTG	120
ATTGACGCTT CCAAACCTCG CGAAGAATAC ACCGAAAACA AAAACAAAAA AACGCGCTTA	180
AGGCCAAGCG ATATGGATT TATTTTAGAA ACTTTCCAAA ATAAAGCCCC AAAATCGGAT	240
TTTTCGCTC TGGTTTCTT TGATGAAATT ACAGAAAAAA ATTATTCTCT AAACCCCGGG	300
CAGTATTTC CTATAGAAGA CACGAGCGAG ACAATCAGCC AAGCGGAGTT TGAAACTTG	360
ATGCAACAAT ATTCAGCGA ACTAGCGAGC CTTTTGATG AAAGCCAAAA TTTGCAACAA	420
GAGATTTTAG AAACTTTAAA AGGGGTTAGG TTTGAG	456

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155

ATGAGAAGAA TTATTAAAAA CACACTTTCA CGCTTAGGCT ATGAAGATGT TTTAGAAGCT	60
GAGCATGGGG TGGAAGCTTG GGAAAACTA GACGCTAATG CCGACACTAA GGTGCTTATT	120
ACGGATTGGA ACATGCCTGA AATGAACGGG TTGGATCTCG TTA AAAAGGT GCGTGC GGAT	180
AACCGATT TA AGGAAATCCC TATCATTATG ATCACCACAG AGGGCGGTAA AGCTGAGGTC	240
ATTACGACTT TAAAGCGGG CGTGAATAAC TACATTGTGA AACCTTTTAC CCCCCAAGTT	300
TTGAAAGAAA AATTAGAGGT TGTTTTAGGG ACAAACGAT	339

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs

201

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156

ATGGCAGAAG	AACAAGAAAA	TACCGCGCAA	CAACCCCAAA	AAAAAAGCAA	AGCCCTTTTA	60
TTTGTCATTA	TTGAAGCGT	GCTAGTGATG	CTTTTATTGG	TGGGGGTGAT	TATCATGCTG	120
CTTATGGGGA	ATAAGGAAGA	ATCTAAAGAA	AACGCTTCTA	AAAACACCCA	AGAAGTCCAA	180
GCTAATCCTA	TGGCGAACAA	GAATCAAGAA	GCCAAAGAAG	GCTCTAATAT	CCAGCAATAT	240
TTGGTGCTTG	GGCCTTTGTA	TGCGATTGAT	GCGCCTTTTG	CGGTGAATTT	GGTCTCTCAA	300
AATGGCAGAC	GCTACCTTAA	GGCTTCTATT	TCGCTAGAAT	TGAGCAATGA	AAAGCTTTTG	360
AATGAAGTCA	AGGTTAAAGA	CACGGCGATT	AAGGACACGA	TTATAGAAAT	TCTATCGTCT	420
AAAAGCGTGG	AAGAAGTGGT	TACTAACAAA	GGCAAAAACA	AGCTTAAAGA	TGAAATTAAG	480
AGCCATTTGA	ATTCGTTTTT	GATTGATGGC	TTTATTAAAA	ATGTCTTTTT	CACTGATTTT	540
ATTATCCAA						549

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157

ATGGGGTGTT	TTAGCACCAT	TTGTTGTAAG	GGTTTAACGC	TTAGCGTTGG	TGGATTTTTG	60
GTGATGATGA	GATTCTTAAT	ATTCAAAGAT	TTTTGCAAAG	ATTTT		105

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2106 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158

GTGGCGCGTC	TTGTGGTTAA	AAGGCGTAAA	ATTGATTATA	AACAAAGCAT	TCAATCTGAC	60
TCTCAATACT	TGCAAGCGAS	CTTGAATCAG	TTTGAAAATA	AAGAAGTGTA	TGAGAATCAG	120
TATTTTTTAG	TTTTAGAAAG	CACTCACTCT	TTGCATGGCG	TTTTGGAGCA	TAAGAAAAAA	180
TCTTTCATGC	ACGCTAATAG	AGAAAAATTT	AAGGATATTC	TCTCTTATAA	AGCGCATTTT	240
TTGCAAGAAA	CTTTAAAAAG	CTTAGAAATC	CAGCTCAAAA	ACTATGCCCC	CAAACCTTTA	300
AACTCTAAAG	AGGTTTTGAA	TTTTATGCA	GAATATATTA	ATGGGTTTGA	ACTCCCTTTA	360
AAACCCCTAG	TAGGGGGGTA	TTTGAGCGAT	AGCTATATCG	CTAGTTCTAT	CACTTTTGAA	420
AAAGATTATT	TCATTCAAGA	AAGCTTTAAT	CAAAAAACCT	ATAACCGCTT	GATTGGGCATT	480
AAAGCTTATG	AGAGCGAAAG	GATCACTTCT	ATAGCGGTGG	GAGCGCTTTT	ATACCAAGAG	540
ACGCTTTTGG	ATATTATCTT	TTCCATAGAG	CCTATGAGCG	TCAATAAAAC	GCTGAGTTTT	600
TTAAAAGAGA	GGGCCAAGTT	TAGCATGTCT	AATCTTGTTA	AAAACGAGCT	ATTAGAATAC	660
CAAGAATTAG	TCAAAACCAA	ACGATTATCC	ATGCAAAAAT	TCGCCCTAAA	CGTTCTTATC	720
AAAGCCCCCA	GTTTGGAGGA	TTTAGACGCT	CAAACAGCT	TAATTTTAGG	GCTTTTATTT	780
AAAGAAAAC	TAGTGGGCGT	TATAGAAACT	TTTGCGTTGA	AAGGGGGGTA	TTTTTCCTTT	840
TCCCTGAAC	GCATCCATTT	AAACCACCGC	TTGCGTTTTT	TAACCTCTAA	AGCCCTAGCG	900
TGTTTGATGG	TGTTTGAAAG	GCAAAATTTA	GGTTTAAAG	CTAATTCATG	GGGGAATAGC	960
CCTTTGAGCG	TGTTTAAAAA	TTTGGATTAT	TCCCTTTTTT	TATTCAATTT	CCACAACCAA	1020
GAAGTGAGCC	ATAATAACGC	TAAAGAAATT	GCCAGAGTGA	ATGGGCATAC	TTTAGTTATA	1080
GGGGCAACCG	GAGCGGTAA	AAGCACGCTG	ATTAGCTATT	TAATGATGAG	CGCTTTAAAA	1140
TACCAAACTA	TGCGCCTTTT	AGCTTTTGAC	AGGATGCAAG	GGTTGTATTC	TTTCACCGAA	1200
TTTTTTAAAG	GGCATTACCA	TGACGGCCAA	TCPTTTAGTA	TCAACCCCTT	TTGTTTAGAG	1260
CCTAATTTGC	AGAATTTAGA	ATTTTTCGAA	TCCTTTTTTT	TGAGCATGTT	GGATCTTGCC	1320
CCTTCAAGGG	ATAAAGAAGC	CTTAGAAGAC	ATGAATGCCA	TTTCTGGCGC	GATTAAGAGC	1380
CCTTATGAGA	CCTTATACCC	CAAAGATTTT	AGTTTGCTGG	ATTTTAAAGA	AACGCTTAAA	1440
AGAACCTCAT	CTAACCAATT	GGGCTTGAGT	TTAGAGCCGT	ATTTGAATAA	CCCCCTTTTT	1500
AACGCTTTGA	ATGACGCGTT	CAACTCCAAC	GCTTTTTTAA	ATGTGATAAA	CCTAGATGCG	1560
ATCACCCAAA	ACCCTAAAGA	CTTAGGGCTT	TTAGCCTATT	ACTTGTTTAA	TAAGATCTTA	1620
GAGAGTCTA	GGAAAAACGA	CAGCGGCTTT	TTGGTTTTTT	TAGACGAATT	TAAATCCTAT	1680
GTGGAAAACG	ATTTGTTAAA	CACTAAAATC	AACGCTTTAA	TCACGCAAGC	CAGGAAAGCT	1740
AATGGCGTGG	TGGTGTGGC	CTTGCAAGAC	ATTTACCAAC	TTAGCGGGGT	TAAAAACGCC	1800
CATAGTTTTT	TAAAGCAACAT	GGGGACTCTC	ATTTTGATC	CGCAAAAAAA	CGCTAGGGAA	1860
TTGAAACACA	ATTTCAATGT	GCCTTTGAGC	GAAACTGAAA	TTTCTTTTTT	AGAAAAACACC	1920
CCTCTGTATG	CCAGGCAGGT	TTTAGTCAAA	AATCTGGGTA	ACGGGAGTTC	CAACATGATT	1980
GATGTGAGTT	TGGAGGGCTT	GGGTGTTTAT	TTGAAAATCT	TTAATTCAGA	TTCCAGTCAT	2040
GTCAATAAAG	TGAAAGCGTT	ACAAAAAGAC	TACCCTACAG	AGTGGCGTGA	GAACTTTTTG	2100
AAGAGT						2106

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

203

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159

```

ATGCAAGAAG ACTGGCAAGC CGTCCAAGAC ACCATTAAAG TGGTTTCAGA TGTGAAAGCG      60
GGGAATTTTG CGGTGCGCAT CACGGCTGAA CCCGCAAGCC CTGATTTGAA AGAATTGAGA      120
GACGCGCTAA ATGGGATCAT GSAYTATTTG CAAGAAAGCG TAGGGACTCA CATGCCAAGC      180
ATTTTCAAAA TCITTGAAAG CTATTCTGGC TTGGATTITA GAGGGCGGAT CCAAAAACGCT      240
TCGGGTAGGG TGAATTGGT TACTAACGCT TTAGGGCAAG AAATCCAAAA AATGCTAGAA      300
ACTTCGTCTA ATTTTGCCAA AGATCTAGCG AACGATAGCG CGAATTTAAA AGAATGCGTG      360
CAAAATTTAG AAAAGGCTTC AAACCTCCCA CACAAAAGCC TGATGGAAAC TTCCAAAACG      420
ATAGAAAATA TCACCACTTC CATTCAAGGC GTGAGCTCTC AAAGTGAAGC CATGATTGAA      480
CAAGGGAAAG ACATTAAAAG CATGTAGAA ATCATTAGAG ATATTGCCGA TCAAACGAAT      540
CTATTAGCCC TAAACGCTGC TATTGAAGCC GCACGAGCCG GCGAGCATGG CAGAGGCTTT      600
GCGGTGGTGG CTGATGAGGT GAGGAAGCTC GCTGAAAGGA CGCAAAAATC CCTCAGTGAG      660
ATTGAAGCCA ATATTAATAT TCTCGTTCAA AGCATTTTCA ACACGAGCGA AAGCATTAAA      720
AACCAGGTTA AAGAAGTAGA AGAGATCAAC GCTTCTATTG AAGCCTTAAG ATCGGTTACT      780
GAGGCAATC TAAAAATCGC TAGCGATTCT TTAGAAATCA GTCAAGAAAT TGACAAAGTC      840
TCTAACGATA TTTTAGAAGA TGTGAATAAA AAGCAGTTT      879

```

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160

```

ATGCCTAAAA GTTTCACCTT ACCGACTTTC GTGTGTTGTT TGTITGTGGG GGTATCTTA      60
AGGAACGCTT TGTCGTTTTT TAAATCCAT AGCGTGTGTT ACAGAGAGGT TTCAGTTATA      120
GGGAATGTGA GCTTGAGCCT GTTTTAGCT TACGCT      156

```

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 546 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

204

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...546
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161

GTGGGGCTTT	TAAATTCTAA	GGCGTTCAAA	CCCTACCGCA	AGATTTTGCA	AATGGTGTTT	60
CAAGACCCCT	ACGCATCATT	AAACCCCTCGC	TTAAGCATTTC	AAAGCATTITT	AATAGAAGCT	120
TTGCGCTTTG	CTTACCCTAA	AGCTTCACAA	CAAGAATGGC	ACCATTTAGC	TGAACTTTGC	180
TTAGAAGAAG	TGTGTTTAAA	CCCTGAATTG	CTTAACTTTT	ACGCTTATGA	GCTCAGCGGA	240
GGGGAGCGCC	AAAGAGTGGC	GATCGCTAGA	GCGATTGCCT	TAAAACCTAG	AATCATTCTT	300
TTAGATGAGC	CAACCTCTGC	TTTAGACAAA	AGCATTCAAA	AAAGCGTGTT	GGAATTATTG	360
TTGAATTTAC	AAGAAAAGCA	GGATTTGAGC	TATTTGTTTA	TCAGCCATGA	TTTAGATGTG	420
ATCAAAGCTT	TTTGGGATAG	GGTGTAGTG	GTGAGTGAGG	GGAAAATCGT	GGAAACAGGC	480
GCTATTGAAG	AGGTGTTTGA	CAACCCCAA	CACGCTTATA	CCAAGCGTTT	GTTGGAATCC	540
AGGCTT						546

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 753 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162

GTGAGTTTGA	TTAAAGTTAG	TGGTGATAAA	AAAGTGATTG	AGGTTTCTAT	TCCTTTAACT	60
TCCATTTTCA	GCAAAGCGCG	TGTGAAAATC	AGACATGCCT	TTAGCGATTG	TGGTATTTCA	120
ACAGCGACTA	GAAAAATCCC	TTTTAGTTTA	AAGCATTATG	TAGAGTGGCA	GATCGGTTAT	180
GATGTCCCCA	TTAAAGATAA	AGAAAAATTT	GAACTCACTA	CTTTAAAAGA	TGAAAAATAT	240
CATTTTTTAG	GGGCTAATAA	TAAAGTAAAA	ACTCTTTATG	AATTGAGCGA	AATGATTTAT	300
TACGCTAAGC	GATTGGGTTT	AATCAGTTTA	GAAAATTTAG	AAAATACTTT	AAAAATTTTA	360
GAAAAACAAA	AACAATTTAT	AGAAGATAAT	TTTATGATTA	CAAGAGAAAG	ATTTAGATCG	420
CATCAATTTG	GTGGCATGGA	TTTTGAAGTC	TCACGCATTT	CTTATCCTTT	GCTCATTTCAT	480
TCTTTTGATG	ATAATGAGTT	GAGCGAAATA	GTTATTAAGG	AACAACAATA	TGGCTCTAAA	540
ACCCAAGCCA	TGCTGTATTT	TTGCTTTTCT	ATTTTGGAGT	TAAAAACCGC	TACCCCTTTA	600
TTAAACAGAA	CCGCTATGCC	CAAAGAACAT	GCCCTTTTGA	TTATCCATGA	AACCAACGCT	660
CTTGTGTTTT	TAGAAATGCT	TAAAATTTTT	GGACTTTTAA	GCCAAGTGCA	CCATAACGAT	720
GTGTTWAAGA	TTTTWGAAAA	AATACTTCAA	AAT			753

205

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163

```

GTGATCACGG CGTGTTTTAA TAGYGAAAAA ACCATTGAAG ACACCATTCT TTCCGTGCTT      60
AATCAAACCTT ATAAAAACAT TGAATACATC ATTATAGATG GGGCTAGCGC GATAGCACTT      120

```

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164

```

GTGTTTGTAG GCCTTTATCA TGGGGCAAGC ATCTTTGATT TAAAATTGA AGTCTATCTT      60
ACTATGCTAA TCTCTTTAAT GCCCTTTGTG GCTACGATTT ATATCAATTT CCCAAAACCC      120
ACAGAAACTT CGCATGGCTA TCGGAGATGG GCTAATGTTA AAGATATAGA ATGCTTTAAA      180
ATTTTATGCA AAGAGGGCTT TTGTAAAGTG GTGCATAGAT TAGGGGTGCA ATTTGATAAT      240
GGCTTTATTC TAGGTAAATT TGTTTTCCA AAGCTTAGAA ATGTGTGCTA TGACAAGCCC      300
TTAGGAACGA TGATTGTTGC ACCCCCTGGT GCGGAAAAAC TGCATGTGTG GCTTTGCCAA      360
ATTTAT

```

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

206

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165

ATGAAACGCC	TTGCTGTTGC	GCTTATTTTG	GTGTTGGGAG	TGGTGTGGGG	GAAATCCTTG	60
CCTAAGTGGG	CAAAAGATTG	CTCAAAAGAG	ATGCGGATTG	AAAAGACCCA	AACCAAAGAT	120
GAAAAAATTT	TAGTGTGTGG	GATGAGCGAT	ATATTGCTTT	CAGATATGGA	TTATAGCTTG	180
TCCTCAGCCA	GACAAAACGC	CTTAGAGAAA	GTGATGGAAG	CTTTCAAGGG	GGATAGAATA	240
GAGATTAAGG	CTGGTGAGCT	AAAGGCCACT	TTTATTGATA	CGGATAAAGT	TTATGTGCTT	300
CTAAGAATCA	CTAAGAAGCA	TGTCGCTTTA	ATGAATGAG			339

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1311 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166

ATGAACCCCC	AGATTCAACC	CGCCACTAAA	AAACCCTTAA	AATCCCTTTT	AGCCGCTAGT	60
TCAGGCAATT	TAGTGGAATG	GTATGATTTT	TACGCTTATG	CGTTCCTTGC	TCCTTATTTT	120
GCTAAGGAAT	TTACCCACAC	CAATGACCCT	ACTCTAGCGC	TCATCTCAGC	TTTTTTAGTT	180
TTTATGCTAG	GGTTTTTCAT	GCGCCCTTTG	GGGAGTTTGT	TTTTTGTTAA	ATTGGGGGAT	240
AAAAAGGGGC	GTAAAACTTC	CATGGTGTAT	TCCATTATCC	TTATGGCGCT	AGGCTCTTTC	300
ATGCTCGCAT	TGCTCCCCAC	TAAAGAAATC	GTAGGGGAAT	GGGCGTCTCT	GTTTTTATTG	360
TTAGCCAGGC	TTTACAGGG	CTTTAGCGTG	GGAGGAGAAT	ATGGCGTGCT	CGCCACTTAT	420
CTCTCTGAAT	TAGGCAAGAA	TGGTAAAAAA	GGTTTTTATG	GCTCTTTCCA	ATATGTAAC	480
TTAGTGGGAG	GGCAACTCTT	AGCTATTTTT	TCGCTCTTTA	TCGTTGAAAA	CGTTTACACG	540
CATGAGCAAA	TCAGCGCGTT	TGCTTGGCGT	TATTTATTTC	CTTTAGAGGG	TATATTAGCC	600
CTACTCTCGC	TCTTTTTGG	AAATATCATG	GAAGAACTA	TGGATAATGA	AGCGACTCCT	660
CAAAAAAAGA	CTAATGTAAA	TAATACAAAA	GAAACCCATA	TCAAAGAAAC	CCAAAGAGGC	720
AGTTTAAAGG	AAITGCTCAA	CCATAAAAAA	GCCTTAATGA	TAGTCTTTGG	GCTAACTATG	780
GGAGGGAGTT	TGTGCTTTTA	CACTTTTACG	GTGTATTAA	AAATCTTTTT	AACCAACAGC	840
TCATCGTTTA	GCCCTAAAGA	AAGCAGTTTT	ATCATGCTTT	TAGCGCTCTC	TTATTTTCATC	900
TTCTTACAAC	CCTTATGCGG	GATGCTTGCG	GATAAAATCA	AACGCACCCA	AATGCTGATG	960
GTTTTTGCGA	TCACAGGGCT	TATTGTAACG	CCTATTGCTCT	TTTATGGTAT	CAAGCATGCC	1020

SUBSTITUTE SHEET (RULE 26)

207

ACTAGCGTGT ATGAAGCCCT ATTTTATGAA ATACTCGCAT TGAGCAGCAT GAGTTTTTAC	1080
ACTTGCAATG CTGGGGTTAT TAAGCGGGAA TTATTCCCTG AACATGTGCG AGCGCTTGCG	1140
GTGGGTTTAG CCTATGCGAT CGCCAATGCG CTTTTTGGAG GGAGCGCGAG TTATATAGCG	1200
TTAGAGTTCA AACAGCATGG TTTTGAAGAG GGGTTTGTGG GCTATGTCAT GTTGAGTATT	1260
GTTATCTTTA TGGTTATGGT TATCATATTC CCTAAAAAA CCTATTGGA G	1311

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167

ATGGACATTA GCATTTTTAG AGAATACGAT ATTAGAGGCA TTTACCCAC CACTTTAGAT	60
GAAAATACGG CTTTATAGTAT CGGCGTGGAG TTGGGAAAAA TCATGCGAGA ATACGATAAA	120
AGCGTGTTTG TAGGGCATGA CGCAAGGGTG CATGGGCGTT TTTTGTGTTGA AGTTTTGAGC	180
GCGGGGCTGC AATCAAGCGG CTTGAAAGTG TATGATTTAG GGCTAATCCC CACACCGGTA	240
GCGTATTTTG CGGCCTTTAA TGAAATAGAC AATATCCAAT GGCCC	285

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168

GTGTGCGACA TTTTTCTGA TGGCGTTTAA TTGGACAAAG CGTTAGTGAT TTATTTCAA	60
GCCCCCTATA GTTTCACCGG TGAAGATGTG TGGGAAATCC AATGCCATGG AAGCCCCCTT	120
TTAGCGCAAR ATATCCTTCA AGCTTGCTTG AATTAGGGG CTAGGCTCGC TAAAGCGGGG	180
GAATTTAGCA AAAAAGCCTT TTAAACCAT AAAATGGATT TGAGCGAGAT TGAAGCGAGC	240
GTTCARCTCA TCCTTTGTGA AGRTGAAAGC GTTTTAAACG CTCTAGCCAG GCAGCTTCAA	300

208

GGGGGA

306

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169

ATGTTTAAAA	AAATGTGTTT	GAGCCTGCTA	ATGATAAGCG	GTGTTTGTGT	GGGGGCAAAG	60
GATTTCGATT	TCAAGCTGGA	TTATCGCGCG	ACTGGGGGGA	AATTCATGGG	GAAAATGACG	120
GACTCTAGTC	TTTTAAGTAT	CACTTCTATG	AACGATGAAC	CGGTGGTGAT	TAAAAACCTT	180
ATTGTCAATA	GGGGAAATTC	AGTCGAAGCG	ACTAAAAAAG	TAGAACCCAA	ATTTGGCGAT	240
AAGTTTAAAA	AAGAAAAACT	CTTTGATCAT	GAATTAATAA	ACTCGCAACA	GATATTTTAC	300
CGCCTGGATT	GCAAGCCTAA	CCAATTGTTA	GAAGTTAAAA	TCATCACGGA	CAAGGGCGAA	360
TATTACCATA	AATTTTCCAA	A				381

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170

ATGACCTTGA	AGCCATATCC	AACCAAAGAG	ACTGCTCTTG	CTAGCCAATT	ATCTGGGCAC	60
TGGTTTTTTC	AGCTTTCGTT	ATTTAATAAA	ACAAACTTTA	ATCCTAATAA	AATTTGGATT	120
CCTTTAGAGT	TCAATAAAAAG	ATCAAAAATA	AAGTTTGATA	AAGATTTAGA	AATCTATTTT	180
GATAGTCATG	AATCGTTCAA	TATCTCTAAA	AAATACTTGC	AAGAAATAGA	TCAAGAATCA	240
CTAAAAAAGA	TCAAACAATC	AAAAGATTTT	TTTTCAATTC	AAAAAATAGA	GAGTAAGCAT	300
GATAATAACG	ATATACTGCA	ACTTGAATTT	TTTGAGAATG	ATACAAGTTT	TCTTTTGTCT	360
AAAGGAAGTT	TTGCAGAAAT	TTTAGAATAC	AACATGCAAT	TAAAAATAGA	TTCTTTAATT	420

209

ACAAAAGAAT	TTAATAAGCT	TTTAGCGATC	GTTCAAGATA	GTCCCAAGA	TAGTTACCAA	480
TTAAAAATTC	GTGTCCGACA	TAACAATAAG	CTTCCTAGAG	AGAAATATAC	GGAACATGAA	540
ATAAACTTG	AAGTTTATGA	TTGCAGAAAA	TCCCACGATC	ACAATGAGCC	AATCATCTTA	600
AGCCAGCAAA	GCACCGGCTT	CCAATGGGCG	TTTAATTTCA	TGTTTGGCTT	TCTTTATAAT	660
GTGGGATCAC	ATTTTAGTTT	TAACCATAAT	ATTATCTATG	TCATGGACGA	GCCAGCCACT	720
CATTTGAGCG	TGCCAGCCAG	AAAGGAGTTT	AGGAAATTTT	TAAAAGAATA	CGCTCATAAA	780
AATCATGTTA	CTTTTGTTTT	AGCCACCCAT	GACCCCTTTT	TAGTGGATAC	GGATCATTTA	840
GATGAAATAA	GGATTGTGGA	AAAGGAAACA	GAAGGCTCTG	TAATTAAGAA	TCACTTTAAC	900
TATCCCCTAA	ATAATGCAAG	CAAAGACTCC	GACGCTTTGG	ACAAAATCAA	ACGCTCTTTA	960
GGAGTGGGCC	AGCATGTTTT	TCATAACCCC	CAAAAACACC	GAATCATTTT	TGTAGAAGGC	1020
ATCACGGATT	ATTGTTATTT	GAGCGCTTTT	AAATTGTATT	TGCGTTACAA	AGAATACAAG	1080
GACAACCCCA	TTCCTTTCAC	TTTCTTACCC	ATTTACGGGC	TTAAAAACGA	TTCAAACGAT	1140
ATGAAAGAAA	CCATTGAAAA	ACTTTGCGAG	TTAGACAATC	ACCCTATTGT	TTTGACAGAC	1200
GATGACAGAA	AATGCGTTTT	TAACCAACAA	GCAACGAGCG	AACGATTTAA	AAGAGCTAAT	1260
GAAGAAATGC	ATGATCCCAT	CACCATCCTA	CAACTCTCAG	ACTGCGATAG	GCATTTCAAA	1320
CAAATTGAAG	ATTGTTTCAG	CGCAAACGAT	AGAAACAAAT	ACGCTAAAAA	TAAGCAAATG	1380
GAATTGAGCA	TGGCTTTTAA	AACAAGGCTT	TTGTATGGCG	GAGAAGATGC	GATAGAAAAA	1440
CAAAACAAAA	GAAATTTTTT	AAAATTATTC	AAATGGATTG	CATGGGCTAC	AAACTTGATC	1500
AAAAAC						1506

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...126
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:171

GTGTATTTTT	TTCTGGCATT	GAGCGGGGAA	AAAGTCTTAC	TGCCCCGCAT	TGGCGGTTTA	60
GAAAAAACG	CGCTAGAAGC	CGGGCTGTTA	AAGGGGGATA	GAATCCTTCT	ATCAACCATC	120
AAAAAA						126

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1050 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172

ATGGAATAAT	TTAACTCAT	CAACTTTTTT	ACCGGTCAA	ACGATGCGGG	TAAAACCAAT	60
CTTTTAGAAG	CTCTTTATAC	CAACACAGGC	CTTTGTGATC	CTACTGCCAA	TCAAGTCAGT	120
CTTCCTCCTG	AACATGCCGT	GAATATTAGT	GAATTCAGAA	AAATCAAAC	CGATGCCGAC	180
AACCTAAAA	CCTTTTTTTA	TCAAGGAAAC	ACCGCTAATC	CCATTAGTAT	CCGCACTGAA	240
TTTGAACATG	CTACTATCCC	TCTTACTATC	CAATACCCCA	CACAAACCAG	TTACAGCAAA	300
GACATCAATT	TGAATAGCGA	TGATGCTCAT	ATGACAAACC	TTATAAACAC	AACAATAACG	360
AAGCCACAGC	TCCAATTTTC	CTACAATCCA	TCCCTTTCCC	CCATGACAAT	GACTTATGAA	420
TTTGAAAGGC	AAAACCTAGG	TTTAATCCAT	TCTAATTTAG	ATAAAATCGC	TCAAACCTAT	480
AAAGAAATG	CGATGTTTAT	TCCTATAGAA	TTATCTATTG	TTAATTCTCT	TAAAGCATTG	540
GAAAATTTAC	AATTAGCAAG	CAAAGAAAAA	GAATTGATTG	AAATCCTACA	ATGTTTCAAC	600
CCTAATATTT	TAAATGCTAA	TACAATAAGA	AAGTCTGTCT	ATATCCAAAT	CAAAGATGAA	660
AACACACCGC	TAGAAGAAAG	TCCCAAAAGG	CTTTTAAATT	TGTTTGGTTG	GGGTTTTATC	720
AAATTCCTTA	TTATGGTGAG	CATTCTTATA	GACAATCGTG	TCAAGTATCT	TTTTATTGAT	780
GAAATAGAAA	GCGGTTTGCA	CCATACAAAA	ATGCAAGAGT	TTTTAAAAGC	TCTGTTTAAAG	840
TTAGCTCAAA	AATTACAGAT	TCAAATTTTT	GCCACCACGC	ACAATAAGGA	ATTTTTATTA	900
AACGCCATCA	ACACGATATC	CGATAATGAA	ACGGGAGTTT	TTAAAGACAT	AGCCTTGTTT	960
GAGCTTGAAA	AAGAAAGCGC	TTCTGRCCTT	ATCAGACACA	GCTATTCTAT	GCTAGAAAAA	1020
GCGCTTTATA	GGGTATGGA	GTTAGAGGC				1050

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1395 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173

ATGGAATTTA	AAAAATGCC	TAATTTTGAA	AAAAAATGTG	CGTTTCTTTG	TTTCTCAAAT	60
TTGGTTTTAC	TTATTGAAAT	CCACTCTAAA	GGACTACACA	TGCAAAAAAA	GAAACCCAAG	120
AACCCGCAAC	CGAATTTATT	TAGCATCTTA	GATAAGGGCG	ATGTTGCAAC	AAACATCCT	180
GTTGAAGAGT	CAGACAAGGC	CAATAAAATA	CAAGAGCCAC	TCCCTTATGT	CGTGAAACG	240
CAATCAATA	AAGCAAGCAT	GATTTCTAGA	GATCCTATTG	AATGGGCAAA	GTATTTAAGC	300
TTTGAAAAAC	GAGTCTATAA	GGATAATAGT	AAAGAAGATG	TCAATTTCTT	TGCCAATGGT	360
GAGATAAAG	AAAGTTCTCG	TGTTTATGAA	GCGAATAAAG	AAGGGTTTGA	AAGGCGCATC	420
ACTAAAAGAT	ACGATCTGAT	TGATAGAAAT	ATTGATAGAA	ATAGAGAATT	TTTTATAAAA	480
GAAATTGAAA	TTCTAACCCA	CACAAACAGC	TTAAAAGAAT	TGAAAGAGCA	AGGGTTAGAA	540
ATCCAATTGA	CCCACCATAA	TGAACGCAT	AAGAAAGCCT	TAGAAAATGG	CAATGAAATC	600
GTTAAAGAA	ACGACCATCT	TAAAGATATT	TACCAAGAAG	TAGAAAGAAG	AAAAGATGGT	660
GGATTGGTAA	GAGAAATAAT	CCCCAGTATT	TCTAGCGCTG	AGTATTTCAC	GCTTTACAAC	720
AAACTGCCTT	TTGAATCAAT	AAACAATGAA	AATACCAAAC	TGAATACTAA	CGACAATGAA	780
GAAATTGAAA	AAGTAAATTT	TGAATTAGCT	AAAGAAGTGC	ATATTTTAAT	CCTAGAGCAA	840
CAATTGCTTT	CAGCAACAAA	TTATTATTCT	TGATAGATA	AAGATGATAA	TGCGAATTTT	900

211

GCTTGGAAAA	TGCATAGGCT	TATCAATGAA	AATAAACTCA	AAGAAAACCA	TCTCAGCGCC	960
ATAAACGCTA	ATAAGATTAA	GCAATTTTTC	TTTAATAATG	GTTCTATTTT	AGGCTGGACT	1020
AAAGAAGAAC	AAAGCGCTAT	ACAAGAAAAC	AGAGATTATT	CTTTAAGAAG	CGCTCTTTTA	1080
AGTTTAGAAG	AAATCGCTCA	AGCAAAAATT	GAATTGCAAA	AATACTATGA	AAGCGTTTAT	1140
GTTAATGGTG	ATGGGAATAA	AAGAGAAATC	AAGCCTTTTA	AAGAAATTTT	AAGAGACACC	1200
AACAATTTTG	AAAAAGCTTA	TAAGGAGCGT	TATGACAAAT	TGGTAAGCTT	GAGTGCAGCA	1260
ATCATTC AAG	CTAAAGAGGG	TGGTAATGAG	CGACAAAATT	CTAGTGCAAA	TAACAATAAC	1320
CCTATTAAAA	ATACAATAGA	GACTAATACT	TCTAACAATA	TTATTCAAAA	TAATGATAAT	1380
ATAATCATCC	AAATT					1395

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174

ATGGCGCTTG	AAGTGGTTTT	ATGGGATTTT	GATGGCGTGA	TTTTTGACAG	CATGCATTTA	60
AAATATGAAG	GGTTTAAGGC	GTTGTTTCAA	AAGCATGGCA	ACGATAGTAA	AGAGGGTTTG	120
AAACAATTTG	AAGTTTATCA	CTATCAAAGT	GGGGGGATTT	CAAGGAATGA	AAAGATCCAA	180
TATTTTTATA	ACGAGATTTT	AAAAACCCCT	ATCGCTCAAG	AAGAAATAGA	TGCATTAGCC	240
CTAGAGTTTG	CGCCTATCAT	AGAGCAAAAG	CTTTTTGATA	GGGGGCATTT	GAATAGCGAR	300
GTGATGGCGT	TTATTGATAA	GCATTATCAA	AATTATATTT	TCCATATCGC	TTCAGCGGCC	360
TTGCATAGCG	AATTGCAAGT	GTTGTGCGAG	TTTTTAGGGA	TTACTAAGTA	TTTTAAGAGC	420
GTTGAAGGGA	GTCCGCCTGA	TAAACCCAAG	ATTATCGCTA	ATATCATTCA	AAAATACGCC	480
TATGACCCAA	GCCGTATGCT	AATGATAGCG	ATAGCGTCAA	TGATTATGAA	AGCGCTAAGG	540
CTAATAAAGT	GGCGTTTTTG	GGCTATAACA	GCAAGGTTT			579

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175

ATGCTCAAAA	AAAAGATTGA	TTTGCATAAA	GATTCTATTA	GGAAGCTCTT	TTTTTATTAC	60
TTCATCCCTT	TAGTTTTTTC	TATGATCTCA	CTTCTACTT	ACTCTATGGT	AGATGACATG	120
TTTGTGGGCA	AAAAACTGGG	TAAAGAAGCT	ATCGCTGCGG	TCAATATCGC	ATGGCCTATT	180
TTTCCAGGAC	TCATTGCGTA	TGAATTGCTT	TTTGGTTTTG	GGGCAGCGAG	CATTGTGGGG	240
TATTTTTTAG	GTCAAAATAA	AACCCATAGG	GCTAGGCTTG	TGTTTAGCAG	CGTGTTTTAT	300
TTTGTGCGTC	TAAGCGCCTT	TATTTTGAGC	ATGGCGTTAT	TGCCTTTTAG	CGAAAATATC	360
GCGCAGTTTT	TTGGGAGCAA	TGACGCTTTA	TTGAACATGT	CAAACGCTAT	ATTGAAATCA	420
TTT						423

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176

GTGAAATGTT	TATTAATAAA	AAAATCACTT	CTATTTGCAC	TGAAACCATT	GCCGGACCTA	60
AAAACGACTA	CCCCTATTTT	AGCGCCTATG	AGCGTGGTGG	CTGGGAGGTT	GRCTSCSCAT	120
TTAGTCCAGC	ATTATTTACT	GGCTTTAGAG	CATGTTAAAG	GGTTTATGGG	TAAGGGGGTC	180
ATACTAGGGG	GTTTGTGCGG	TGCSCAAAGG	GCTAAAATCG	TCGTAATTGG	AGGCGGTGTG	240
GTTGGCATGG	AGAGCGCGAA	AGTCTTAARC	CAAATGGGGR	CTAAAGTAAC	GATTTTAGAA	300
TTAGACTACG	CTAAATTACA	AAACCACCCT	TATTATCATT	TGTATGATTT	AGAAGTCTTA	360
AGCGTGAATG	AAGCCAATAT	CATTCAAGCC	TTAAACGGGR	CGGTGGGGCT	AGTGGGAGCG	420
GTRCTGTTA	CARCGAGCCA	AACCCCTAAA	GTGRTCTTAA	GAAGGCATTT	AAAATAC	477

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

213

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177

ATGCTTGCAA	AAATCGTTTT	TAGCTCATTG	GTTGCGTTTG	GAGTTTTGTC	GGCTAATGTG	60
GAGCAGTTTG	GTTTCATTTTT	CAACGAGATA	AAAAAAGAAC	AAGAAGAAGT	GGCCGCAAAA	120
GAAGACGCTC	TTAAAGCTCG	CAAGAAGCTC	TTAAACAATA	CGCATGATTT	CTTAGAAGAC	180
TTGGTTTTTA	GAAAACAAAA	AATCAAAGAG	CTTGTGGATT	ACAGAGCTAA	AGTTCTTTTA	240
GATTTAGAAA	ACAAGTACAA	AAAAGAAAAA	GAGGCTCTAG	AGAAAGAGAC	AAGAGGTAAA	300
ATCCTTACTG	CTAAGTCAAA	GGCTTATGGT	GATCTAGAGC	AAGCCTTAAA	AGATAACCCT	360
CTTTATAAGA	AACTTCTTCC	TAACCCTTAT	GCTTATGTTT	TAAACCAAGA	AACATTCACG	420
CAAGAAGATA	AGGAGCGTTT	GAGTTATTAC	TACCCCAAG	TGAAAACGAG	CAGTATTTTT	480
AAAAAACTA	CCGCTACCAC	TAAAGATAAG	GCTCAGGCTT	TGCTTCAAAT	GGGTGTGTTT	540
TCCTTAGATG	AAGAGCAAAA	CAAAAAAGCG	AGCCGATTAG	CTTTATCTTA	CAAGCAAGCG	600
ATTGAAGAAT	ATTCCAATAA	CATTTCTAAT	TTATTGAGCA	GAAAAGAATT	GGATAATATA	660
GATTATTACT	TGCAGCTTGA	AAGAAACAAA	TTTGACTCCA	AAGCAAAAGA	TATTGCTCAA	720
AAAGCCACCA	ACACGCCTAT	TTTTAACTCG	GAACGCTTGG	CGTTTAGCAT	GGCGATTGAT	780
AAGATCAATG	AGAAATACTT	AAGGGGCTAT	GAAGCTTTTT	CTAACTTGTT	GAAAAATGTC	840
AAAGATGATG	TGGAGTTGAA	TACTTTGACT	AAAAACTTCA	CCAATCAAAA	ATTGAGTTTC	900
GCACAAAAC	AAAAATTGTG	TTTGTGGTT	TTAGACAGCT	TCAATTTTGA	TACCCAATCC	960
AAAAAATCTA	TATTAATAAA	GACTAATGAA	TACAATATCT	TCGTAGATAG	CGATCCTATG	1020
ATGAGCGACA	AAACAACAT	GCAAAAAGAA	CACATACAAGA	TATTTAATTT	CTTCAAAACA	1080
GTGGTTTCTG	CATACCGGAA	CAATGTTGCC	AAGAATAACC	CCTTTGAA		1128

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178

ATGGATTTCG	TAGGGTTTGA	AGATTTAAAA	TGCAAAGACA	AAGAAAATC	TCAAAAAGTT	60
TTTGTGATCC	GTAACGATAA	GTTAGGCGAT	TTTATTTTAG	YGATTCCCGC	TTTAATCGCT	120
CTCAAGCATG	CTTTTTTAGA	AAAAGGCGTA	GAAGTGATTT	TGGGCGTGGT	TGTGCCTAGC	180
TATACCACCC	CAATTGCTTT	AGAATTCCCT	TTCATTGATG	AAGTTATCAT	AGAAGACAAC	240
CATTTAGCCA	CCACCCYCAA	AAACCGCTCC	ATTGACGCTC	TTATCTTTTT	ATTTTCTAAT	300
TTTAAAAACG	CCAAACTCGC	TTTCAGTTTG	AGAAAATCCA	TCCCTTATAT	CCTAGCCCCA	360
AAGACCAAAA	TCTATTCTTG	GCTTTATCAA	AAGAGAGTGC	GCCAAAACCG	CTCTTTATGC	420
TTAAAAACCG	AATACGAATA	CAATTTGGAC	TTAATCCATG	CGTTTTGTAA	AGACTACGAT	480
CTCCCTAACG	CTCAACTTAA	AAAAATCGCA	TGGAAGCTTA	AAGACAAATC	CAAAGAGCGA	540
TCCATCATCG	CTTCAAAACT	CAACGCTAAT	GTTGATCTAT	TGTGGATTGG	CGTGCAATG	600
CATAGCGGAG	GCAGTTGCCC	CGTATTGCCC	GCTTCGCATT	TCATTGAGTT	GATTGCAATC	660
TTGCATGAAA	AATTAAAGTG	TGAGATCAAT	CTTATTTGCG	GGCCAGGCGA	GAGAAAAGCC	720
ACAGAAGAAC	TCCTTTAAGA	AGTCCCTTTC	GTCACCTCT	ATGATACGAG	CCATAGTTTA	780
GTGGATTTAG	CCAAATTGTG	CGCGAATTTA	AGCGTCTGTA	TCGGGAACGC	TTCAGGCCCT	840
TTGCATGTGA	ACGCTTTATT	TGACAACCAA	TCTATCGGGT	TTTACCCTAA	CGAACTCACC	900
GCCTCTATTG	CCAGATGGCG	GCCTTTCAAC	GAACAATTTT	TAGGCATCAC	CCCGCCTAAT	960

214

GGCTCAAACG ATATGGGTTT GATTGACATT CAAAAAGAAA GCGAAAAGAT TATGGGATTT 1020
 ATCACAAAAA ATCTTTCTCA TCACATGCAA GAAAGA 1056

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179

GTGGGTGTCT TATCCCTCAA AATAGAGGCA ATTTCTAATT TTTATGGGTT ATGCGTTTTA 60
 GGGGTGTGT TAGCATGTTT TTATCTTTTA GACGCTTATT ATCTCATGCA AGAAAGGCTG 120
 TTTAGGGAGC AATACCAATG GCTAATAAAA AACCGACTTA AAACCGATGA AAGGCTGTTT 180
 GAAGTCTTCC CTATTCATCA AACTTGCCAA TCAACGCAAT TCTTATCGCC ATGCGTTCGT 240
 TTAGTCTTTT CCCCTATTGG GCGT 264

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180

ATGTCTTTAG GGGCAGTGGT CAGCTCACTC CTTTGCCATA AGTTAGAGGG GGCAATATTA 60
 GATCTGAGAG CGTATCGTTS RARAGCTTAT TATCACGAAA ATAAAGATAC YTTGCTTATT 120
 AAAGGCCAAA AACGCCTTCT TTACAATTAT ATTAAAGCCC ATATTGYTTT AAAGTGGCTA 180
 TGGACAATTA GAAATCGCAC GTRATCATTG GGAAAATTTA CTCAAAATCC AACCGAACAA 240
 CCGCCACGA ATAACCACAC CATTCAATGG AAAAACRGAA AACATTCTAA TGGACAGAAT 300
 TTTAGTGATT GGTAT 315

215

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181

ATGAAAAAAA	CAACCTCTTT	TGTATTGGGC	TTATTATTCA	ATAGCTCTTT	AAGCGCTGTT	60
GATGGGATTT	CTCAAACCGA	GCCTTCTTCT	TTGAATTTGG	CTGAAGATAG	CCTGCCTTTG	120
AACCATTTCTA	ACGCCCAAAA	ACTCTCTTTA	AAAAACGCAT	GGAATAGGGT	GTGTCTAAT	180
CATGAAGGCT	TGCATGCGCA	GAATACGCCA	TTAAGCGAGC	GACTAAAA		228

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182

GTGAAAAAAG	TAGAATCCAT	GAATGTGGTG	CCTTTCATTG	ACATCATGCT	TGTGTTGTTA	60
GTGATCGTGC	TCACAACGGC	GTCTTTTG TG	CAAACCTCAA	AGCTTCCTAT	TAGCATTCCT	120
CAAGTGGATA	AGGATAGCAC	TGATTCTAAA	GATGTGTTGG	ACAAAAAACA	AGTTACGATC	180
GCTATTTCTA	ATAAGGGTTC	TTTTTATTTT	GACGATAAAG	AAATCAGCTT	TGAAAAATTTA	240
AAACACAAGG	TTTCCACTTT	GGCTAAAGAC	ACCCCTATTG	TCTTTGCAAG	GCGA	294

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

SUBSTITUTE SHEET (RULE 26)

216

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183

ATGGGATCTT	ACACATTCCC	TCTCATTTTG	AAGCCAATAT	TTATAAACAA	AGTGCCTGTA	60
ACGATAGATT	TTTATGCGAA	CGCCAATTAC	TTTTTGATTT	ATGGTGCGTT	AGCGAATGCG	120
GTGGTGGGGA	GCATCAACGC	CTTAAACGAT	GAAATCAGGT	TCAAACGCAA	CGCCCAAATA	180
GAAGAAGCTG	AATTAGGGAC	AGACGGGATT	AAGATTAAGC	CTATCGCTTT	GTATAACCCT	240
AGTGAGGGGT	ATTTGAATTA	CGCGCTCTCT	AGCGTGTTTA	TTTTCATCTT	ACACCAGGTG	300
ATGCTCATTG	CAAGCAGCAT	GTTTACTAGC	TCCAGGCGTT	TGGAATTGGC	CCTTTTAGAC	360
AAGAAACAAA	TCGCTTTAAG	GCTGTGCGCA	AGACTCTTGG	TGTTTCATGG	GGCGTTTAGC	420
GTTTTGTFTT	TATGGTATTT	TGGGGCGCTG	TTTTCTTTTT	ATGGGATCGA	ACGGCATGGA	480
AGCGCT						486

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184

GTGATTATGA	CTAAGCTTGA	TGGCACTTCT	AAGGGCGGAG	CGATTTTARG	CGTGCTGTAT	60
GAGTTGAAAT	TACCCATTCT	TTATTTAGGA	ATGGGCGAAA	AAGAAGACGA	TTTGATCGCT	120
TTTGATGAAG	AACGCTTTAT	AGAAGATTG	GTTGATGCGG	TGTTTGTTGA	ACAA	174

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

217

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185

GTGTGTGGGG CTCATGGAAA GAGCAGTATC ACGGYCATGT TGAGCGCGAT TTGCCCCGCT	60
TTTGGASSGA TTATTGGGCG GCATTCTAAA GAGTTTGATT CCAATGTSSG AGAGAGCGCG	120
GATATGAGTT TGGTTTTTGA ASCCGATGAA AGTGATTCAA GTTTTTTTAT TTTCCAACCC	180
TTTTTGGCGG ATTGTGCC	198

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186

GTGAATGAGT TAAAAAACTC TAAGCAAGTT TTAGGGAATG GGAAAGCCGA TCTGAGCAAC	60
GAAAACACCA AGGTAAGGCA GACTAAAACA RATCTGACTG AAAAAAATCA AAGGCTAACC	120
ACAGAAAAAA CAGAATTAAA TAACAAGATT ACTGGGTTAG CCACAGAAAA AGAAAGGTTA	180
GCCGCAGACA AAGAAAACCT AACTAAAGAA AGCAGACAAA GAAAACCTAA C	231

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 555 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

218

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187

```

ATGGATTTAC AACAAATTGA TGAGCTAGAA AATAAGTTTG AAGAACAAGA AGAACAAGCC      60
CAAGATACCC CCCTAAACA AGAGCCTAGC ACAAAGGAAG TAAAAATCCC TAAAAAAGG      120
GGGCGTAAAA AAAGCTTGTT AGATGAAGAT AAGAAAAAGA GCTTTAACAT TGCCTTTAGT      180
CCTTGTGTGA TAAAGAACT TAATGAATTT TTGCTAGAAT TTGGCTCATT TAAAGAGACA      240
CGAAGCACTT TTATTGAAGA AGCGCTTATT AGGCATTTAA AACACAGAAA AAACACCCAA      300
GAGCAAAAGC TTTTAAAGCA ACTAGAAAAGA TTACAAAACA AAGAAAAGGG AATAATGAAA      360
ACAATGAAC TGAATGAATT TTTTACGCAT AAGATAATCT ATAAAGACAC CCCTTTAAAG      420
TTTAAGGATA CACTAGAACA AGAAATCAGC CAAGCTAGTT TAGTAGAGAA GTTAATCTTA      480
GCTAATATCT TAGCCAATAT GGTGTTTGCT AAGATAAGCA ATGAGAATGC CCCTAAAATT      540
CTTATTTTCA CGGCT

```

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188

```

ATGGGGTGCT ATGGGATAGG CATTAGCCGG TTGCTCAGCG TGATTTTAGA GCAAAAAGC      60
GATGATCTAG RCTGTGTGTG GACGAAAAAT ACCGCTCCTT TTGATGTGGT GATCGTGGTT      120
TCTAACCTGA AAGATGAAGC GCAAAAAAAA CTCGCTTTTG AAGTGTATGA AAGACTGCTC      180
CAAAAGGGCG TTGATGCGCT GTTAGATGAC AGAGACGCTC GTTTTGGGGC GAAGATGAGG      240
GATTTTGAAT TGATTGGGGA ACGATTAGCC TTGATTGTTG GGAAGCAAAC TTTAGAGAGT      300
AAGGAATTTG AATGCATCAA ACGCGCTAAT TTAGAAAAGC AAACGATCAA AGACATAGGA      360
ATTAGAAGAA AAAATTTTAG AAATGTTAGC GAGCGAATAA GGGGAGGGAA TGGAAAAAYT      420
AGTGATTGGC TC

```

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189

ATGGAAATAC AACAAACACA CCGCAAAATC AATCGCCCTT TAGTTTCTCT CGTTTTCAGCA	60
GGAGCGTTGA TTAGCGCCAT ACCGCAAGAG AGTCATGCCG CCTTTTTCAC GACCGTGATC	120
ATTCCAGCCA TTGTTGGGGG TATCGCCACA GGCAGTCTG TAGGAACGGT CTCAGGGCTT	180
CTTAGTTGGG GACTCAAACA AGCCGAAGAA GCGAATAAAA CCCCAGATAA ACCCGATAAA	240
GTTTGGCGCA TTCAAGCAGG AAAAGGGCTT	270

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 804 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190

ATGTCAGAAA AAGAAAGACT GAATGAAGTG ATCTTAGAAG AAGAGAATAA TGGGAGTGGT	60
ACTAAAAAGG TGTTTTTGAT CGTGGCCATA GCCATTATCA TTTTGGCGGT GCTTTTAATG	120
GTGTTTTGGA AAAGCACCAG AGTCGCTCCT AAAGAGACTT TTTTACAAAC CGATAGTGGC	180
ATGCAAAAAA TAGGCAACAC TAAAGATGAG AAAAAAGACG ATGAGTTTGA AAGCTTGAAT	240
ATGGAATTCT CCAACAAGA AGACAAGTTA GACAAAGTGG TGGATAATAT TAAAAACAA	300
GAGAGTGAAA ATTCTATGCC CATTCAAACC GATCAAGCTC AAATGGAGAT GAAAACAACA	360
GAAGAAAAAC AAGAATCTCA AAAAGAATTA AAAGCTGTG AGCCTATTCC CATGAGCACT	420
CAAAAAGAAT CTCAGGCTGT GGCTAAAAAA GAAACCCCCC ATAAAAAGCC TAAAGTAGCG	480
CCAAAAGATA AAGAAGCGCA TAAAGRTAAA GCTAAGCATG CAGCTAARGA GCCAAAAGTC	540
AAAAAAGAAG CTCGTAAAGA AGTTTCTAAG AAAGCTAATT CTAAAACCAA TCTTACTAAA	600
GGGCATTATT TGCAAGTGGG GGTTTTTGCG CACACGCCA ACAAAGCCTT TTTACAAGAG	660
TTTAATCAAT TCCCCATAA AATTGAAGAT AGGGGGGCTA CTAAACGCTA CCTYATAGGY	720
CCTTATAAGA GCAAGCAAGA AGCCTTAATG CATGCCGATG AAGTCAGCAA GAAGATGACT	780
AAACCGGTTG TCATAGAAGT GCGG	804

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 513 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

220

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...513
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:191

GTGGAATATT ATGCGTTTAA TTTCAGCGTG TTGGATTTTG TCTTAATGGG GAAAGCGACG	60
CATTTGAATC TGTTGCTAT GCCTAAAGCT AAGCACATTA AAGAAGCCAC GAGCGTTTIA	120
GAGCGCTTGG ATTTAGAGTC CTTAAAAGAT CAAGGCATTA ACGATTTGTC CGGCGGTCAA	180
AGGCAGATGG TACTTTTAGC CAGAAGCTTG TTGCAAAGAA CGCCCTTATT GTTACTGGAT	240
GAGCCTACGA GTGCGTTAGA TTTAAAAAAC CAAGCCCTTT TTTTGTATGC GATTAAAGAT	300
GAGATGAAAA AACGAGAATT GAGCGTTTGA GTCAATATCC ATGATCCCAA TTTGGTTGCC	360
AGGCACTCCA CGCATGTGGT CATGCTCAAA GATAAAAAAC TTTTTTTGCA AGCTTCCACG	420
CCAATCGCTA TGACTTCACA CAATTTAAGC GCGCTTTATG ACACGCCCTT ARAAGCGATC	480
TGGCATGATG ATAAGCTTGT GGTGTATGCG TTG	513

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192

ATGATGGCAC ATTCACCTAT TTTGGTTTCA AAAACATCAC TCTCCAACCT GCTTATTTTT	60
GTGGTTCAAC CTGATGGGAA ATTGAGCATG ACTGATGCCG CCATTGATCC TAACATGACT	120
AAATTCAGGAT TGAGATGGTA TAGAGTTAAT GAAATTGCAG AGAAGTTTAA GCTCATTA	180
GACAAAGCCC TTGTAACAGT GATCAATAAA GGCTATGGGA AAAATCCATT GACAAAAAAT	240
TACAATATCA AAAACTATGG TGAATTGGAG CGTGTGATTA AAAAGCTCCC TCTTGTGAGA	300
GATAAA	306

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 711 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

221

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193

GTGCTGAATG	AAGAGCAAAA	TTCATTAGAA	GAAAAAGGGG	GCGAAAAACAA	AAACGAAAAA	60
GAAACCCCC	TAAAGGGCAT	TCATTCTAAA	ATCCCCTCTT	TGAAGCAGGC	TTTGGAGCAG	120
ACGATTAGTA	AAATCAAAAG	CTCTAAAGAG	TTTTTCAAAC	AGCTTCTACA	CAATAAAAAA	180
AAGCTTTATA	TCGCGCTTGG	AATATTGCTT	TCACTCATCG	CGCTCATTGT	GGCTTTGAGT	240
TTGTTACTAG	GGCATAAAAA	AGAAAATAAA	CAAACCTCTT	TACAAACTAA	TACCGCCACC	300
ACCAATAACG	AAACGCCTAA	CGACACCAAT	AACGCAGAAG	CCGAAGGGCA	AATAGAAAAT	360
TTAGACTTGC	CTGATTTAAT	CGGCAAAGAC	TCTTTGAAAA	GAAACGATGA	AAGCCAAGTG	420
GATGCGATGA	TGCAAAAAGC	GAGCCTTTTG	TATGAGCAAG	GGCAAAAAGA	TGAAGCCTTG	480
CATTGTGTTG	ATAAGATCGC	TTCTTTCTCG	CAAGGGATTG	CGAGCCATAA	TCTAGGGGTG	540
ATTAAATTCA	AAGAAAAGGA	TTTAATGGG	GCGTTGGATT	TGTTTGATTG	CAGTATCGCT	600
TCTAAGAAA	ACGCGAGCGT	GRGCGCGATT	GATGCGTTAG	TTACGGCTTA	TCATTTGCAA	660
GATGCGGATT	TGTATTATCA	TTATCTAAAA	ATTGTRAAGA	GACACTTTGT	A	711

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 675 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194

ATGAATACAA	GCTTATTGAC	CCAAGCACAG	GTTTTAAGCT	CTAAAGAAAA	TCAAATCCAT	60
CGCCTTTTGT	TAGAGCTTTT	AGAAGAGGCT	AAGCTTCATT	TTGAGCCTAA	GCTTTATATC	120
ATTAAACGCCC	CTTACATGAA	CGCTTTTGGG	AGCGGGTGGG	ATGAATCTAA	TTCCCTTATC	180
GCTCTTACAA	GCGCTTTAAT	AGAGAGGTTA	GATAGAGACG	AATTAAAAGC	CGTGATCGCT	240
CATGAGCTCA	GCCACATACG	GCACAACGAC	ATCCGCTTGA	CCATGTGCGT	GGGGATTTTG	300
AGCAATATCA	TGCTATTGGT	GGCTAATTTT	AGCGTGTATT	TTTTCATGGG	GAATCGCAAG	360
AATAGCGGGG	CGAATTTAGC	CCGAATGATT	TTATGGGTTT	TACAGATCAT	CTTGCCTTTT	420
TTAACGCTCC	TTTTGCAAAT	GTATTTGAGC	CGCACACGAG	AATACATGGC	CGATAGCGGG	480
GCGGCGTTTT	TAATGCATGA	CAATAAGCCC	ATGATCAGAG	CCTTACAAAA	GATTTCTAAC	540
GATTACACCA	ACAACGATTA	TAAAGAAATA	GATAAAATA	GCACCCGATC	AGCGGCCTAT	600
CTTTTAAACG	CTGAAATGTT	TAGCACCCAC	CCTAGTATTA	AAAATCGTAT	CCAATCCTTA	660
AGAAAGCGTG	TGATC					675

222

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195

ATGTTTAATA	TTAAAAGGAC	TTTTTTAATA	ACGATCATAA	GTTTTTTTCT	CATTGTTTCCT	60
AATTGGTTGA	AAGCTATTGA	TTTGCCCAT	GTTTCAAATC	TCAAAATTTA	CCAAACAGTT	120
TATTGCATGC	TGATACCGAG	TTATGTTTTA	ACCAACAAAA	GTITTTGCAGA	TATTTTGAACA	180
GGCTATACAT	CTATTGGTGC	ATCAGGGAGT	GGAAAGAGTT	CAGGGCAGGG	TGTGATCGAA	240
GCGCTTAGCA	CACCATTAGC	CACAAGTTTA	GCCGCTAGCA	ATCTGCTGAA	ATATTTGAAT	300
ACTTTAGGTC	CTTTATGGGG	ATCGGCGTGG	GCAAGTGTTG	CTACAGCTAT	ACAAGGTTTT	360
GCTCTAACGC	CATCAAGTGG	CTGTAATTTT	GGTTGGAACG	CATTGATAAA	TAAAAACATA	420
GATGTATCCA	TGGATAGCGT	ACTAGACAAT	TTGAGCAACA	AGATTTCAGAA	TTTTACCAAA	480
GGCGGTGTTG	AGGACAATGT	GAAAGGCAAT	ATTCTTTTAC	AAATAATTGG	CTCAATAACC	540
GCTCAAGCTT	CTACGAATAT	TACAGCTGAT	GGTTTAATTT	GGCTGATTGG	TAAAGAATTC	600
ACTGCAATA	AACTGCAAAA	CAACACTATA	GCCATGCTTG	CTTTTGCCGC	ATTAGAATCT	660
GTGTCAAAG	GAGCGGACGC	TGCTGTTCTT	CCTGCATATG	GTGTAGTCAA	TCTGCCTGAT	720
ATTATCATAG	GGCAAGGGTC	ATATCTTGAT	TTTGTTTCTT	ACCTAATTTA	TATTGTTTTT	780
GGGATTTTTG	TTTTTATTTT	TTTTATGAAA	TTGAGAGATA	TTTCAAACGG	CATTTCAGATT	840
AACATAGGTT	TTGAATACAT	GCGATTGTTT	GGGGGGACAT	TATTCAAAAT	GGCGATGGTC	900
TCTTTTATCG	CCTATGCAGG	TTTTGGTTAT	CTTTATAAAA	TCTCTTATTC	TATTTATTTT	960
GGTTTAGCAG	GTGCTTTTGG	GCTGAATCAA	GTTCTTTTTT	GGGCTTTAGA	TTTAGTGCTG	1020
AATTACACTG	TTAATTCAT	TTTACCTGCG	GTAAGAGCTG	TTTTTTCTAA	TGTTGGCAAC	1080
AACGCTCCTA	GTTTGTTTACA	AGGCTTGCAA	GTGGCAGGTA	TTTCTTTATT	CGCTATTTTT	1140
ATGCAAGTAA	CTATCATTTAT	GAGAATAAGC	ACTGTTGTTG	TGAAACCTTT	GATAGCGGGG	1200
GCTTTTAGCG	GTATTGTTTT	CCCTATTGCA	GTATGTTTGA	TCGTGCTAGA	TTGGTTCAAA	1260
GATTCTATGA	AAAACATATT	GATATGGTTT	ATTAATAATC	TGTTTATCTT	GGTTCTAGCT	1320
ATTCCTATTT	TGCTCTTTGG	TGTTTGGCA	TTATTGGCAT	TCAATTGAC	CATAACGCCC	1380
TCTGTTGCTA	TACAAAACAT	CAATCAAGGG	GGATTGGGTA	TCGATTCAAC	TATTGCGAGT	1440
TTGATCACTC	TATTTATTTT	AAAAGGTTTC	ATAGAGACGA	TTATTGAGAG	CGTCAATGCG	1500
ATCGTTAACA	CCATTTTCAG	CTCTGTCTCT	ATGGATGGTA	GCAGAATGGA	TAGAGAAAGA	1560
GATGCCCTTAA	TGGTGGGAAG	AGTTGGTGGA	TCTATGTTTA	AAGGA		1605

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

223

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196

ATGGCGTTTT	GGCAGGCTAT	CCGGTGGTGG	ATTTTAAAGT	TACCCTTTAT	GATGGGAGCT	60
ACCATGATGT	GGATTCTTTC	AGAAATGGCG	TTTAAATCG	CTGGYTYTAT	GGCGTTTAAA	120
GAAGCGAGTC	GTGCGGCTAA	CCCGGTTTTA	CTAGAGCCTA	TGATGAAAGT	GGAAGTGGA	180
GTCCCTGAAG	AATACATGGG	CGATGTGATT	GGCGATTTAA	ACAGAAGAAG	AGGGCAAATC	240
AATTCTATGG	ACGATAGATT	AGGTTTGAAA	ATCGTGAATG	CTTTCGTGCC	GTTAGTGGA	300
ATGTTTGGTT	ATTCTACGGA	TTTGCGATCA	GCCACTCAAG	GGCGTGGGAC	TTACTCTATG	360
GAGTTTGACC	ACTATGGCGA	AGTGCCTAGC	AATATCGCTA	AGGAAATCGT	GGAAAAACGC	420
AAAGGC						426

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 459 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197

ATGCAGAAIT	TGCCGGGTAT	GGCGAGAGCG	GCGATGCTAA	CCACATCATC	AGCCCCAGCC	60
CCTGAGGGTG	AAGGGGCTTT	TAGAGCCATG	AAAATGGCTT	CAGAAATGGC	GAAAGTGGA	120
GTAGGCTATG	TGAACGCCCA	TGGGACAAGC	ACGCATTATA	ACGATTGGTA	TGAAAGCATT	180
GCGTTAAAAA	ATGTGTTGGC	TCTAAAGAAA	AAGTCCCTCC	TGTTAGCTCC	ACTAAAGGGC	240
AGATTGGGCT	TGCTTGGGTG	CTGCGGGGTT	AGAAGCCGTT	ATTCTATCAT	GGCCATGAAY	300
CAAGGGATCT	TACCTCCTAC	CATTAATCAA	GAAACGCCCTG	ACCCAGAATG	CGAYCTGGAT	360
TATATCCCTA	ATACAGCCAG	AGAAAAGCAA	GTGAATGCCG	TGATGAGTAA	CTCATTTGGT	420
TTTGGTGGCA	CTAATGGTGT	TGTGATTTTC	AAAAAAGCC			459

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

224

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198

ATGATACTAA AAAATTTGAT TTTGTTATTT TTAGCAAAGA GAAAACTTAT TTTCATAGAA	60
GCTAATTTTT ATACCATTAG TGGGAGCAAG CTTAATGAAG TCGCAAGATC CTATCAAGAC	120
TTAGCTTTAA AATTTGAAGC ATTTCTTAAT TACGAATTTA TTTGGATAAC TGATGGCATA	180
GGTTGGCTAG ACGCTAAAAG CAAGCTCCAA GAAGCTTACA AATCTGTAGA AATCTATAAC	240
TTAAGCTATG TGAATGATTT TATATCAAAG GTGCAAAAA	279

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199

ATGGAATCAC AACTCATGAA ACTCGCCATT GAAACTTATA AAATCACTTT GATGATTTCT	60
TTACCGGTAT TATTAGCGGG CTTAGTGCTG GGGCTGTTAG TCAGTATTTT TCAAGCGACC	120
ACCCAAATCA ATGAAATGAC TTTGTCTTTT GTGCCTAAGA TTTTAGCCGT GATTGGGGTG	180
CTGATTTTAA CCATGCCGTG GATGACGAAC ATGCTTTTAG ATTACACCAA AACCTTAATC	240
AAGCTCATTC CTAAATCAT AGGC	264

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

225

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200

ATGAAATTTT TTACAAGAAT CACTGACAGC TACAAGAAAG TTGTAGTAAC TTTAGGGCTA	60
GTGGTAACAA CCAATCCTTT AATGGCGGTC ACCAGTCCTG CAACAGGCGT TACTGAGACT	120
AAAAGTTTGG TTATTCAGAT CATTTCTGTT CTAGCGATCG TAGGTGGTTG CGCTTTAGGG	180
GTCAAAGGCA TAGCAGATAT TTGGAAAATC TCTGATGACA TCAAAAGAGG TCAGGCGACT	240
GTTTTTGCTT ACGCGCAACC CATAGCTATG TTAGCGGTGG CAGGTGGCAT TATCTATTTG	300
AGCACTAAGT TTGGCTTCAA TATTGGCGAG AGTGGAGGAG CTAGC	345

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201

ATGAAAAATC CCCAAGCTAA TGTTTTTAAA CTCTTTTAA ATCAAGTGGC TGACCAAAAA	60
TACATAGATA TGAATGATGA AAAAAACTAT GACCCAAGAG AACCTGAACC CCCTTATGGA	120
ACAAAAGGGG CGTTAGATGA GATTATAAGG ACAGATGCTA GGAGTTGGGC AAACACTCCT	180
GATGATGAAT TTGGGAGCAT TATGCTTCT TTTAAGCGTT TTATGTATGT CTATAAGAC	240
CCAAAAGTGC GTGAAGCTAC TTCTAAAATG AGCTTTGATT ATGAAGAATT AAGAACGGGC	300
AATATCAGTA TTTACATTGT AATCGCTCAA ATTGATATAG GCACACTTTC TTCTTTAGTA	360
AGAGCCTTT TAGAGAGTAT TGCTAAAAAC CTTATGGTCA AAGAAAGCTC TAAACCTGAA	420
GAGCGTATTT TTATCATTGC TGATGAATTT GTTAGATTG GTAAGTTGCC TTTCTTGTTA	480
GAAATGCCAG CACTTGTGTC CTCTTATAAT GTTGTCCTT TATTCATCAC GCAAGATTAT	540
GCTATGATTA GAAATACTAT AGCGATGATG ATT	573

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1053 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202

ATGATAAGTG	AGATTATTAA	GTTTCAATTA	AAAGGAATAA	AAATGATTAG	ATTAAAAGGT	60
TTGAATAAAA	CTTTAAAAAC	AAGCTTATTA	GCTGGGGTTT	TACTAGGTGC	TACTGCTCCC	120
TTAATGGCAA	AGCCTTTATT	AAGCGATGAA	GACTTATTGA	AACGAGTAAA	ACTACACAAT	180
ATCAAAGAAG	ATACGCTGAC	TAGCTGTAAT	GCTAAGGTGG	ACGGCTCTCA	ATACTTGAAT	240
AGTGGTTGGA	ATTTATCTAA	AGAATTTCCG	CAAGAATATA	GAGAAAAGAT	TTTTGAATGC	300
GTAGAAGAAG	AAAAACATAA	ACAAGCCCTT	AATTTAATCA	ATAAAGAAGA	CACTGAAGAT	360
AAAGAAGAAC	TTGCAAAAAA	AATCAAAGAA	ATTAAGAAA	AAGCTAAAGT	TTTAAGGCAA	420
AAATTTATGG	CTTTTGAAAT	GAAAGAACAC	TCTAAAGAA	TCCCAAATAA	AAAGCAACTT	480
CAAACCATGC	TTGAGAACGC	TTTTGATAAT	GGAGCTGAAA	GTTTTATTGA	TGATTGGCAC	540
GAACGCTTTG	GGGGTATAAG	TAGAGAGAAT	ACTTATAAAG	CACCTGGCAT	TAAAGAATAT	600
AGTGATGAAG	GAAAGATATT	AGCCTTTGGC	GAAAGAAGTT	ATATTAGACA	ATATAAAAAA	660
GATTTTGAAG	AAAGCACTTA	TGATACTAGA	CAAACCTTAT	CTGCTATGGC	TAATATGAGT	720
GGCGAAAACG	ATTATAAAAT	TACTTGGTTA	AAACCCAAAT	ATCAGCTCCA	TAGTTCAAAT	780
AATATTAAAC	CCTTAATGTC	AAACACAGAG	TTGTTAAATA	TGATAGAGCT	AACCAATATC	840
AAAAAAGAAT	ATGTTATGGG	CTGTAATATG	GAAATAGATG	GTTCTAAATA	TCCCATTCAT	900
AAAGATTGGG	GATTTTITGG	TAAGGCAAAA	GTCCCAGAAA	CTTGGAGAAA	TAAGATTTGG	960
GAATGTATTA	AGAATAAAGT	AAAGTCCTAT	GACAACACTA	CCGCTGAAAT	AGGAATAGTT	1020
TGGAAAAAAA	ATACTTATTC	TATCTCTCAT	CAC			1053

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1053 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203

ATGGCTGATA	TTTTAAGCCA	AGAAGAAATT	GATGCGCTTT	TAGAAGTCGT	TGATGAGAAT	60
GTGGATATTG	AAAATGTCCA	AAAAAAAGAT	ATTATCCCCC	AACGCAGCGT	AACCCCTCTAT	120
GATTTCAAGC	GCCCTAATCG	TGTGAGTAAG	GAGCAATTGC	GCTCTTTTAG	GAGCATCCAT	180
GATAAAATGG	CTAGGAATCT	TTCCAGTCAA	GTCTCTTCTA	TCATGCGTTC	TATTGTAGAA	240
ATCCAGCTTC	ATAGCGTGGA	TCAAATGACT	TATGGCGAAT	TTTTGATGAG	TTTGCCTAGC	300
CCTACGAGTT	TTAATGTCTT	TTCCATGAAG	CCTATGGGGG	GAACGGGGGT	TTTAGAGATT	360
AATCCTAGCA	TCGCTTTCCC	TATGATTGAC	AGACTATTAG	GGGGTAAGGG	GAGCGCGTAT	420
GATCAAAACA	GGGAGTTTAG	CGATATTGAA	TTGAATTTAT	TGGATACGAT	TTTACGCCAG	480
GTGATGCAAA	TTTTAAAGA	AGTGTGCTCG	CCTGTGGTGG	AGATGTATCC	TACCATTGAC	540
GCTAAAGAAT	CCAGCGCGAA	TGTGGTCCAA	ATCGTCGCTC	AAAATGAAAT	TTCTATCATG	600
GTGGTTTTAG	AGATTATCAT	TGGGCATAGC	CGTGGGATGA	TGAATATTTG	TTACCCGGTG	660
ATTTCCTAGC	AGAGCATTC	TTCTAAATG	GGGAGTAGGG	ATTTTCATGCT	TTTACGAAACG	720
AACTCCAAAA	AGAGCCGTAA	TAAGGAATTG	CAAGCACTAT	TGAGCGGGGT	GAGCGTGGAT	780
ATGATGGTGT	TTTTGGGCGC	GSTGGAATTG	AGTTTGAAAG	AAATGTTGGA	TTTAGATGTG	840
GGGGATACTA	TCCGGTTGAA	TAAAGTCGCT	AACCATGAAG	TGAGCGTGTA	TGTACATAAG	900

227

AAAAAGCGTT ATTTAGCGAG CGTGGGGTTT CAAGGGTATA GGAAAACCAT TCAAATTAAA	960
GAAGTGTTTT ATAGCGAAAA AGAACGCACT AAAGAAATTT TAGAAWTGCT WGAAGAACAG	1020
CGCAGGAGGC AAAGTTGGGC GRTGTTATGG AGC	1053

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204

ATGCCCCACGA TGTAGCGGT TGGTTTTTGG GTGTTGGTTT TTTTATCCAC GAGCAATGCG	60
GTGAATTTAA CCGACGGGTT AGACGGATTA GCGAGTGTGC CTAGCATTIT CACCCTCTTA	120
AGCCTTTCTA TCTTTGTGTA TGTGGCAGGG AATGCGGAAT TTTCTAAATA CTTGCTCTAT	180
CCTAAAGTCA TAGATGTGGG GGAATTGTTT GTGATTTTCG TAGCATTAGT GGGATCGCTC	240
TTTGGCTTTT TGTGGTATAA CTGCAACCCG GCAAGCGTGT TTATGGGCGA TAGCGGGAGT	300
TTGCAATAG GAGGGTTTAT CGCTTATAAC GCTATGTTT CGCATAATGA AATCTTGCTC	360
GTTTAATGG GGTCTATTTT TGTAATAGAA ACTCTGTCTG TGATCTTGCA AGTAGGGAGC	420
TATAAAACCC GTAAAAACG CCTTTTTTTA ATGGCACCCA TCCATCATCA TTTTGAACAA	480
AAGGGTTGGG CAGAAAATAA GGTGATCGTG CGTTTTTGA TCATTTCTAT GCTGAGTAAT	540
TTAGTCGCTC TTTTGAGCTT GAAGGTGTGT	570

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205

GTGCGTTTTG AAAATTTTCAT CAACCGCCTA GCCTTTTACA TGGCCACAGG GAGCGGTAAA	60
ACGATCGTCA TTATCAAACCT GGTAGAGCTT TTAAGCGTGG CTATGGGAAT GGGTTTGATC	120

228

CCTAAGAAAA	ATATCATGTT	TTTTAGCGCG	AACGAGCATT	TAATCAAGCA	ATTTGAAAAA	180
GAAATTGAAA	AATACAACCG	CAATAAGGAC	TATTCCAAAC	AAATTGATTT	CAAAAACCTT	240
AAAAGCGTTA	AGAATAAGGA	TTTTTATCGT	GCTCCAAAAG	ATTCTTTAAT	GAAAGAAATC	300
GCTCTTTTTT	ATTACCGCGC	AGATTTAATG	AGCGATGAAG	AAAGCAAGGA	AAACCTTTTA	360
AATTATAAGG	ATTGTTGGGA	TAATGGGGAA	AATTATGTGA	TTTTAGATGA	AGCGCATAAG	420
GGGAATAAGA	CTGAAAGCAA	AAGACAGGCG	ATTTTATAGC	TGCTGCTCTT	AAAAGGGTTT	480
TTATTCAATT	TCAGCGCCAC	TTTCACTGAA	GAAAGCGATC	TCATCACTGC	GGTGTATAAT	540
TTGAGCGTGG	GCGAGTGGGT	GAAACTTGCG	TATGGTAAAG	AGTCTGTTTT	ATTGAAGAAA	600
AACAACCTTA	ACGCTTTTAA	GGAATTGAAA	GATTTAAACG	ACAGGGAAAA	AGAAATCGCT	660
CTTTTAAAGG	CGTTATTGCT	TTTAGGCATG	CAAAAACGCT	ATAAAGTAGA	AGGCTATTTT	720
CATGACCCCT	TAATGCTCGT	GTTACGCGAT	TCTGTGAACA	TGGAAAACAG	CGATGCGRAA	780
ATCTTTTTTA	AAACTTTAGC	GCGCGTGATT	GAAAATGATG	ATGAGAGCGA	TTTTTCAAAA	840
GCTAAAGACG	ATTATTAGA	GGAATTAAAG	AATCCGGAAT	TCCTTTTTAG	CGATGGCAAA	900
GATAAAGAAA	AAGACTATAA	AATTGAGGTC	TTTAAAGAGA	GTTTAAAGGG	CATGGATTTT	960
AAAGGCTTAA	AAGAAGCAGT	TTTTTATGCC	AGTAATGGGC	ATATTGAAGT	CATCATTAAC	1020
CCTAAAAACA	ACCAAGAAAT	CGCTTTCAG	CTCAACACGA	GCGATAAAGT	CTTTTGCCTG	1080
ATTAGAATAG	GCGATATTAC	AGAATGGATC	CGTGAAAAAT	TAAAGAGCGT	GAAGGTGGTG	1140
AGTAAGAATT	TGAGCTTCAA	AGAAGAGAGC	TATTTACAGC	AGATTGATAA	GAGCAGTATC	1200
AATATCTTTAG	TGGGGTCTCG	TGCTTTTGAC	ACTGGGTGGG	ATAGCACAAG	GCCTAGCGTG	1260
ATTTTATTTT	TAAATATAGG	GCTTGATGAT	GACGCTAAAA	AGCTGGTGAA	ACAATCTTTT	1320
GGCAGGGGCG	TAAGGATTGA	AAGCGTCAAA	AACCAACGCC	AAAGGTTAGC	GTATTTAGAG	1380
ATAGATGAAG	CCATTAAAGA	ACAAGCTGAA	ACCAAACGCT	GCAATGCTGG	AAATGCTTTT	1440
TGTGATACCT	ACCAACCATG	CAAGCCT				1467

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206

GTGTTTAAAA	ATTCCCTCTT	TGGTATATCA	ATCTCCATGC	TTATCACTTG	GGTTTAAACC	60
GCTTGATATT	TGATTTTTAT	CCTTTTTGTC	CCGAATTTTA	CCCTTACGCA	TCCCAATTTT	120
CATTTCACTC	CGTTTGAAAA	AACCTATTTT	CAAATTCCTAG	GACTTGTTGG	TATGTAAAGT	180
TCTATTATTT	TCACCGGGTT	TTTGGCTGAT	AAAATCAAAC	CGCACAAAGT	TTGCATGGCT	240
TTTAGCSGCA	CCTTTGGGTT	TTTGGCTTTT	TTATTCTTTA	AGGAATTTTA	TTCTAACGCG	300
CCAAGTTTAG	TCAATACTAT	AATTTTATAC	TTTTTAGCTT	GCTTTTGGCG	GGGCATTATG	360
AATTTTGGCC	CCATTTTCAT	GAGCGATGTG	TTTAGCGCTA	RAATCCGTTT	TAGCGGGATT	420
TCCTTTGCTT	ATAACATAGC	CTATGCTATA	ACCGCTGGCT	TTACCCCTCA	ACTTTCAAGC	480
TGGTTAAACG	CAAAAGCTAT	AGCAGTGCCT	GAAAGTTTGC	AAAGTTATGG	TTTAAGCTTT	540
TATATCCTTA	TAGTTTCTTT	AATTGCTTTT	ATTACATCGC	TTTTAATGGC	GCCAATTTAT	600
CACAAATCTA	ATACCCAACA	CGAAGTGTGG	CCCACGGCA			639

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs

SUBSTITUTE SHEET (RULE 26)

229

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207

ATGAAAAGCG ATAAACCCCTT TTTAGAACGC TATTTTTATG ACCCCACTCT TTTGCAAAAG	60
GGGTTGATTT TCGCGCTCTA TCCTTTTTCT TTAATCTATC AATGTATTGC CACAATTAAA	120
CGAAAAACCG CTAAAAAGCA TGATTTTAAA ATCCCCATTA TCAGCATAGG CAACTTGATC	180
GCTGGGGGAA GCGGTAAAAC GCCCTTCATT TTAGAAATCG CTCCAAGATA CCAAGAAGTG	240
GCGGTGTTT CTAGAGGGTA TCAACGGGAT TCTAAAGGTT TAGTGGTGGT GAGCGTTAAA	300
GGAAACATTT TAGTTCCTCA AAAAACAGCG GCGGATGAAG CCTATCTTTT AGCCTTAAAT	360
CTAAACAAG CGAGCGTGAT TGTGAGCGAA AAAAGGGAGC TAGGCGTTTT AAAAGCCCTT	420
GAATTAGGAT CAAAGATCGT GTTTTATAGAC GATGGTTTTA GGTTTAATTT CAACCAATTC	480
AATGCGCTTT TAAAACCCAA AGTCCCCCCC TACTACCCTT TTTGTTTGCC TAGCGGGTTG	540
TATAGAGAAA ATATTAAAAG CTATAAAGAA GCCCATTTAG TCATTACAGA AGATAAGGAT	600
TATCAAAGAA TCACCTCTAT CACTAACCCC ACCAAACGCA TGCTTTTAGT AACGGCTATC	660
GCTAACCTTA GCAGGCTTGA TGCGTTTTTA CCCAAGAAG TGGTTAAAAA ATTGTATTTT	720
AGAGACCATG CCCCTTTTGA TTTGAAGCTT TTAGAAAAAG AGTTTTATCA AAATAACGCC	780
ACCTCCTTAT TGTTACTTC AAAAGATCTC GTCAAATTAC AAGATTGCAA ATTGCCTTTA	840
AGCGTATTGG ATTTAAACT AGAAATTTGC CCTAAAGTTT TAGAGGAGAT TGATCGTTAT	900
ATCCTTTCTT ATCCTTGTA TATAAAGAA CATCTA	936

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208

ATGCTTTTAG GGGCAGTGAT CAGGCTTATT TTTTGTATA AGTTAGAGGG GGTAATATTA	60
GATTAAAGC GCATCAATT CAAATCCTAT TACCCAATA ATAAAAATGC ATTATTTATC	120
AACAATAAGA AAAATCCATT ATCTAGTRCT TCAAAGTTCA TATTGCTT	168

230

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209

ATGCTAGAAA	CCACTATTGA	TTTTTCTCGT	TACAGCAGCG	TGAAAATCGG	TGCGCCTTTA	60
AAAGTGAGCG	TTTtagaaaa	CGATAATGAA	ATCTCTCAAG	AACACCAGAT	CATAGGATTA	120
GCGAACAACC	TTTAAATCGC	TCCTGACGTG	AAAAATCTCG	CTTTATTAGG	AAAAAACTAC	180
GATTATATTT	GCgATAAGGG	TGAGTGGGTG	GAGGTAGGGG	GAGCGGCCAA	TGCGTCTAAA	240
ATTTTAAATT	ATTTTAGGGC	GAATGATTTA	GAGGGTTTAG	AGTTTTTTAGG	GCAATTGCCT	300
GGCACTTTAG	GGGCGTTAGT	TAAAATGAAT	GCTGGCATGA	AAGAATTTGA	AATAAAAAAT	360
GTTTTAGAAA	GCGCTTGCGT	TAATGGCGAA	TGGCTAGAAA	AAGAAGCTTT	GGGGCTAGAT	420
TATCGCAGCA	GCGGGTTTAA	TGGCGTTGTT	TTGAGGGCTA	GTTTTAAAAA	GACGCATGGT	480
TTTAGAGAAG	GGGTTTTTAA	AGCGTGTAAG	AGCATGCGCA	AAAGCCACCC	CAAATTGCCT	540
AATTTTGGGA	GCTGTTTTCA	AAACCCGCCT	AACGATTATG	CGGGCAGGCT	TTTAGAGGGC	600
GTGGGCTTAA	GGGGTTATTG	TCTAAAAGAG	TGGGCTTTGC	CAAAGAACAT	GCGAATTTTT	660
GGTGAATTTG	GGGGGCGCAG	AATT				684

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210

ATGCTCAAAA	ATGGCGATAA	GATTCCGGAC	GCTATTTTtag	TGGATATTGA	GATGCCTAAA	60
ATGGATGGCT	ACACTTTTCG	CTCTGAAGTG	CGTAAATACA	ATAAATTCAA	AAACCTGCCC	120
TTGATCGCCG	TTACCACTCG	GGTAACTAAA	ACGGACAGAA	TGCGCGGCGT	TGAATCCGGC	180
ATGACTGAAT	ACATCACCAA	ACCTTATAGC	GGTGAATATT	TAACCACCGT	AGTGAAGCGC	240
AGCATTAAT	TAGAAGGAGA	CCAATCG				267

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211

GTGTTTGAGC	CGGTTATCGC	TTACAAGCTT	TTCCATTCTT	TTGTGATTTT	AGGGTGCGCG	60
ATTGAAACTT	TAACGACTAA	ATGCGTGGAA	GGCATCACGG	CTAATGAAAA	GATTTGCCAC	120
GATTATGTTT	TTAACAGCAT	TGGCATTGTT	ACCGCGCTCA	ACCCTCATAT	CGGCTATGAA	180
AAATCCGCTA	TGATCGCCAA	AGAAGCCTTA	AAAAGCGATC	GCTCTATCTA	TGATATCGCT	240
TTAGAAAAGA	AAATCTTAAC	CAAAGAGCAA	CTGGACGATA	TTTCAAGCC	AGAAAACATG	300
CTAAGYYCTC	ACGCTTTCAA	AAAGCATAAA	GAC			333

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212

ATGTTGCGTT	TATTAGCCCA	AAAAAGCGCT	ATTAAACTCA	TTCTTATCCC	CCCAAGCGCG	60
AACGCTTTAG	GCATCGCTTC	TATTTGCGAA	TTGAGCGAAG	AAGTTTTTGA	ACATGAAAAA	120
ATCGTAGGCA	TTGCGGCTCA	AGGGGATTTC	ACTATCAATA	GCGACGATAG	GGGTTTTTGG	180
GAAAGACGCT	GTCAG					195

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

232

- (A) LENGTH: 804 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213

ATGAAAAAAC	TTCTTTTACT	CTTAGAGCAT	AAGATCGTAA	AAATTGGCTT	AATTATTGTG	60
ATTGTGTTAG	TGGGTTTTIT	TCTTTTTTAT	GAACAAGAAA	TCAAAGAAAA	AGCTGTTAAT	120
GTTTCTCAAG	GTAAATTCCC	CACTTCATCT	TATTTGTTTC	AAGCTTACGA	AGGCATTAAG	180
AATAAAATAG	ATACTATCAA	TCAAGTGAAG	CCAAACGATG	AAACTAAAAG	CGTTAATGAG	240
AATATAGAAA	AAACACAAAA	AGATTTAGAT	GATTTTAAATG	CGCTAGTGCA	AAAGTTACCA	300
AATTTGCCCTA	AGGACTTTAA	TAAAACACTT	ATTAAACCAC	AAAGTCCATT	TTTCAACTAC	360
AATACCCTA	ACGAAGATGA	AAAAAACC GC	CTGGTGATT	TAGCGTCTCG	TATTAGCAGC	420
CAAAAAGAAA	CGCAACCTCC	CATTTCTATA	AAAAATAGCG	TTTCTCACAT	AAAATCCAAA	480
GAAAAACGAG	AACTTGAAAA	AGAATGGGCA	AAACCTAGTG	TTTCTTTTGG	TTCTTTTTC	540
TTGCTTTCCA	GTTCTTCTTC	TTTTCTTTCT	TTTGAAGTTT	CTTTTMTATC	AAGGGGAATA	600
GGATTGGATT	GTGAGAAGCT	CAAATCCTTT	TTAAAAGCTT	TTTCAAGTTC	GCTATTTTCC	660
TTATTATCTT	CATTGTTTTG	CCATCCACTT	TCTCTTTTTC	GCTCTCTAAT	AGGATTAATC	720
TTTTGTTTTT	CTAAGTTTTT	TAGAGAGCTA	GTGAATGCGT	CTAACAATTC	GCTTGAGTTT	780
TCATCATTTGT	CAAGGCTAGG	ATCA				804

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214

ATGGGAGCGA	TAGCGAGTTG	TTACGCGCAT	CAAATCATCT	TAACTTCAGA	CAATCCTAGA	60
AGCGAAAAACG	AAGAAGACAT	CATTAAGGAT	ATTTTAAAAG	GCATCAATAA	TTCTTCTAAA	120
GTCATTGTAG	AAAAAGACCG	AAAAAAGGCC	ATTTTAAACG	CTTTAGAAAA	TTTAAAAGAC	180
GATGAGGTGT	TGTTGATTTT	AGGCAAGGGC	GATGAAAACA	TTCAAATCTT	TAAAGACAAA	240
ACGATTTTTT	TTAGCGACCA	GGAAGTCGTT	AAAGATTATT	ATCTCAATTT	AAAACAAGGA	300

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215

GTGATGGACA	AACTCACTAA	AAGCTTGCAA	ACGCAAAAAA	ACTTCGCTTA	TTTAGGCAAA	60
ATCAAGCCCC	AACAACCTGC	TGATTTTCATC	ATTAACGAAC	ACCCTCAAAC	CATCGCCTTG	120
ATTTTGGCCC	ACATGGAARC	CCCTAATGCG	GCTGAAACTT	TGAGCTATTT	CCCTGATGAA	180
ATGAAAGCCG	AGATTTCCAT	TAGAATGGCG	AATTTTAGGC	GAAATATCGC	CCCAAGTGCT	240

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216

ATGCGGTATT	TTAGAAGCGC	TTTTTTATTA	TTTTTCATGA	CGCTTTTTTT	TGTTTCTTGC	60
TCTAAGCACC	CTTTTTCTAA	GCAAACCCCT	AAGACTAAGG	AGCGGATCCG	ACAAGAAGAA	120
GCCAATAAAA	AAAGAGAAGA	GACTTTGAAT	GCCTTGCGCC	AATTCAGACT	CATTTACATT	180
AACACGCCCG	TTTTTCGCTT	TTATGATTAC	GGCAGCATCA	AAACCGATAA	AGACCACAAT	240
ACTGAAGTAA	CCCTTTTATA	GCTCAGCCAA	AAAGTGGGCG	ATATTTACAT	GAATAAACGG	300
AGCATTGTGT	TTAGCCAAAA	ATGTTTCGGC	AAATGGATTG	CTGCAAGGGA	TTTGTTTGGC	360
AAGGTGAGCT	ATGGGGATTT	GTTTGATGAT	ATTGTTTTAG	GGAGGGATAT	TTTTAAAGGT	420
TTAGGGAAAC	GCCACCTAAC	CCCTGAATAT	GTGATCCAAA	GGTTTCAAAA	AAGCGGGGAA	480
ATTATCCTTT	ATGAAAGAAA	AAATGGCCTG	ATTCTTTTCC	AAAACCTGAC	TCAAAAATT	540
GCTATTAGGA	TTGAACCCTA	TGAGCCTTCT	TTGCAAGATT	TAGAAGACAA	TGAAAACGCT	600
GATAGCGAGC	TTCAA					615

234

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217

ATGCGCATG AAGAAATGG CGTGATTCT CTAGCCTTTA GTAACGGGGT GGTAGAGCCG	60
GTCGCTCGCA TCGGTATTW AGCTTTCCT AACGATCAAG GCTTAAGGAA AATCGGCGGT	120
AACCTCTATG AATGCAAGA AGGCACCATT AATGGCGAAA ACAGACCCCT AAGSGGTAAC	180
CCCATTTTAG GGTGGGACGA AGAGGGCAAG CTCAAGTTT GGAAATCAG GCACAAATAT	240
TTAGAAACGA GCAACGTGAA TGCCGGGAAC GCCCTAACCA ATCTCATTTT AATGCAAAGA	300
GGCTATTCTA TGAACGCTAG AGCCTTTGGC GCGGGCGATG ACATGATCAA AGAAGCCATT	360
AGCTTGAAAA AA	372

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218

GTGGAAGCGC GTTATTATTA TGGGGACACT TCATACTTTT ATTTGCATGT GGGAGTTTTA	60
CAAGAGTTTC CTCACCTTGG ATCGAATGAT GTGGCGTCTT TAAACACCTT TAAAATCAAT	120
GCCGCTCGCA GTCCTTTAAG CACCTATGCA AGAGCGATGA TGGGTGGGGA ATTGCAATTG	180
GCTAAAGAAG TGTTTTGA TTTGGGCGTG GTTTATTTCG ACAATTTGAT TTCCAACGCA	240
AGCCATTTTC CTTCCAATTT AGGAATGAGG TATAGTTTC	279

(2) INFORMATION FOR SEQ ID NO:219:

235

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219

GTGGAGGAGC TAGCTAAATT GATCAACAAT AATAATAACA ATAAAAAACT GAGAGGCTTT	60
TTTTTGAAAG TTCTCTTAAG TCTCGTTGTT TTCAGTTCGT ATGGGTCAGC AAATGACGAT	120
AAAGAAGCCA AAAAAGAAGC GCTAGAAAAA GAAAAAAACA CTCCCAATGG GCTTGTTTAT	180
ACGAATTTAG ATTTTGATAG TTTTAAAGCG ACTATCAAAA ATTTGAAAGA CAAGAAAGTA	240
ACTTTCAAAG AAGTCAATCC CGATATTATC AAAGATGAAG TTTTGGACTT CGTGATTGTC	300
AATAGAGTCC TTAAAAAAT AAAGGATTG AAGCATTACG ATCCAGTTAT TGAAAAATC	360
TTTGATGAAA AGGGTAAAGA AATGGGATTG AATGTAGAAT TACAGATCAA TCCTGAAGTG	420
AAAGACTTTT TTACTTTCAA AAGCATCAGC ACGACCAACA AACAACGCTG CTTTCTATCA	480
TTGCACGGAG AAACAAGAGA AATTTTATGC GATGATAAGC TATATAATGT TTTATTGGCC	540
GTATTCAATT CTTATGATCC TAATGATCTT TTGAAACACA TTAGCACCAT AGAGTCTCTC	600
AAAAAATCT TTTATACGAT TACATGTGAA GCGGTATATC TA	642

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220

GTGGGGGGCA TTGTGGCAAA CATGAACGAT CTTTCAACTT ACATGGTTGA GAATTTACTC	60
ATGGGTTTGT ATCTTTTTC TAGCGCTTTA GATTGGGCG TGAAAAAGC CATTAACTA	120
GCGAGCTCTT GCGCTTATCC TAAATACGCC CCTAACCTT TAAAAGAGAG CGATTATTG	180
AACGGCTCTT TAGAACCAAC GAATGAAGGC TACGCTTTC CAACTCTCT GTRR	234

(2) INFORMATION FOR SEQ ID NO:221:

236

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221

```

ATGAAGAAAA GAAACATGT ATCCAAGAAA GTGTTTAATG TCATTATCTT GTTGTGGCA      60
GTATTCACCTC TTTTAGTCGT CATTACAAA ACCCTTTCAA ACGGCATTCA CATACAAAAT      120
TTAAAAAATTG GAAAACTTGG CATTTCTGAA TTATACTTAA AACTCAATAA CAAGCTTTCT      180
TTGGAAGTTG AGCGGGTTGA TCTCTCTTCT TTCTTCCATC AAAAACCCAC TAAAAAGCGT      240
TTAGAAGTTT CTGATTTGAT TAAAAATATC CGTTATGGCA TTTGGGCGGT GTCTTATTTT      300
GAAAAACTTA AAGTCAAAGA AATCATTTTA GACGATAAAA ATAAAGCCAA TATCTTTTTT      360
GATGGGAATA AATACGAGTT WAGAATTTCC AGGAATCAAA GGGGAATTTT CCCTAGAAGA      420
CGATTAAAAA TATCAAGCTT AAAATCATCA ATTTGCTTTT TAAAGATGTT AAAGTCCAAG      480
TGGATGGCAA CGCCCACTAT TCRCCCAAAG CCAGGAAAAT GCGGTTCAT T      531

```

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222

```

GTGTCATGTT GGGGAGCGTC AAAAAAGCGG TTTTtagGGT TTTGTGTTTG GGGGCGTTCT      60
GTTTATGCGG GGGGGTTAAT GGCAGAGCAA GATCCTAAAG AGCTTATATT TTCAGGTATA      120
ACTATTTACA CGGATAAAAA TTCACTAGA GCTAAGAAAT ATTTTGAAAA AGCTTGCAAA      180
TCAAACGATG CTGATGGCTG TGCAATCTTA AGAGAGGTTT ATTCTAGTGG TAAAGCCATA      240
GCGAGAGAAA ACGCAAGAGA GAGCATTGAA AAAGCTCTTG AACACACCGC TACTGCTAAA      300
GTTTGTAAAT TAAACGATGC TGA AAAAATGC AAGGACTTAG CAGAGTTTTA TTTTAATGTA      360
AACGATCTTA AAAATGCTTT AGAATATTAC TCTAAATCTT GTAAGTTAAA TAATGTTGAA      420
GGGTGTATGC TGTACGAAC TTTTATAAC GATATGATAA AGGGTTTGAA AAAAGATAAA      480
AAAGATCTAG AATATTATTC TAAAGCTTGC GAGTTAAATA ACGGTGGAGG GTGTTCTAAA      540
TTAGGAGGGG ATTATTTTTT TGGTGAAGGC GTAACAAAAG ATTTCAAAA AGCTTTTGAA      600

```

237

TATTCTGCCA	AAGCTTGTGA	GTTGAACGAT	GCTAAAGGGT	GTTACGCTCT	AGCAGCGTTT	660
TATAATGAGG	GTAAAGGCGT	GGCAAAGGAT	GAAAAGCAAA	CGACAGAAAA	CCTTGAAAAG	720
AGTTGCAAGC	TAGGATTAAA	AGAAGCATGC	GATATTCTCA	AAGAACAAAA	ACAA	774

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223

GTGGCTCTCA	CTTTGGGGGC	TAGAGGGGGG	GTGTATTTGT	GTGGGGGGAT	TATCCCACGA	60
TTCATGATT	ATTTTAAAC	TTGCCCCCTT	AGAGCGCGTT	TTGAAACGAA	AGGGCGCATG	120
GGAGCGTTT	TCGCTTCCAT	CCCTGTGCAT	GTGCTGATGA	AAAAAACTCC	CGGACTTGAT	180
GGGGCGGGCA	TTGCGTTAGA	AAATTATTTA	CTGCATGATA	GAATA		225

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

ATGAAAGGTT	TAACAATGAA	AAAATTAGTT	TTTAGCATGC	TTTTATGTTG	TAAAAGCGTG	60
TTTGCAGAGG	GGGAAACTCC	TTTGATTGTC	AATGACCCAG	AAACCCATGT	AAGTCAAGCC	120
ACTATCATAG	GCAAATGGT	AGATAGTATC	AAAAGATACG	AAGAGATTAT	TTCTAAGGCT	180
CAAGCTCAAG	TCAATCAGTT	ACAAAAAGTC	AATAACATGA	TAAATACGAC	TAATTCCTTG	240
ATTAGTAGTA	GTGCTATCAC	TTTAGCCAAT	CCTATGCAAG	TTTTACAAAA	CGCTCAGTAT	300
CAAATAGAGA	GCATTAGATA	CAACTATGAG	AATTTAAAGC	AAAGCATAGA	AAATTGGAAC	360
GCACAAAATT	TGTTAAGAAA	CAAATACTTA	CAGCAACAAT	GCCCTTGGCT	TAATGTCAAT	420
GCTCTTACTA	ACAATAAGAT	TGTCAATCTT	AAAGATCTCA	ATAACCTAAT	CACCAAAAAT	480

238

GGCGAACAAA	CCCAAACCGC	AAGAGATGTG	CAAAATCTCA	TTCAGTCCAT	TAGTGGCAGT	540
GGCTATGGAA	ACATGCAATC	ACTTGCTGGG	GAATTGAGTG	GTAGAGCGTG	GGGGGAAATG	600
TTGTGTAAAA	TGGTAAACGA	TAGTAATTAT	GAAAGCGAGC	AAGCTCTTTT	AGCAACAGGC	660
AATAACCCAG	AAGAGCAAAA	ACGAAGATTT	TTGCTTAGAG	TAAAGAAAAA	GGTTAATGAT	720
AATAAGCAGT	TAAAAGATAA	ACTTGACCCA	TTTCTAAAAA	GACTTGATGT	CCTACAAACT	780
GAGTTTGGTG	TAACTGACCC	TACAGCTAAC	CATAATAAGC	AAGGGATACA	TTATTGCACA	840
GAAAATAAAG	AGACAGGTAA	ATGCGACCCT	ATTAAAAATG	TATTTAGGAC	AACTCGCTTA	900
GATAACGAAT	TAGAACAAGA	AATCCAAACG	CTCACACTTG	ATTTAATCAA	AGCCTCCAAT	960
AAAGACGCTC	AAAGCCAAGC	CTACGCAAAT	TTCAATCAAA	GGATTAAATT	ACTTACTCTA	1020
AAATATTTAA	AAGAAATTAC	CAATCAAATG	CTCTTTTAA	ATCAAACAAT	GGCAATGCAA	1080
AGCGAGATTA	TGACAGATGA	TTATTTTAGG	CAAAATAATG	ATGGCTTTGG	GGAAAAAGAA	1140
AACCATATAG	ACGAACAATT	AACGCAAAAA	AGAATAAACG	AAAGAGAAAG	AGCTAGAATA	1200
TACTTTCAAA	ACCCTAATGT	TAAATTTGAC	CAATTTGGCT	TTCCCATTTT	TAGTATATGG	1260
GAT						1263

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225

ATGAGCGTGA	ATTTATTGGA	ATTGTTAAAA	CTCGCTGTGC	CTTTAGCGGT	TATTTTGAGC	60
GTTCAAGTGG	CGGTTATGAT	CCTTTATGTG	GTGCTTGTA	CCTTTAGCGT	ATGCCGGAAG	120
GATTATGATG	CGGCGGTGTT	GTGCGCGGGG	CATTGCGGTT	TTGGGCTTGG	AGCGACCCCA	180
ACGGCTATGG	TGAATATGCA	AACCATCACC	AACCACTATG	GGCCATCGCA	TGTGGCGTTT	240
ATCGTCGTGC	CTTTAGTGGG	AGCGTTTTTT	GTTGATATTA	TTAACGCTTT	AGCGATTAAA	300
GGCTTTTTGC	TTTTGCCTTT	TTTCCCTAGT				330

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

239

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226

ATGCAACTAA	GCCCCCTTACA	AAGCGCGCTG	TTATATTTCC	GTTACTTTAT	TTATCCGGAA	60
AAAAAAACAA	GGAGCTTTGA	TTTAAGCGAT	TTAATTTTAA	TTGTCATGGT	TTTTTTAGTC	120
CTAGCTTTGG	GGCTGTTGAT	GAGCGAAGAA	ATTTCTATCA	GCTACAATGA	AGCGAAAGAC	180
TTTTTTTATA	GCGATGCGTG	GTTTGTCAAA	ATCGCTCAAA	AAAGCGTAGC	CATTTTAAGG	240
CCAAAACGAT	TTGGCTTTAA	GATTGCCTTT	TTTGATCGCT	CACGTCATCA	ACATGTTTTT	300
ATTCTACCTC	ATAGGGCGAA	AGATTTTAAA	AAAGCC			336

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227

GTGTATGCGC	TCATGGTGGC	GTTTTTTGCT	TACATGAGTT	ATTGCTTGGG	GTATCAATTC	60
TCCAAATTCG	TTTCTAAAAA	CAACATTCA	TCGCTCTCAT	CGCTTTTATC	AAGCTGTGTG	120
CGCGTGGTCT	CTGTGCTAAT	CTTGTCGCTC	AGTAGCCTAG	AGTTGCGTTA	CTTCTCACCC	180
CTAACTATCA	TAACCATGCA	TTTTGCCCTA	ACGCTTATCA	TCCTCTTTTT	CTTTTTGTAT	240
AAGGCTAAGC	CGTTTGATGA	G				261

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228

SUBSTITUTE SHEET (RULE 26)

240

ATGAGGCTCTT	GGATGAAGAA	AAAATACTTC	ACGCTTTTAT	TGCAAAGTAG	TGTGGTATTA	60
GCGGTTTTTTA	TAGGGTGTTC	TTCTACCAGG	AATCATACTT	TTTCAGCCCT	TAGTAATCAA	120
GAAAATACAG	ACGATAAGCT	CCCAGTGGTC	CATTCCATTA	AAACGATTAA	CGATGTGAGT	180
TCAGTGGGCT	TTGAATGGTC	TAAAGTCGCT	GACACTTATG	ACATTGACGG	GTTTGTTTTG	240
TATCGTTTTGA	AAAAAGACTC	CAAGCTTAAA	AGAATCGCCA	CCATTAAAAA	CCCTTATGCG	300
ACCCACTATT	ATGATGAGGG	GTTAGAAACA	GAGAGTTCCT	ACACTTACCA	ATTAGCCACC	360
TACAAGGGCG	ATAAAATTTC	CAAACTTTCA	GAACCCATTT	TAGTAAAAAC	CTCCTTTATC	420
AATCCTGTAG	AAAGCGTGT	TGCAAGCCTT	GAATACCCCTA	AAAGCGTGAA	AGTCTTTTGG	480
AGCCCGCACC	CAAATCCCAG	CGTTTCTAAA	TACATCATTC	AAAGGCAGAA	TAAAGACGGC	540
AAATTTTTTAA	ATGTGGGGGC	TGTAAAAAAC	CGCTTATTCG	TGGAGTTTTT	TGATAAAGAT	600
TTAGAAGATG	GGCAAAAAATA	CCGTACCAA	ATCATCGCCG	AAAATTTTCAT	GGGGGATAAA	660
TCCAGGCCCTA	GCGTGATAGT	GGAGGGGAAA	ACCAAAGACT	TGCCCCAAGA	AATCGCTAAT	720
GTTAGAGTGA	GTCAAAACCT	CACACGACAA	ATTGAATTGA	GTTGGGATAA	ATCCCCAGAA	780
GAAGATGTGA	TAGCTTATCG	CATTTACGCT	TCCAATAACC	GCAACGATAA	ATACAAATTC	840
ATCGCTCAAA	CCACCAACAC	TTCTATGTG	GATAAGATAG	AAAAAGACAA	TCTCACTCGT	900
TATTATAAAG	TCGTCGCCGT	AGATAAAACG	CATCTTGAAG	GGGCGTTACC	CAAAGAGCCT	960
GCCATGGGTG	AGACCTCTGA	TAGGCCTGAA	GCCCCATCA	TCACTAAAGG	GACTATTCAA	1020
GACTCTTTCGG	CCTTGATCCA	ATGGGAAAAC	AACCCAAGCC	CTAAAATAGC	CACCTATGCG	1080
GTGTATCGTT	TTGAAGCCAA	CTCCAAAACC	CCTTTGCGTT	TTGGGAATAT	CACACAAAAC	1140
CAGTTTCGTG	ATAAGGACAT	GAAAGTGGGC	GTGGCTTATC	GCTATCAGGT	GGTGAGCGTG	1200
GATAAAGATG	GTTTAGAGTC	GCACCCAAGC	AAAGAAGTGC	GTTTGTTTTT	AGAGCGC	1257

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229

ATGCTTCCTA	CTAAAACACG	CATTAGAGAT	CCGAACAAGC	AAGAACTTAC	ACAACCAAAA	60
ATAAAAGGAT	TGAGTATGGG	AAAAATTTTA	GCTTCTTTGT	TGGGTGGCGG	AACAAATCTT	120
TTTACAGGTT	TATCCAGTGA	TTTGTTTTCT	ATGATATTAA	ATTTTTTGTT	CTTCCTGATG	180
TTAATGATGG	GACTTAATGA	AGCATTAGGG	AAAAAATTTA	ACTTGCTAT	GGACAATATC	240
AAGAATTTTA	TGGCAGAAGT	GCTGAAGAAT	GGATTTCGATA	GTATCAAAAA	CATGGGATCT	300
GCTTTGGTTG	GTAATGGTTT	TGGTAGCAGC	AAATCAGACA	AAACCACTAA	TAAAATGAGT	360
GTCCACACAG	TAAGACTC					378

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

241

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...216
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:230

ATGGCGAACA TGATGATGGC AGCGGCCATG TTAGGGATTG ATTCTTGCCC GATTGAAGGG	60
TATGATCAAG AAAAAGTGGG GGCTTATTTA GAGGAAAAAG GCTATCTAAA CACGGCAGAA	120
TTTGGCGTGT CGGTAATGGC CAGTTTTGGT TATCGTAACC AAGAGATTAC CCCTAAAACC	180
CGCTGGAAGA CAGAAGTTAT TTATGAAGTG ATTGAA	216

(2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...333
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:231

ATGGCCGGGC TTGTTTIGAT GGTGCTGCTC GCCAGTTATG AAAGCTTTGT TTCTAAATTA	60
GACAAGGTGG ATGCTAGCGA AATCACTTGG CTAAACACA CAGATTTTAA CGCTTTAAAA	120
TTAAAGGTTT CCTCTCCAT TGTAGCCATT TCGGCGATT TCTTGCTCAA ACGCTACATG	180
AGTTTAGAAG ACGTTTATC CAGTATTCCT AAAGACACGC CCCTATCGCA TAACCCTATT	240
TTTTGGCAAG TGGTGATCCA TTTGGTGTTC GTGTGTTTTCAG CGCTGTTAAC CGCTGTTACC	300
AATAACATCG CTTTTTCGCA GAAAGAAAGG CAT	333

(2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

242

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...426

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:232

ATGATTACGA TCGTTATTGC AAAAGCGGGG AATATAGTCA AAGYCGATAT TTTTACGCAC	60
ATTAGCGATA TTAAATGGG GCTTATTAAA GGAGGTCAAT GGGGGGTAT TGGTTTAGGC	120
AATATCGGTA AAAGAGTCGC CAAGCTCGCT CAAGCTTTTCG GGGCAAAGGT GGTGTATTTT	180
TCCCCTAAAG ATAAAAAAGA AGAATACGAG CGCTTGAGTT TAGAGGAATT GCTTAAACA	240
AGCGGTATTA TCAGCATTC A TGCCCCCTTA AATGAAAGCA CGCGCGATT AATCGCTCTG	300
AAAGAATTGC AAAGCTTAAA AGATGGGGCG ATTTTAATCA ATGTGGGGCG TGGGGGCATT	360
GTGAATGAAA AGGRTTTGGC TTTRRTTTTA GAAACCACAG ATTTGTATTA CGCGAGCGAT	420
GTGTTT	426

- (2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 189 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...189

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:233

GTGAATTTCA ACGCTAAAAA TATTTCAATT GATAATTTGG TAGAAATCAA TAATCGTGTG	60
GGTTCGGAG CCGGGAGAAA AGCCAGCTCT ACGGTTTTGA CTTTGCAAGC TTCAGAAGGG	120
ATCACTAGYA GTAAAAATGC GGAATTTCT CTTTATGATG GCGCCACGYC AATTGGCTT	180
CAAACAGMG	189

- (2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 930 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

243

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234

ATGCGAACGC TCATTCTGTC GCTTCTAAAA CATGCGATTT TAATGGGCAT GCTTTTAAAA	60
GAATGCCAAG AAAAGTTAAA GCGTTCTTTA AATTTGAGTG CTAATCATTG CGTCTTGAGC	120
GCGGGGTATG GGGCGAGTTC AGCGATTAAG AAATTTCAAG AAATTTTAGG GGTGTGTATC	180
CCTTCAAAAA CGAAGAAAAA TTTAGAGCCG TATTTGAAAG ATATGGCTTT AAAGCGTGTG	240
ATTGTAGGGC CTTATGAGCA TCATTCTAAT GAAGTTAGCT GGCCTGAAGG CTTGTGTGAA	300
GTGGTGCGTA TCCCTTTAAA TGAACATGGT TTATTGGATT TAGAAATTTT AGAGCAAAC	360
TTAAAAAAA CCCCTAACAG CTGGGTTTCT GTGAGCGCGG CTTCTAATGT AACGGGAATT	420
CTTACGCCCTT TAAAAGAACT TTCATCATTG TGTAAGGAAT ATAGGGCTAT TTTAGCTTTG	480
GATTTAGCGA ATTTTAGCGC GCATGCTAAC CCTAAAGATT GCGAATACCA AACCGGTTTT	540
TATGCGCCTC ATAAGCTTTT AGGGGGCGTT GGAGGGTGCG GTCTTTTAGG CATTCTTAAA	600
GATTTGATTG ACACGCAAAAT YCCTYCGAGT TTTAGCGCAG GGGGCGTGAT TAAATACGCT	660
AATCGCACAC GGCGTGAATT TATTGATGAA TTGCCTTTAA GAGAAGAATT TGGCACGCCA	720
GGATTGTGTC AATTTTACAG GAGCGCTCTA GCGTATCAAT TAAGAGATGA ATGCGGTTTG	780
GATTTTATCC ATAGAAAGA AAACAACCTT TTAAGGGTGC TTGTGTATGG CTTAAAAGAC	840
TTGCCCCGTA TTAATATTTA TGGGAATTTA ACGGCGAGTC GTGTGGGGGT AGTGRCTTTT	900
AATATTGGAG GGATTTCRCC CTATGATTTA	930

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235

GTGGCATGCA ACACCGCGAG CGCTCTGGCT TTAGAAGAGA TGCAAAAGTA TTCTAAAATC	60
CCTATTGTGG GCGTGATTGA GCCAAGCATT TTAGCGATCA AGCGGCAAGT GGAAGATAAA	120
AACGCCCTTA TTTTAGTGCT AGGGACAAAA GCGACGATTC AATCCAACGC CTATGACAAC	180
GCCCTGAAAC AACAAAGGCTA TTGAACATT TCGCATTTAG CTACTTCTCT TTTTGTGCCT	240
TTGATTGAAG AAAGTATTTT AGAGGGCGAA TTGTTAGAAA CTTGCATGCA TTATTATTTC	300
ACTCCCTTAG AGATTTTACC CGAAGTGATC ATTTTAGGTT GCACGCATTT TCCCTTAATC	360
GCTCAAAAAA TTGAGGGCTA TTTCATGGGG CATTTTGCCC TTCCAACGCC CCCCTACTC	420
ATCCATTCCG GCGATGCTAT TGTAAGATAT TTGCAACAAA AATACGCCCT TAAAAACAAT	480
GCATGCACAT TCCCTAAAGT GGAATTTTCA GCGAGCGGCG ATGTGATCTG GCTAGAAAGA	540
CAAGCTAAAG AATGGCTCAA ATTG	564

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

244

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236

GTGTTGTGGG TGCTATATTT TTAAACAGT TTATTTATTT GCTCTTTGAT TGTTTTGTGG	60
TCTAAAAAAT CCATGCTCTT TGTGGATAAC GCTAATAAAA TCCAAGGCTT CCATCATGCA	120
AGAACCCAC GAGCCGGGGG GCTTGGGATC TTTCTTTCTT TTGCGTTGGC TTGTTATCTT	180
GAACCTTTTG AGATGCCTTT TAAGGGGCCT TTTGTTTTCT TAGGGCTATC GCTAGTGT	240
TTGAGCGGTT TTTAGAAGA CATTAACTT TCATTAGCC CCAAATAACG CCTTATTTTG	300
CAAGCTGTAG GGGTCGTTTG CATCATTTCA TCAACGCCTT TAGTGGTGAG CGATTTTTCG	360
CCCCTTTTGA GCTGCCTTA TTTCATCGCT TTTTATTCG CTATTTTTTA TGCTGGTGGG	420
TATCAG	426

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237

ATGGCGTGTA AATTTTGCCC TAAGATCAGA AAAACAGATT GGATTTTAT TTAAATCGCC	60
GCTTTAGGCT TTTATTCAGT TAATAAGCTA GGGTATGCGC CCAAATTCAA TACCCCACT	120
CCAAAATCTT CACGCCCTCT TTCACGCCCT ATTGAAAAGC CTAACAATAT GACTGAAGAA	180
GAAAGGAAAA AGCGTTTAT AGAGTTGCAA AAAGCATGCT TACTTCATAA AGACAAAAG	240
GCATGCGAAG AGGTTTTT	258

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

245

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...363
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:238

GTGGATTCCA TTTTAATTGA TGAAGCGAGA SCTCCTTTAA TCATTTCAGG GCCTGTGGAT	60
AGGCGCATGG AAAATTACAA CAAGGCTGAT GAAGTCGCTA AAAGCATGCA AGTGGAAAGTG	120
GATTTACCA TAGACGAAAA AAACCGCGCG ATTTTAATCA CTGAAGAGGG GATTAAAAAA	180
GCCGAAAATC TCTTTGGCGT GGATAATTTA TACAAAATTG AAAACGCCGC CCTATCGCAC	240
CATTTAGACC AAGCCTTGAA AGCGAATTAC CTCTTTTTTA TTGRTAAAGA TTATATTGTA	300
GCCAATAATG AAGTGGTGAT TGTAGATTRA TTTACCGRCC GTTTGYTTGA AGGGGAGGCG	360
CTT	363

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239

ATGACGATCA CCACCCTATC TTTTTTATTC ACAACGCCAG AAGTGTTTGT CAATCAGGAT	60
TTCCCATGGC TTTCTGGGGC TGGAAAGCTA GTGGTTAAAG ACTTGCCGTT ATTTGCTGGA	120
GGCTTGTTTG TGGCCGATT TGATCGAAAC GCTATTTGGA GGGTAAAGGG TTTTGCT	177

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

246

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...426

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:240

GTGTTTTCTG	GCAATAAAAG	GGCTATAAAT	TATCGCACGA	TTGTCAGCGC	CTTTGTGATT	60
CAAGTGGCTT	TAGGGGCGTT	GGCTTTATAT	GTGCCTTTGG	GCAGAGAAAT	ACTGCAGGGT	120
TTAGCTAGCG	GCATACAAAG	CGTGATTGGT	TACGGCTATG	AGGGGGTACG	CTTTTTATTT	180
GGCAATCTCG	CTCCAAACGC	TAAGGGCGAT	CAAGGGATAG	GAGGCTTTAT	CTTTGCGATC	240
AACGTTTtag	CGATCATTAT	CTTTTTTGCT	AGCTTGATTT	CACTTCTATA	TTATTTAAAA	300
ATCATGCCTT	TAGTAATCAA	CCTCATCGGS	GGGGCGTTGC	AAAAATGCTT	AGGCACTTCT	360
AAAGCAGAAA	GCATGAGCGC	AGCGGCTAAT	AYTYTTGTGG	CGCACACCGA	AGACRCCCTT	420
AGTCAT						426

- (2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...240

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:241

ATGCTGGTGG	GTATCAGTAA	CGCTATTAAT	ATCATTGACG	GGTTTAACGG	GCTTGCATCT	60
GGGATTGCG	CGATCGCGCT	TTTAGTCATT	CATTATATAG	ACCSTAGCAG	TTTGTCTTGT	120
TTGCTCGCTT	ACATGGTGCT	TGGGGTTTAT	GGTGTTAAAW	TTCCCTTCAG	GAAAGATTTT	180
TTAGGWCAT	CGGGGGGGCG	TATTTTTTGG	GTTTGGTGWR	CGGRATTTCT	CTCTTGCAAT	240

- (2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

247

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242

ATGCTACATA AAAAATATCG TCCTAATGTT GCGGCCATTA TCATGTCGCC AGACTACCCCT	60
AACACATGCG AAGTTTTTAT CGCTGAGCGC ATAGACATTG AAGGGGCGTG GCAGTTCCCC	120
CAAGGAGGCA TTGATGAGGG AGAGACCCCT TTAGAAGCAC TCTATAGAGA ATTACTAGAA	180
GAAATTGGCA CGAATGAAAT AGAGATTTTG GCGCAATACC CTAGA	225

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243

GTGATGCTAA TGGCAATTTT TACCCCTTAT ATTCTTATTT TGAAAATGAT GAAAAAGTCT	60
ATGAGTTTAT TCGCCATAT GGGGTGGAG CAAATTTTTT GCAACAGAGA CATTAAAGAT	120
TTAAATGATT TTGTTTTTGG TATAGAAGTG GGGCTTGATA GCAATGCGAG AAAAAATCGT	180
AGCAGAAAAG CTATGGAAAA TCATCTTATC GGTCTTTTGG TCCAAGCTCA ATTAAATTTT	240
AAAGAACAAG TAGATATTAG AGAATTTGAG GATTTACGCC AGGCTTTTGG AAATGATACT	300
AAAAAATTTG ATTTTGTAT TTTTAGCAAA GAGAAACTT ATTTTCATAG AAGC	354

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...627

248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244

ATGATCCGTC TAGCCGCGTT TTTTITAGCT CTCGCTTGCG CGATTACGCC AAAAAGCCGC	60
CTTCTTTTAA AAAATGTCTT GCTCAACCCC ACTCGCATAG AAGCTTTTGA GGTTTTGAAA	120
AAAATGGGCG CTCATATAGA ATATGTTATC CAATCCAAAG ATTTAGAAGT TATTGGCGAT	180
ATTTACATAG AGCATGCCCC TTTAAAAGCG ATCAGTATTG ATCAGAATAT CGCCAGCCTT	240
ATTGATGAAA TCCCCGCTTT AAGCATCGCT ATGCTTTTGT CAAAAGGCAA AAGCATGGTG	300
AGAAACGCTA AAGATTACG AGCCAAAGAA AGCGATAGGA TTAAAGCGGT TGTTCCTAAT	360
TTCAAAGCTT TAGGGATTGA GTGCGAAGAA TTTGAAGACG GGTTTTATAT AGAGGGATTA	420
GGAGATCGCA GTCAATTAAA GCAGCATTIT TCTAAGATTA AACCCCTAT TATCAAGAGT	480
TTCAATGATC ACAGGATTGC GATGAGTTTC GCTGTTTTAA CTTTAGCGTT GCCTTTAGAA	540
ATTGATAATT TAGAATGCGC GAACATTTC TTCCCAACCT TTCAGCTTTG GCTCAATCTA	600
TTCAAAAAAA GGAGTCTCAA TGGAAAT	627

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245

GTGGGGAGTT TGAAATTTTT AAACGCTATG GGGGTTGATT TAAAGGTAA AGAGAGCGCT	60
AATATCATGG TAGGCTTTGC GAAAAATAAG ACCTTATGCG CGTTATTCAT TTTAGAAGAG	120
CGTTTGAAAG CTAACGCTAA AGAAGTCATT CAGGCTTTAC AAAATCAAGG CTTGGAATTA	180
GAAATTTTAA GCGGGGATAA TGAAAGCTCG GTTAAGGAGT GCGCG	225

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...363

249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246

ATGGAGGCTT TAAACGCTTT GAACGCGCAA AGTGATGAGC AAATTTTATG CGAGGGTTAT	60
TTTGTGTTGT TGCAAAATCTT AGAGCCTATG ATCCCGCACA CGGCATGGGA ATTGAGCGAG	120
AGGCTTTTAA AAAGAGAGAA TTCAAGCCT ATAGAAGTAG ATGAAAGCGC TTGATAGAA	180
GACTTTATGA CTTTAGGGCT TACCATTAAAT GGCAAAAGGC GCGCGGAATT GAAAGTCAAT	240
ATTAACGCTA GCAAAGAAGA GATTATTATT TTGGCTAAAA AAGAATTAGA GAAATATTTA	300
GAAACGCGA GCGTTAAAAA AGAAATTTAT GTGCCTAATA AACTTGTTAA TTTTGTACC	360
GCA	363

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247

ATGAAAGAAA GTATTAAATA CTTGCTAGAA AGCGTGGGGC TAGTGCTTTT AATGAGCGTG	60
AATCCGGGCT TTGGCGGGCA GAAGTTTTTA GATCTAGTGC TAGAAAAGTG CTTGAAAGTT	120
AAAGAACTGA TCAAACGCTA CAACCCTAGC TGTCTTTTAG AAGTGGATGG GGGCGTGAAT	180
GATAAAAATA TCPTTGAACCT CCAACAAGCG GCGGTGGATG TGGTGTTTC AGGGAGTTAT	240
ATTTTGAAT CCAAAGATYG TAAGCTGGCT ATTGAAGCT TACAGAATGT CAGACAACCT	300
CTTGCA	306

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248

SUBSTITUTE SHEET (RULE 26)

250

GTGCATGACG	GCGTGCTTGG	GTGGGTAGGC	TTCACCTTGA	TTGCGAGCAT	GTATCACATG	60
ACCCCTAGGC	TTTTCAAAAG	AGAGATCTAT	TCAGGAAGAC	TTGTGGATT	CCAATTTTGG	120
ATCATGACTT	TAGGGATTGT	GCTTTACTTT	TCGTCCATGT	GGATTGCAGG	GATCACGCAA	180
GGGATGATGT	GGAGGGATGT	GGATCAATAC	GGGAATCTCA	CTTACCAATT	CATTGACACG	240
GTTAAGGCGC	TAATCCCTTA	TTACAATATT	AGAGGCGTTG	GGGGTCTTAT	GTATTTTATT	300
GGATTTATTA	TTTTTGCTTA	CAATATCTTT	ATGACAATCA	CGGCAGGCAA	AAAATTAGAG	360
CGTGAGCCCA	ATTACGCCAC	SCCTATGGCA	RRA			393

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249

ATGATAACGC	TCTTTAGTTT	TGGAGCGTTC	GCTTACTATT	TCGTGCTTTC	TCAAATCAGT	60
CACGAAACT	ATCAAAACGA	AATGCGCCAT	TACCAGTTTG	TTACCACTAT	CAATGAAATT	120
TTAAATAACT	ACTCTGATTA	TAGAGCCATA	GAAGATTACC	TCTATAAAAT	TGGCTTTAGA	180
GAAACCACAA	TAGAAAATTT	AGAAAAGGTT	TTAGCCAAAA	GACGCCACCA	GTTGCACCAC	240
AGAAATATTT	GGTATGCTGA	AGTGTTTAAA	TTCAGCGATA	TGGTTTTTAT	CCTTTTAAAA	300
AAGGATGAGC	ATTTTGTGCT	TTATAAAGAT	TTGCATTTCG	TTTCTTATAG	GAATTATTTT	360
TTAGCCATTA	CGGTGGGTTT	ATTATTGATT	TTATTCTCTT	TTTTATTTGT	TTTGCAGAGT	420
TTATTGCCCT	TAAGAGAGTT	AAGATCTCAA	GTGAAACGCT	TCGCTCAAGG	GGATAAAAGC	480
GTGAGTTGTA	AAAGCAAGCA	AAAAGATGAA	ATAGGGGATT	TGGCTAACGA	ATTTGACAAT	540
TGCATCCAAA	AAATCAATGC	GATGAATGAA	TCTCGGGTTT	TATTTTTCG	CTCTATCATG	600
CATGAATTAC	GCACCCCTAT	CACTAAGGGC	AAGATACTAA	GCTCTATGCT	CAAAGAAGAG	660
CTGTCTTGCA	AACGCTTTTC	ATCTATATTT	GATCACTTGA	ACATGTTGAT	TGAGCAATTT	720
GCCCGCATTG	AGCAGCTCGC	TTCCAAAAAT	TATGGGAGCA	ATAAAGAAAA	ATTTTAAATG	780
AGCGAATTGA	TAGATAAGAT	TGAAAAATG	CTTTTAATTG	ATGAAGATAA	AAAAAGCCCT	840
ATCCATGTAT	CCTCTTCAAA	TTACATCATT	GAAGCGGATT	TTGAATTGTT	TGCTATAGCG	900
TTAAAAAACA	TGATAGACAA	TGCGATCAAA	TACAGCGATG	ACAAACAGGT	GTTTTTGGAT	960
TTCATAGGGA	ATAATTTAGT	GGTGTCCAAT	AAAAGCAAAC	CTTTAAAAGA	AGATTTTGAA	1020
AAGTATTTGC	AACCCCTACT	TAAATCTTCT	AACCCAGCC	AAGCCCATGG	GTTTGGGTTA	1080
GGCATGTATA	TCATTAAAAA	CGCTTTAGAG	GCTATGGGAT	TGAATTTGAG	CTATCATTAT	1140
AGCAATGGAA	GAATCTGTTT	CACTATCCAT	GATTGCGTTT	TTAATAGTTT	TTACGATTTA	1200
GAAGCGGATA	ATGAAGAGCT	ACCCCCCCCC	GAAAATTTGA	GAGAGGTGAA	GGGAATGAAG	1260
GGAACAGAAA	AAGCCAATTG	TGGGGTTAAA	GAAAAACAAA	AAGAGAGAAC	ATGTTCAAAC	1320
GAT						1323

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

251

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250

```

GTGCTTCTCC TTTCTCGTAT GGGTATCGCT TTTGCCCACT CTATTTTGTG GTCCATCACG      60
GCTTCTTTAG TCATTCGTGT CGCGCCAAGA AACAAAAAAC AACAGGCCTT AGGGCTGTTA      120
GCGTTAGGGA GTTCGTTAGC GATGATTTTA GGGTTGCCGC TTGGGAGGAT CATTTGGGCAA      180
ATTTTGGATT GGCGATCCAC TTTTGGCGTG ATTGGGGGCG TTGCGACTCT TATAATGCTG      240
CTTATGTGGA AATTGCTCCC GCATCTACCG AGTAGAAACG CCGGCACGCT CGCAAGTGTT      300
CCTATATTAA TGAACGCCCC GCTTTTAGTG GGGATTATT TGCYTGTA TCATGGTTAT      360
TTCTGGGCAT TTCACCACTT A

```

(2) INFORMATION FOR SEQ ID NO:251:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251

```

ATGCGCATT TCATAAGGTT ACTTTCATTT AAAATGAACG CTTTTTTAAA ACTCGCGCTC      60
GCTTCTTTGA TGGGGGGGCT TTGGTATGCT TTCAATGGCG AAGGCTCTGA GATTGTGCGT      120
ATAGGGATTT TTGTGTTGAT CTGTTTGTGTT TTTTATATCC GCCCTGTGAG TTTCCAAGAC      180
CCAGAAAAAC GAGAAGAATA CATAGAACGG CTTAAAAAAA ACCATGAGAG GAAAATGATC      240
TTACAAGACA AGCAAAAAGA AGAGCAAATG CGCCTCTATC AAGCCAAAAA AGAGCGAGAG      300
AGCAGGCAAA AACAAGACCT TAAAGAACAA ATGAAAAAAT ACTCA

```

(2) INFORMATION FOR SEQ ID NO:252:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

252

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...258
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:252

GTGCGATCTT GCAAACAGAT TTTTGATAAG GGTTTAAAGC CCTATTATAA ACATTCTGTT	60
TGCTTAAAGC CTTTITTTAG GTTTGTGTTT CTCAAAATTC ATGCTTATCA ACAGCGTTAT	120
AGAGCGTTTG CTCTAACGCT CTTTCTTGT AAGTTTTTA ACGCTTGTA GATTTTTATT	180
CCCATAATTG ATTTTAAAT CGTTTTTATC CCTATTCTAA AACACCAAGC CAAGCTAAAA	240
AGAGTCTCTA ATGCCTAT	258

(2) INFORMATION FOR SEQ ID NO:253:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...132
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:253

ATGTGTGGAA TGGGGTTTAT TGGCTTCAAA ACAAACTTA CTAAACAAA GGCATTATT	60
ATATTGATCC CAATCTTTCA GGACAGAGCG GTCAAAGCG CAACACGCTC AGCACCTATA	120
CAGCTAATTT GT	132

(2) INFORMATION FOR SEQ ID NO:254:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1680 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

253

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...1680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254

ATGGGGAATT	TTAATAGCTA	TGGCGATTTG	GTGTTTAACC	TCAGTCATTC	AGTTAGTCAT	60
GCTATTATCA	ATACTCAAGG	CACAGCGACG	ATCATGGCCA	ATAATAACCC	TTTGATCCAA	120
TTCAACGCTT	CTTCAAAAGA	AGTGGGTACT	TACACGCTGA	TTGATAGCGC	TAAAGCCATT	180
TATTACGGGT	ATAACAACCA	AATCACAGGA	GGCAGTAGCC	TGGATAATTA	CCTTAAGCTT	240
TATGCGCTCA	TTGATATTAA	TGGCAAGCAC	ATGGTGATGA	CTGACAACGG	CCTAACCTAT	300
AACGGGCAAG	CCGTGAGCGT	TAAAGATGGC	GGTTTAGTTG	TAGGCTTTAA	GGACTCTCAA	360
AATCAATACA	TTTACACTTC	CAITCTTTAT	AATAAAGTGA	AAATCGCTGT	TTCTAATGAT	420
CCTATCAATA	ACCCACAAGC	CCCCACTTTA	AAACAATATA	TCGCTCAAAT	TCAGGGCGTT	480
CAAAGCGTGG	ATAGCATCRA	TCAAGCTGGG	GGAAATCAAG	CGATTAATTG	GCTCAATAAA	540
ATCTTTGAAA	CTAAAGGAAG	CCCTTTATTC	GCTCCCTATT	ATCTAGAGAG	CCACTCCACA	600
AAAGATTTAA	CCACGATCGC	TGGAGATATT	GCTAACACTT	TAGAAGTCAT	CGCTAACCCCT	660
AATTTTAAAA	ATGACGCCAC	TAATATTTTA	CAGATCAACA	CCTACACGCA	GCAAATGAGT	720
CGTTTAGCCA	AGCTCTCTGA	CACITCAACT	TTGCGCCGTT	CTGATTTCTT	AGAACGCTTA	780
GAAGCCCTTA	AAAACAAGCG	ATTCGCTGAT	GCGATCCCTA	ACGCTATGGA	TGTGATTTTA	840
AAATACTCTC	AAAGGAATAG	AGTTAAAAAT	AATGTGTGGG	CGACAGGAGT	TGGAGGGGCT	900
AGTTTCATTA	GTGGAGGTAC	TGRAACTTTA	TATGGTATCA	ATGWAGGGTA	TGATAGGTTT	960
ATTAAGGGCG	TGATTGTGGG	AGGTTATGCC	GCTTATGGGT	ATAGCGGGTT	CCATGCAAAC	1020
ATCACTCAAT	CAGGCTCTAG	CAATGTCAAT	GTGGGCGTTT	ATAGCCGAGC	GTTTATCAAA	1080
AGAAGCCGAG	TAACCATGAG	CITGAATGAG	ACTTGGGGAT	ACAATAAAAC	TTTCATCAAC	1140
TCCTATGACC	CCCTACTCTC	AATCATCAAT	CAGTCTTACA	GATACGACAC	TTGGACGACT	1200
GACGCTAAAA	TCAATTATGG	CTATGATTTT	ATGTTTAAAG	ATAAAAGCGT	TATTTTAAAA	1260
CCCCAAGTAG	GCTTAAGCTA	TTATTACATT	GGTTTGCTCT	GTTTAAGGGG	CATTATGGAT	1320
GATCCTATTT	ACAACCAATT	CAGAGCCAAT	GCTGACCCTA	ATAAAAAATC	CGTTCTAACG	1380
ATCAATTTTG	CCCTAGAAAAG	TCGGCATTAT	TTCAATAAAA	ACTCTTATTA	TTTTGTGATT	1440
GCGGATGTGG	GCAGAGACTT	ATTCATTAAT	TCTATGGGGG	ATAAAATGGT	GCGTTTCATC	1500
GGTAATAACA	CCCTAAGCTA	TAGAGATGGT	GGCAGATACA	ACACTTTTGC	TAGCATTATC	1560
ACAGGCGGGG	AGATAAGATT	GTTCAAAACC	TTTTATGTGA	ATGCGGGCAT	AGGGGCTAGG	1620
TTTGGGCTTG	ATTATAAAGA	TATTAATATT	ACCGGAAATA	TTGGTATGCW	SYATRCTTTT	1680

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255

ATGGAGTCGA	ATCAWTCAC	CCCCATGGCA	TTAATATCAT	GCTCACCTAA	CGCTAAAGGG	60
GCGGACATTA	AAGGCTATAA	CGGCTTAGTG	GGGGAATTGA	TTGAAAGGAA	TTTCCAACGC	120
TATGGCGTGC	CGTTACTGCT	TTCTACGCTC	ACTAACGCC	TATTGATTGG	GATCACTTCG	180
GCTTTAAACA	ACAGAGGCAA	TAAAGAAGAG	GTGACTAATT	TCTTTGGGGA	TTATCTTTTA	240
TTGCAATTGA	TGAGGCAAAG	CGGCATGGG	ATCAATCAAG	TGGTCAATCA	AATTTTAAGA	300
GACAAGAGCA	AGATCGCCCC	CATTGTGGTG	ATTAGAGAGG	GGAGTAGGGT	CTTCATTTTC	360

254

CCCAATACTG ACATCTTCTT CCCTATACCC AGAGAGAATG AAGTCATCGC TGAGTTTTTG 420
AAG 423

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256

GTGAATTTTT ACCTTCGCC CAAAGATTAC CACCACTACC ACGCCCTTG CGATTTAGAA 60
ATTTTAGAGG CTCGTTATTT TCGGGGAAA TTACTACCAG TCAATAAGCC CTCATTACAC 120
AAAAACAAA ATCTGTTTGT GGGCAATGAA AGG 153

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...699

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257

ATGGATATTT TAAAAGCAGA GCATTTAAAC AAACAGATTA AAAAAACCAA AATCGTTTCA 60
GATGTTTCTT TAGAAGTGAA AAGCGGCGAA GTGGTGGGGC TTTTAGGGCC TAATGGGGCG 120
GGTAAAACCA CCACCTTTTA CATGATATGC GGGCTTTTAG AGCCTAGTGG GGGGAGCGTT 180
TATTTAAACG ATGTGGATTT AGCTAAATAC CCCTTACACA AGCGTTCTAA CTGGGGCATA 240
GGCTACTTGC CCCAAGAATC CAGTATTTTT AAAGAATTGA GCGTGGAAGA GAATTTGGCC 300
CTAGCAGGGG AGAGCACTTT TAAAACTCT AAAGAGAGCG AAGAAAAAAT GGAAAGCTTG 360
CTTGATGCTT TTAATATCCA AGCCATAAGA GAGCGCAAGG GCATGAGCTT GAGTGGGGGA 420
GAAAGAAAGC CGCTAGAAAT CGCTAGGGCT TTAATGAAAA ACCCTAAATT CGTGCTGTTA 480
GATGAGCCTT TTGCGGGCGT GGATCCGATT GCGGTGATTG ACATTCAAAG AATCATTGAA 540
AGCTTGATTG GATTAAACAT TGGCGTGTG ATTACTGATC ACAATGTGCG AGAGACCTTG 600

255

AGCGTGTGCC ATAGGGCGTA TGTGATCAAA AGCGGCACGC TTTTAGCGGC GGGAACGCTA 660
 ATGAAATTTA TGAAAACGCT TTGGTGCCTA AGTATTATT 699

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258

ATGAAAGAAA TCGTTACAAT AGAGAATGTG TCTTTTAACT ACCACAATCG CGCTATTTTT 60
 AAGGATTTTA ATTTAAGCAT TCAAGAAGGG GATTTTTTAT GCGTTTTAGG GGAGAGCGGG 120
 AGCGGTAAAA GCACGCTTTT AGGCTTGATT TTAGGGCTTT TAAACCCAG TCTGGGGAGC 180
 GTTAAATCT TTAATGAGAC CCTTCAAAC AACGCTTTT TACGCCAAA AATAGGCTAT 240
 ATCGCTCAGG GCAATTCCTT ATTCCCTCAT TTAAACGCCT TACAAAACAT GACTTTTTGC 300
 CTTAATTTAC AAGGCATAAA CAAACAAGCC GCTCAAAAAG AAGCCAAAGC CTTAGCGTTA 360
 AAAATGGGGT TAGACGAGAG CCTTATGGAT AAATTCCTTA ATGAATTGAG TGGGGGGCAA 420
 GCCAAAGAGT GGGCATTATT AGGGGGATTA TCCACAGGCC AGAACTCATT TTAT 474

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259

ATGATTTTCC CCGAGCGCTT TCAAAACGCC TTTTATAGGT TAAGCGAATT GTTTTACTAC 60
 GCTTCCAGCT TGAGTTTTTA TACGATTTTG TCTTTATCGC CTATTTTGT GTTCGTGTT 120
 AGTCTTTTGT TGTCTCATTA CTGCGAAGCG CACAGCGGTG AAATGGAAGC CTTGATTTTC 180
 CCTAACGCTC CTAACTCAT TGGCGCGATT AAGGATTTTT TAGAAAATT TAAAAAACA 240
 GACATGACCT TAGGCACGCT TGAAGAGGTG TCTATTGTGG TGGCGTTGGT GCTTTTTTGT 300

SUBSTITUTE SHEET (RULE 26)

256

GAAACTACC	GCTCCATCGC	GTCAAAAT	TTTGACGCAA	AGCCCAGAGA	TTATGCGCAT	360
TTTAAGGGTA	AAGAAATCTT	TTTATTTTGG	GGGTTTGGCA	CGACTTTAGT	GTTTTTATTC	420
GCTTTCCTT	TGGTGGTGTT	TTTGATATT	AAGATCCAAG	TGTTTTTTGA	AGATAAAGAT	480
TCAAGCTTGT	TGCATGTTTT	AAGATGGATA	GGCACTTACG	CGTTTTTTTT	GATCCTTTTT	540
ACCATTCCCA	CGAATAAGGT	GTTTAACTA	YYA			573

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260

ATGTTTTGA	TGATTTTCAC	AAGCATCTTG	AAGATAGCGT	TAAAAGTTTT	ATCAGAGCGA	60
AAAAAAATC	GTTATGGTTT	TCCTAGAATC	TTTGATGTTG	CAGACATAGA	ACAAGAAGAG	120
AGGGAAGTCA	TTGAATGGCG	AGAAAAAAG	AAAGCGTCAA	AACAAAGCTA	TAAACAAAAC	180
CTTCAAATCA	ATAAAATCGC	TAACGATTTA	AAGCGTGATA	AGATAGTGGA	TAAAAGAACG	240
ATTTTAAGCG	TGATAGACGC	TGATATAGAG	CGTGGTTTTA	TCCCGCCTAA	AGATTTGTTA	300
AAACAATTAG	AAAAAATTAG	CGCTTCTCTT	TCTAAAGACA	TCGTAATAAC	GATAAAGCAA	360
GTAGAAAAAT	TAGAGCTTAA	CTATGCGCTA	ATAGACAATA	TCCAACATAA	CACGCTTGAT	420
GACACGCTTG	ATTTTACCTT	TATTGTTGGG	GATTCCTTGA	GCGTTCAGTC	GCTTTATGTT	480
ACCTTTAATC	TTGTGATTGA	TATTGATAGA	CCCATGAGCG	AGCAGTTTCT	CAACCWTATT	540
GGGAAATTGG	GGAGTTTGA	ATCTAGAGAG	CAAGCGTTAG	AGTGGGTGCG	ATTATCGCAA	600
ACTAACTGA	TCATTGAAAC	GCCTAAAGAA	GCCTTAAAAA	ATGCCGAATT	ATCACAAATT	660
GAAGAAATAT	TGACCGGCTG	TATTTTAAAT	GGCGCTTACC	GCCTTCAAAA	CGATCTTAAG	720
AAAGGGCGA						729

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261

GTGAGTGAGG	TCGCGAGCGT	GGGGGGCTTT	GTGAAGGATT	ATGAAGTAAC	GCTTCAAAAC	60
GATTCTTTGA	TCCGTTATAA	CTTGAGTTTA	GAACAAGTCG	CTAACGCGAT	TAAAAATTCC	120
AATAACGATA	CCGGTGGGGG	CGTTATTTTA	GAAAACGGGT	TTGAAAAAAT	TATAAGATCG	180
CATGGCTATA	TCCAATCTTT	AAACGATTTA	GAAGAAATTG	TGGTTAAAAA	AGAAGGGGCT	240
ATCCCTTTAA	AAATCAAAGA	TATAGCGAGC	GTTAGGCTAG	CGCCCAAACC	GCGCAGAGGG	300
GCGGCTAATC	TCAACGGCGA	TAAGGAAGTG	GTGGGCGGGA	TTGTTATGGT	GCGCTATCAC	360
GCTGACACTT	ATAAGGTGCT	TAAAGCCATT	AAAGAAAAAA	TCGCCACCTT	ACAAGCGAGT	420
AACCCTGATG	TGAAAATCAC	CAGCGTGTAT	GACAGGAGCG	AATTGATTGA	AAAAGGCATT	480
GACAATTTGA	TTCACACGCT	CATAGAAGAA	AGCGTCATTG	TGCTAGTCAT	TATTGCGATT	540
TTCTTACTGC	ATTTCAGGAG	CGCTTTAGTG	GTGATTATCA	CTCTGCCTTT	AAGYGTGTGC	600
ATCAGTTTCT	TGCTCATGSG	TTATTTTCRAT	ATTGAAGCGA	GCATCATGAG	TTTGGGGGGC	660
ATTGCAATCG	CTATAGGGGC	GATGGTGAAT	GCGGCGATTG	TGATGGTG		708

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262

GTGGAACTT	TTCTTAGAAT	TTTTGAAAAA	GATATTTTTA	ACACGCCCTA	TAAATTAGAA	60
GTCATTACG	CTACTGAGGG	GGGGGCTAGG	ATTAAAGGGA	CTAAAGAAAT	GCCCTTTAAA	120
GAAGTGTGCG	AAAAAWTAGA	CAAATCCAAG	CCAAAGCCTC	CTATCAATCT	TATTTATCCC	180
ACCCAATCAG	AACAGGCTAA	AAATTTAAAG	ATCGCCAAGA	AAAAATGCGA	AGAGATCATC	240
AAATACGCCA	ATGAGAAAAA	AACGCAAGTT	GAAGAAGCGT	TTTTAAAGGT	GGCAGAGTTT	300
TTAGAAAAAG	TGAAAAAGCT	TCATGAAAAA	AACAAATTAG	AAGAGTTGGA	TTTTGAAGAA	360
TTAGAAAAAT	TGAGCGCTGA	AATTGATAAC	GTTAAAGAGC	TTTTTGATGA	CAAACGATTC	420
AATTCGTATT	TTATGGATGC	GATACAATCT	TACATTTTCC	ACCAGGAATT	GCATATCGCT	480
GAAATCGTGT	GTAAAAAAAC	GAGTAATGAA	GACGGGATTA	AGGGC		525

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

258

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263

ATGAAAACGC	CTTGCAACGC	CTATTTTCTC	AAAACGCCAC	CCAAAAACAA	AAAAAGAAGA	60
GTTTATGTTA	ATTTAGCGGT	GTTTCCTTTT	TTATTGCTAG	CGAGCGCTTT	ATGGCTCATT	120
CCTAGAAGTG	CCATAGAAGR	AAAGCCCTTA	GTCGTGGCGA	CAAAACCTAG	CAGCGAGCAG	180
TATATTTTGG	GCGAAATTTT	AAGCCTTTTG	TTAGAAAAAC	ACCATATCCC	TATCAAGCGA	240
GCGTTTGGCA	TTGGTGGGGG	GACGATGAAT	ATCCATCCGG	CATTGATTAG	GGGCGATTTT	300
GATTTGATG	TGGAATATAC	CGGCACCGCT	TGGGTGAACA	CGCTCAAAAA	CCCTTTGACT	360
CAAAAAGTGG	ATTTTGA AAC	GATTAAAAAG	CGTTATGAGA	AGGAATTTAA	TCTTTTGTGG	420
GTGGGACTTT	TGGGCTTTTA	TAACACCTAT	TCTTTAGCGA	TTTCTAAAGA	AGACGCTCAA	480
AAATACGCAA	TTGAACTTT	CAGCGATTTA	GCCTTTCATA	GCCCCGAATT	TGATTTTGGA	540
GCGGAGYTTG	ATTTTTTTGA	AAGAGAGGAC	GCCTTTAAGG	GCTTAATCAA	AGCTTATCGC	600
TTTCATTTTA	GAAGTTTGCA	TGAAATGGAY	ATTAATTTGC	GTTATAAAAG	TTTTGAATCC	660
CTCATAAGAT	YAACGCTT					678

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264

GTGATGGTTT	ATAAACTCCC	CAAACACCAG	CAAATAAGG	TCATGATTTT	AGGCTTGGGC	60
TTAGCGATGA	TCACTCGTAT	AGGGCTTTTA	GGGAGCTTGT	TTTTTCATCAG	CCATTTGCAA	120
AAGCCTTTAT	TCGTATAGC	GGGCATGAGC	TTTTTCATGCC	GTGATGTGGT	GCTGCTTTTA	180
GGGGGGGCGT	TTTTGGCTTT	TAAGGCGTTA	GTGGAATTAA	AAAGAGCAGA	TCTATCC	237

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 630 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

259

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265

ATGTTTGTGG	TTTTTATAGA	AGGTTTGGT	TTAGCGATT	CTTTGTGCGC	GGCGGTGGGG	60
GCGCAATCCT	TGTTTATTGT	GGAAAGGGGG	ATGGCTAGGA	ATTATGTGTT	TTTGATTGTC	120
GCCTTGTGTT	TTATGTGCGA	TATGTCTTA	ATGAGCATGG	GCGTGTGTTG	CGTGGGGGCT	180
TATTTGCGTA	AAAACCTTTA	TTTGAGCTTG	TTTTTGAATT	TATTTGGGGC	AGTTTTTACC	240
GGATTTTACG	CTTTTTTGGC	TTTAAAAACC	CTTTTTTCAA	CCTTTAAAAA	AAAGCAAGTC	300
CAAAACCCCTA	AAAAATTATC	CTTAAAAAAG	ACCTTATTAT	TCACTTTAGG	CGTTACCTTA	360
CTCAATCCTC	AAGTGTATTT	GGAAATGGTG	TTTTTAATTG	GCGCGAGCGC	TATGTCTTTT	420
AACCTAGTGC	AAAAAATCGT	CTTTCTAGCT	GGCACTTTAT	CGGCTGCCTT	TTCTTGGCTT	480
TTATTGTTAT	GCACCATGTC	CTTACGCTAT	GGCTCTAAAC	TTTTGAACAA	CCAAAAAATC	540
TTTATGGGCG	TGAATCTCTT	TGTAACCGCT	ATCATGGGAA	CGCTCAGCGT	TACTTTATTC	600
AGGGATTTTT	TAGCGTTATT	GAGCAAAACC				630

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 888 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266

GTGAAGCCAA	AGAGCATGAA	AGAGAAGCTA	AGAGGCGCTA	TGGTGAATAT	CTTAAGGATA	60
AAAATGATTG	AAATAAGCGA	ATGGTTGCAA	AAACTAGACG	ATGCCTTAGA	TAAAGTTGTT	120
GCTAAAAAAG	AGCCAGAGAG	TTTTCTCAAG	CCGATCATTT	CACCAATAGA	GGACTACCAA	180
AAGAGTGTC	GGCAAATTCA	AGCGCAATTC	ACAGACGCGC	CGAAGTTCAA	TGAAGAGGGT	240
GCTTACCCTC	AATTTTTAAG	CTGTGGTTTA	TTGCAAGTTA	GGGGCAAAAA	TGGTGCTAAC	300
ATGGAATTTT	TATTGCCTAA	AGTTTATCCT	TTCCCCCCTA	AAAGCTTGTA	TATAGAGCAT	360
GAAAAAGACG	GGCAGTTTTT	GAGAGAAATG	CTCATGCGCT	TACTCTCCAG	CGCGCCTTTA	420
GTGCAATTGG	AAGTGATCTT	AATTGATGCG	TTGAGCTTGG	GGGGCATTIT	CAATCTGGCC	480
AGAAGGCTTT	TAGATAAAAA	CAATGACTTT	ATTTACCAGC	AAAGGATTTT	GACCGAAAGC	540
AAGGAAATAG	AAGAAGCCCT	AAAGCATTTG	CATGAATATT	TAAAGGTTAA	TTTGCAAGAA	600
AAATTAGCCG	GTTTTAGAGA	TTTTGTGCAT	TATAATGAAA	ACGCCAAAGA	CTCCTTGCCT	660
TTAAAGCGC	TTTTTTTAAG	CGGGGTGGAT	GCTTTGAGTA	AAGACGCGCT	TTATTATCTA	720
GAAAAGATCA	TGCGTTTTGG	CTCTAAAAAT	GGGGTTTTGA	GCTTTGTCAA	TTTGAGAGAC	780
GAAAAAACA	ATCAATCCGC	AGAAGATTG	AAACGCTATG	CGGAGTTTTT	TAAAGACAGG	840
ACAAGTTTTG	AGTGSTTAA	ATACCTTAAT	GTAGAAATCA	TCAGCGAT		888

(2) INFORMATION FOR SEQ ID NO:267:

260

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267

GTGCTTATAA GCGTGATGAT AGGCCAAAAT CAAGTCTTAG GCTTTATAGG GACTAATTTT	60
AAGCAAGAAT TAGTCGTGGA TTTCATTGTC CCAAGCGCTG AAATCAACAT AGGCRRTCAA	120
GTGYTAACGA GCGGGCTAGA TGGGATTTTT GGAGCGGGGG TGTTTGTGGG TGAAGTTTCA	180
AGCGTTGAAG ATCATTACAC TTATAAAAGC GCGGTGTTGA AAAACGCTTT TTTAAGCGAA	240
GCCAAACTTT TAAGGCATGT GTTTTAAAGC GGTGTGAAAA AC	282

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268

ATGGAAGCGC AATTACGATT TACGGSTCTT GGAGGGCAAG GCGTGTGTT AGCGGGAGAG	60
ATTTTAGCTG AGGCTAAGAT CGTGAGCGGG GCTATGGCA CTAAGACTTC CACCTACACT	120
TCGCAAGTGC GTGGAGGTCC CACTAAAGTC GATATTTTGT TAGATAAAGA TGAAATTATT	180
TTCCCTTATG CTAAAGAGGG CGAGATTGAT TTCATGCTTT CAGTCGCTCA AATCAGCTAC	240
AACCAATTT	249

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 609 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

261

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269

ATGCAAGCTT	GGGTGGATAA	GCCGGTATTG	TTAGAGCCAG	ATAGTAACGC	CCAATACGCC	60
GCTGTCATTG	AAATTGATGT	GGCAGAAATC	ACGGAGCCTA	TTTGGCATG	CCCTAATGAC	120
CCTGATGACG	TCGCTACTTT	GAGCGAAGTT	TTAGCGGATA	CGACCCGCAA	AAGACCCAC	180
GCTATTGATG	AAGTGTTTAT	TGGCTCTTGC	ATGACGAATA	TTGGGCATTT	CAGAGCCTTT	240
GGTGAAATCG	TTAAAAACGC	CCCTCCCACT	CAAGCACGCC	TTTGGGTAGT	GCCACCCACT	300
AAAATGGACG	AACAAGAGCT	TATTAATGAG	GGCTATTATG	CGATTTTGTG	GGCTGCCGGG	360
GCAAGGACTG	AAGTACCAGG	CTGTAGCTTG	TGCATGGGCA	ATCAAGCGAG	GGTTAGGGAT	420
AATGCGGTCTG	TTTTTCTAC	TTCCACACGG	AATTTTGATA	ATCGTATGGG	TAGAGGGGCT	480
AAAGTGTTAT	TGGGCAGTGC	GGAGCTTGGG	GCGGCGTGCG	CTTACTAGG	GAGGATCCCC	540
ACTAAAGAAG	AATACATGAA	TTTAGTGAGT	GAAAAGCTAG	AGAGCCAAAA	AGACAAGATC	600
TATCGCTMC						609

(2) INFORMATION FOR SEQ ID NO:270:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 660 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270

GTGGGCAATG	CCGGGGTGGC	TTTAGCGGGT	TTGATGAGCG	ATGAAATTTA	TTTGTGCGCT	60
TTAGATTGCG	CTTATATCAA	AGGGTTTAAA	AAGCACGCTC	AAAATTCCTA	TTATGGAGAT	120
GAAAAAGAGA	TTGACACCTC	ATCTTTAATC	AGCGTAGAGG	GTAATGTTGA	AGGTTATGAA	180
ACTTTTAGCG	ACTCGCTTTT	TTTGCTCTCT	AAAGAAAGGA	TTGAAGAAGC	CCTTCATTAT	240
TACCAGCCTA	AAAAAGTCTA	TAAATTAAGC	TATGGGGCGA	AAATCAAGCA	CGCCGTTAGC	300
CTCAATCACT	CTCAAGTGAA	ATTGAAACAA	ATCAACAAAC	AAGACGCTAT	CGTTCGCATT	360
AAAAGCATGT	TTAGCCCTAG	AAGTAATCAT	GCTAAGGATT	TAAAAAATTT	ACAAAAAAAT	420
CTGATTCGTT	TTAAAGAGGA	TTTTTTCACG	CATTTAACAA	CGCCTTGTA	AACCAAGCAA	480
GAAGCATTTG	AATGGGTGGA	TAGCTTGAGT	GGATTTTGCC	AAACAGCCAG	CGCTAAAACC	540
CCCACTATAG	GCATTTTATT	TGAAGGGAGT	GTCGCCCATA	TCTTACAAAG	CGTTCCTAATC	600
GTTCATTGTC	ATCTTAAAGA	AAATGAGCTG	ACGCTTTTAT	CAAATCTCT	CAAAACGCCT	660

262

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271

ATGCAAAAAA	GTATATTCAA	AATAACTCTG	TTGTTGGTTT	TCCTCTTTTT	AAGGAATGCT	60
GTTGGTTTAG	ACGATAAAAA	AGCAGCTCCT	AAAAGCGTTC	AAAATACCCC	TAAAAATTTA	120
CCCCCTATCC	AGTTAAGGCT	CGATCAAGCC	TATGAAGACC	TTATCAAAAT	GTTAGACAAT	180
ATGGGAAAAA	GCACGCAGTA	TGAGTTCCCT	AAAATTAAAG	AAATCCTAGA	ACAAAGCGAA	240
GAGGAATGGC	TAGGAGTCGC	CCATGAAGAA	TGTGTGGCGT	TAGTCATGTT	AATAAGCCCT	300
AAGGCTTCTA	TTGAAAACAG	CCCGATTTAT	AAGAAATTGCT	ATGAAGCTTA	TGTGAAACAA	360
AGAAATCCATG	ATTTATATGA	TTTTTATATA	GAGGGCAAAA	AAGTGAAAAG	AAAAATCAAG	420
AAAGCCCATG	AGCATGAAAT	GGCCCTCAAC	AAATCCCAAC	CCTTAAAAAA	GGAACCGCCT	480
AAAAGCGAGA	ATAAAAAGGG	CTTAACAAAA	CCTAGCTTGA	AAGACGCAAA	GATCCCTAAA	540
GGGTATTACT	TGCAAAATTGG	GGCTTTTTTA	AATTCGCCCA	GTAAGGATTT	TTTGCAAACG	600
CTCAAAACTT	TCCCTCACCA	AATGGAGGAA	AAAGACTCCC	TCACGCATTA	TTTGATTGGC	660
CCTTATAAAA	CCAAAGAAGA	AGCCCTAAAA	CAGCTTGAAA	ATGCGGCTAA	AAGCTTTAAA	720
AATAAGCCTG	CGTTGGTAGA	GAAG				744

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272

ATGCAAGAAA	TCTTAATCCC	TTTAAAAGAA	AAAAGCTATA	AAGTGTTTTT	GGGGGAAGTG	60
CCTGAAATAA	AATTGAAACA	AAAAGCGCTC	ATCATTAGCG	ATAGCATCGT	GGCCGGGTTG	120
CATTTGCCCT	ATTGTTTGA	GCGCTTGAAC	GCCTTAGAAG	TCAGAGTGTG	CGTGATAGAG	180
TCCGGGGAAA	AATACAAAAA	TTTTCATTCA	TTAGAGCGGA	TTTAAACAA	CGCCTTTGAA	240

263

ATGCAATTAA	ACCGCCATTC	TTTAATGATA	GCCCTTGGTG	GGGGAGTGAT	AAGCGATATG	300
GTGGGGTTTG	CGAGCAGTAT	TTATTTTCAGG	GGGATTGATT	TTATTAATAT	TCCCTACGAC	360
TTTACTCGCT	CAAGTGGATG	CGAGCGTGGG	GGGGAAAACA	GGGATCAACA	CGCCTTATGG	420
CAAGAACCTA	ATCGGATCGT	TCCACCAGCC				450

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273

ATGCGAATAC	TTCATTATGG	AGGTGAGCTC	CCATGCGATT	GTCCAAAACG	CATCGCTGGG	60
CTTGATTTTCG	CTCTTAAAAT	TCTCACCAAT	ATCACAAGCG	ATCATTTAGA	TTTCCATCAA	120
AATATAGAAA	ATTACAGGGA	CGCTAAAAAC	AGCTTTTTTA	AAGATGAGGG	CTTAAAAGTC	180
ATCAACAGAG	ATGAAACAAA	CGCCCTTTT	AACCCCATTA	ACGCGCGCAC	TTACGCACTG	240
GATAAAAAAG	CGCATTTGAA	TGTTCAAGCC	TTTTCGCTCA	ACCCTTCCAT	TAGCGCGTCT	300
TTATGCTACC	AACACGATTT	AAGAGATCCC	AATCTTAAAG	AAACCGCCCT	GATCCATTCC	360
CCCCTTTTAG	GGCGTTACAA	CCTTTATAAT	ATTTTAGCGG	GCGTTTTAGG	GGTTAAATG	420
CTCACTCAAT	TGCCTTTAGA	AACGATCGCA	CCGTTATTGG	AAAACTTTTA	TGGGGTTAAG	480
GGGCGTTTGG	AAATTGTACA	TTCTAAACCT	TTAGTGGTCG	TGGATTTTGC	CCACACAACA	540
GACGGCATGC	AACAAGTTTT	T				561

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274

GTGAGCATT	AAGAAGAGAG	CCAAACCTTA	GCCGATATTA	CTTCCAAAA	TTATTTTCAGG	60
-----------	------------	------------	------------	-----------	-------------	----

264

ATGTTTTCTA	AACTTTCAGG	CATGACAGGC	ACGGCTCAAA	CCGAAGCCAC	AGAATTTTTA	120
GAAATCTACA	ATTTAGAAGT	GGTGTCATC	CCTACTAATC	TAGCGATCAA	GCGAAAAGAT	180
TTGAACGATC	TGATCTATAA	GAGTGAAAAA	GAAAAATTTG	ACGCTGTGAT	CCTTAAATT	240
AAAGAATTAC	ACGATAAGGG	TCAGCCCGTT	TTAGTCGGCA	CGGCTAGCAT	TGAAAAGAGT	300
GAAACCTTGC	ACGCTTTACT	CAAAAAAGAG	CGCATCCCTC	ACACCGTTTT	AAACGCCAAG	360
CAACACACTA	AAGAAGCTGA	AATCATCAAA	GACGCCGGGC	TTAAAGGGGC	GGTTACGATT	420
GCGACCAACA	TGGCAGGCAG	GGGCGTTGAT	ATTAAGCTCA	CTGATGAAGT	TAAAGAACTT	480
GGGGGGCTGT	ATATCATTTG	CACTGAAAGG	CATGAGAGCC	GTAGGATTGA	CAATCAATTA	540
AGGGGGCGAA	GCGGGCGTCA	AGGCGATCCG	GGAGTGAGTC	AGTTTTATTT	GAGC	594

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275

GTGGTGGCTG	ATGAGGTGAG	AAAGCTCGCT	GAAAAACCC	AAAAGCCAC	TAAAGAAATC	60
GCTGTCGTGG	TTAAAAGCAT	GCAACAAGAA	GCGAACGATA	TTCAAACCAA	CACCCACGAT	120
ATTAATTCTA	TTGTAGGCTC	TATTAAGGGT	GATGTGGAAG	AGCTTAAATC	CACCGTAAAA	180
AATAACATGA	TTGTCGCGCA	AGCCGCAAAA	TACACCATCT	ACAATATCAA	TAACCGGGTG	240
TTTTGCGGTG	TGGCTAAACT	CGATCATGTG	GTCTTTAAAA	ACAATCTTTA	TGGCATGGTG	300
CSTTTGGTCT	CAATTCCTTT	GACATTACCA	GCCCATAAGA	GTTSCCGTTT	AGGCAATGG	360
TATTATGAGG	GTGCGGGTAA	AGAAAACTTT	GCTAACACTT	CAGGCTATAG	AGCTTTAGAA	420
AGCCACCATG	CGAGCGTGCA	TGCTGAAGCT	AATGATTTGG	TTAAAGCCGT	TCAAGAAGAT	480
CACGTCACCG	ATTCAAAATA	CCTAGAACAT	AAAGTGCATT	TAATGGAAGA	TAGCGCTAAG	540
CATGTCAAAG	AAAATATTGA	TAAGATGTTT	TATGAAAAAC	AAGATGAACT	CAATAAAATC	600
ATTGAAAAAA	TTCAAAAAGG	CGAA				624

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

265

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276

```

ATGAATACAT CAAAAAAATT AGGTAACCCC TTGCTTTTTT TGCATGATAA TAAAATTTTG      60
TTGTTTGTGCG TAGGGGTGAG CATGGGCGGG TGGGCCACTT CTAAATCTA TCAATTTGAA      120
AGCGCTTTAG AGCCGATTCA TTTTAAGTTT GCGCGAAAAC TCTCTTTAAG CCCTTTTTTA      180
AATTTGAGCC ATTTAGTAAG GAATAAGCCT TTAAACACCA CTGATGGCGG GTTTATGCTA      240
CCACTCTATC ACGAATTAGC CACCCAATAC CCCTTGTGTG TGAAATTTGA CCAACAAAAT      300
AACCCAAGAG AGCTTTTAAG GCCTAATACC TTAAACCACC AGCTCCAACC AAGCTTAACC      360
CCCTTTAAAG ACTGCGCTGT CATGGCGTTT AGAAACCATT CTTTTAAAGA TAGCCTCATG      420
CTAGAAACCT GTAAACCCCC CACTGATTGG CAAAACCCA TTTCTACAAA TCTTAAAAAC      480
TTAGATGATT CTTTAAATTT ACTCAATTTA AATGGAATAT TGTATTGAT CCACAACCCCT      540
AGCGATTTAT CACTGCGTCG TAAAGAACTT TGGCTTTCTA AATTAGAAAA CCYCAACTC      600
RTT                                                                    603

```

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277

```

ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT TTGCCTTCCT      60
GTTTTTGTCT ACCCAGAAAC GCTGGTGAAG GTAAAGATG CTGAAGATCA GTTGGGTGCA      120
CGAGTGGGTT ACATCGAACT GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTCGCCCCC      180
GAAGAACGTT TTCCAATGAT GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC      240
CGTATTGACG CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
GTTGAGTACT CACCACTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT AAGAGAATTA      360
YGCWGGTGGT GCCATAACCA T                                                                    381

```

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

266

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278

GTGAACGTGG GCGTGCCTTT TAGCTATCAA GTGAGCGCGA CCTTTCAAAA CTCACGCCTT	60
TCTAGTTTGC TAGAACTTT AAAAAAGAGT TTTTATAGAA AGCCCTTAAT TGAGAGCAGC	120
GCGAATAAAA TCGCGGATAT TTTTCTAAA GCGGTGTTGT TTTTAGCCTT TGTGAGCTTT	180
TTATTGTGGC AATTGGTTT GGGGGTAAT TTTGAAAAAS GCTTTAATGG TGTGTAT	237

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279

ATGCTAATGG TTAATGGCTA TCAAATCAG ATGCATAAGG GTTATAAGGT AGGGTTTTTT	60
ACAAGCGGTT ACAACCCTGA TTTCGCTCAA ACCATTCAAA ATAGAAGCTA TTTGATGAGC	120
TCTTATGAGT TATCGTTTTT AAGAAAT	147

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280

267

ATGGTGCAAT	TTCAAAACAC	GCTTATAAAA	TTCCATGCCC	TATCCTTTAA	AAACGCAAAT	60
TTAATTTATA	ATGCAAAATT	AAACAAAACA	TGCTATAAAG	AAAATTCAAA	TACTATCAIT	120
TTAAGGATTA	AAATGCTCAC	CCAAGAAGAT	GTCTTAAACG	CGTTAAAAAC	GATCATCTAC	180
CCTAATTTTG	AAAAGGATAT	TGTCAGCTTT	GGTTTTGTTA	AAAACATCAC	CTTGCATGAC	240
AACCAATTAG	GGCTTTTAA	AGAAATCCCC	TCAAGCTCTG	AGGAAACGAG	TGCGATTTTA	300
AGGGAAAATA	TCTCCAAAGC	GATGCAAGAA	AAAGGCGTGA	AAGCTTTGAA	TTTGATATT	360
AAAACCCCGC	CTAAACCGCA	AGCTCCAAAG	CCCACCACTA	AAAATCTGGC	TAAAAACATC	420
AAGCATGTGG	TCATGATAAG	CTCAGGCAAG	GGCGGTGTGG	GTAAAGCAC	CACCAGCGTG	480
AATTTAAGCA	TCGCTTTAGC	GAATTTAAAC	CAAAAAGTGG	GGCTACTAGA	CGCTGATGTG	540
TATGGCCCTA	ATATCCCTAG	AATGATGGGC	TTGCAAAACG	CTGATGTGAT	CATGGATCCT	600
AGCGGTAAAA	AACTCATTCC	TTTAAAGCT	TTTGGCGTTT	CTGTGATGAG	CATGGGGCTT	660
TTGTATGATG	AGGGGCAGAG	TCTCATTTGG	AGAGGACCCA	TGCTCATGCG	AGCGATTGAG	720
CAGATGCTAA	GCGATATTAT	TTGGGGGGAT	TTAGACGTGC	TGGTGGTGGA	TATGCCCCCA	780
AGGAACAGGC	GATGCGCAGC	TCACGCAGCC	CAAGCCGTGC	CACTCAGCGC	AGGAATCACC	840
GTTACTACGC	CTCAAATCGT	GAGTTTAGAT	GACGCTAAAC	GGAGTTTGGA	CATGTTTAA	900
AAACTACACA	TTCTATTG	GGGCATTGTA	GAAAATATGG	GGAGTTTGT	GTGCGAGCAT	960
TGCAAGAAAG	AGAGCGAGAT	TTTTGGCTCA	AATTCCATGA	GTGGATTATT	AGAGGCTTAT	1020
AACACGCAGA	TTTAGCCAA	GCTCCCTTTA	GAGCCTAAAG	TGCGTCTAGG	GGGGGATAAG	1080
GGTGAACCGA	TTGTGATTT	TCATCCCACT	AGCGTGAGTG	CTAAAATTTT	TGAAAAAATG	1140
GCAAAGGATT	TGAGTGCTTT	TTTAGACAAG	GTGGAAGGG	AAAAACTAGC	CGATAATAAG	1200
GACATCCAGC	CCACACAAAC	GCATGCTTAT	TCGCAT			1236

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281

ATGGGTGTGG	TGATTGGCGA	GACCACAGAG	ATTGGAGATG	ATGTTACCAT	TTATCATGGC	60
GTAACCTCTG	GGGGTACGGG	CAAGTTTAA	GGCAAACGCC	ACCCTACTTT	AGGCAACCGA	120
GTGGTAGTTG	GGGCAGGGGC	TAAGGTCTTG	GGCGCGATTT	GCGTGGGCGA	TGATGTGAGG	180
ATTGGGGCTA	ATGCGGTGGT	GCTTTCAGAT	TTACCCACGG	GTTCTACGGC	TGTAGGTGCT	240
AAAGCCAAAA	CCATCACAAA	GGATCGT				267

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

268

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282

ATGCTATCTT	TTATAAGCGC	GTTTGATAAA	AGGGGCGTTT	CAATACGCCT	TCTAACAGCC	60
TTGTTACTGC	TTTTTAGTTT	GGGTTTGGCT	AAAGATTTAG	AAATCCAAAC	TTTTGTGGCT	120
AAATACCTTT	CTAAAAATCA	AAAAATACAA	GCCCTACAGG	AGCAAATTGA	CGCTTTAGAT	180
TCTCAAGAAA	AAGTCGTTAG	CAAAATGGGAT	AACCCTATTT	TGTATTTAGG	CTATAACAAC	240
GCTAACGTGA	GCGATTTTTT	CAGGCTGGAT	AGCACCTTAA	TGCAAAACAT	GAGCTTGGGT	300
TTGTCTCAAA	AAGTGGATT	AAATGGTAAA	AAACTCACGC	AGTCTAAAAT	GATCAATTTA	360
GAAAAACAAA	AAAAAATATT	AGAGCTTAAA	AAAACCAAGC	AGCAATTGCT	GATTAATTTA	420
ATGATAAACG	GCATTGAAAA	CTATAAAAAC	CAACAAGAAA	TAGAGCTTTT	AAACACAGCG	480
ATTAAAAATT	TAGAAAACAC	CCTCTATCAA	GCCAACCATT	CCAGTTCGCC	CGATTTAATA	540
GYGATYGYCA	AGTTTGAAAW	TTTAAAAATC	GCCAWT			576

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283

GTGCCGGCTG	TTGGGGGGGC	TTTGATTGG	ATYCYTATAG	YGATTATGA	GCTTTATCAT	60
GGGYATGTGA	ATGAGGYTAT	TTTTAYYGT	TTGTATTCCA	TTTGTTAAT	TGGTGTGTTG	120
ATTGATAGCG	TGATCAAGCC	AATTTTAATC	GTTTTTATCA	AAAAAAGAAT	CTTTAAAACC	180
ACCCTTAAAA	TCAATGAAAT	ATTGATTTTC	TTTTCTATGA	TTGCTGGGAT	TTCTCAATTT	240
GGTTTTTGGG	GGATTATCGT	AGGGCCTACC	ATCACGGCGT	TTTTTATCGC	GTTACTGCCA	300
TTGTATGAAA	ATTACTTTAT	TCAAAAGGAG	CAAAAACAT	GCGAATGT		348

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

269

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284

GTGGTTGTCA TTATTTTAGT GGTGCTTATC ATTCAAACA GCTCTTCTTT AAAAGAAGAG	60
AGAGAGCAAG AACGCGCTAT TAAGCCCGAC ACCAAAAATA ATTCTTTCAA TGAACTAAT	120
CCTACAGAAG AAAAAAAGTT AGAGCCAACG CCTAAATTAG AAGAAAAACA CAAAGAACAA	180
GACAAGCAAG GCAAAGAAGC GATCAAAGAA AATCCTAATA CCATTACAT TATCCCTAAA	240
CGAGATATTT GGGTAGAAGT GATTGATTTA GATGAGAAAA AAAACTCTTT TCAAAGGTT	300
TTTAAAAAAA GTTATCCTTT AGAGGCTAAA AACCACCGCT TGTTGTTACG CTTTGGGCAT	360
GGGCATCTTA TTCCTAAAAA CAACCATCAA GAACAAGATT ATAACGACAG CAAAAC TAGG	420
CGGTTTTTAT ACGAGCCAAA TAAAGGTTTA ACGCTCATCA ATGAGGCCCA ATACAAAGCG	480
CTCCAGCAA	489

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285

ATGGATGAAA TCTATCAAAT CGCTAAAAAT AAAACCCTAA TCGTTATCGC CCACCGCTTA	60
AGCACGATTG AACGCTGTGA AGTCATCATT GACATGAGCC AACACAAAGA CAATCTCGGC	120

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

SUBSTITUTE SHEET (RULE 26)

270

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286

```

GTGGCGGGCA GCTTTATTAT TGCTCTTTTT AGCGTTTTAG CGGATCAATT TGTGAGCGTG      60
TTTCAGCATG AAAACGCCTT GCAACGCTTA TTTTCTCAAA ACGCCACCCA AAAACAAAAA      120
AAGAAGAGTT TATGT                                     135

```

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287

```

ATGGTAGCTT TAAGCAACGC TCTTTCAAGG GTTTTTGGTT CTGTGGCTGG CTATAAATTC      60
CCTTCTTTTA TCCAAAAAAG CATCAACGCT CTTTATGTTA AGATCTTTAA AATTGATTTG      120
AGCGAGTTTG AGCCTTTAGA AAATTATAAG AGTTTGAACG CTCTTTTCAT GCGCTCTTTA      180
AAAAAAGAAC GCCCCTTTGA CAAAGCCCCT ATATTTCAT TGCGCCTTGC GATGGCTTTA      240
ATCACTGAAT GCGCTTTTTT AGACAACGAT AGCGCTTTAC AAATTAAAGG CATGCCCTAT      300
AAAGCGCATG AATTAGTGGG CGAAATCAAC CCCTTAAGCC CTCTTTTTTC TATG          354

```

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...600

271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288

ATGGCAGTGT TAAAAAAGAT GATAGGTTTG GTGGCGGTTT TAAGCGTTT ATTAGCCAGA	60
GACAACCCTT TTGAGCCTGA AATCAATTCC AAGAATTGTC AAGGGGGCTT TAGCGGGATC	120
TATGATGACT ACCTCAAAGA AATCCATGTG GATTTGCCCA CGAGCGCTAG GATCTTAAAA	180
AAAATCACGC TCACFTACCA AGATATTGAT GGCTCTATCC ATTCTAAAGT CGTGGGTATT	240
GATAAAAGCA TTGATTGGCA CTACCCCTTA AAACCTTCCC AACACACCCT TAATCAAGAC	300
GCCTTTGAAA AACGCTACCA GATCCAAGAT TTGATTTTT TAATGGCAA CAACACGATG	360
ATTTTGCGTT CCCCTTATAA AATTTGCGC TCTTTTGTT TAGTCAATCC TTATAGAATC	420
GTGTTAGACA CGCAAAAAGG CCCTTTGGAT ATTTATCAA ACATGGATT AAACCAGAAG	480
TTTTTTTCTC ACATTAAAGT CGGCACGCAC AAAGATTATT ACCGCATCAC GCTCATTTTA	540
GACGGGAAAT ACCGCTATCT TTTGGAAGAA AAAACGGGG CGTATGAATT AAAACTGAAA	600

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289

ATGGGCGGAT TCACAAGCAT ATGGCATTGG GTCATTGTTT TATTAGTGAT TGTGTTGTTA	60
TTTGGGGCTA AAAAGATCCC AGAATTGGCT AAAGGTTTAG GCAGTGGGAT TAAGAATTTC	120
AAAAAAGCCG TGAAAGACGA TGAAGAAGAG GCTAAAAACG AGCTAAAAAC CCTAGACGCT	180
CAAGCAACAC AAACCAAAGT GCATGAAACT AGCGAAATTA AAAGCAAACA AGAAAGT	237

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290

SUBSTITUTE SHEET (RULE 26)

272

GTGCGTTTGA	ATGCGGCGGT	TGTGGTGGAT	GGCAAGTATA	AAATCGCGCT	CGAAGACGGG	60
GCAAACGCTT	TAGAATACGA	GCCTTTAAGC	GATGAATSGS	TTAAAAAAT	CAACGYCCTA	120
GTCAAACAAG	CCATTGGTGA	TAACCAAAAT	AGAGGCGATG	ACGTGGCGGT	GAGTAATTTT	180
GAGTTTAACC	CTATGGTGCC	TATGATTGAC	AACGCCACCT	TGAGTGAAAA	AATCATCTAT	240
AAAACCCAAA	AAATTTTAGG	TTTATTTATG	TTTTTAATCA	AGGTATATTT	GGTGTTTATA	300
GTGTTATTCA	TTTTCTATAA	AAAAGTGATC	GTGCCTTTCA	GCGAACGCAT	GCTGGAAGTG	360
GTGCCTGATG	AAGATAAGGA	AGTGAAATCC	ATGTTTGAAG	AAATGAACGA	AGAAGAAGAT	420
GAGTTGAACA	AACTCGGCGA	TTTGAGGAAA	AAAGTAGAAG	ATCAATTAGG	GCTTAATGCA	480
AGCTTTAGCG	AAGAAGAAGT	AAGATATGAA	ATTATTTTATG	AAAAGATTAG	AGGAACCCCTT	540
AAAGAGCGTC	CTGATGAAAT	CGCCACGCTC	TTTAAACTCT	TAATCAAAGA	TGAAATCTCT	600
TCAGACAGCG	CGAAAGGT					618

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291

GTGTGTTTTA	TATTGCCTTT	TGTTTTAGGG	GTTTTAGGCA	CGCAAATCTT	TAAACAAGAG	60
ACCCCAAGAC	AGCTCCCTAT	CGTGGTGGTG	GATTTGGATA	AGACCACTAC	AAGCCATCAA	120
GTGGCGTTTG	AATTAGGCGC	AACGAGTGCG	GTTGAAATCA	AATACCAAGT	GACTAGCCTT	180
TCAGAAGCTA	AACGCTTTTT	AAACTCCGCT	GAAGTGATG	GGGCGTTAAT	TTTGCCTAAG	240
GATTTGGAGA	GAAAAATCAA	AATGGGGCGA	AAAGTGSAT	TTGCCCTTTT	ATTA	294

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...591

273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292

```

ATGAAAGGCT TATGGCTTGT AATCTCTTTA GTTTTGTGTG GTTTTTGTG GGCTAATGAA      60
TCTTATGTTT TTAACAATTC TAAGGGGCGT TTAACAGAAA AAAGCGTTGC GTTTATAGAG      120
GGCGTTTCTA AAGAGCTTTA TCTTAAACC GCGTGCGTT TTGCGATTGA TATGACGGAT      180
TTTGAAAAAA ATCCTATCGC TCTAGCGAAT AAAAAAGAGC GCCAAAGCTA TCAAGAGGGC      240
TTTTTAAAGC AGCTCAAACC CCCTTTTGTG GTATTCTTTT TCTACCATGA CGCTCAAAAA      300
ATAGAATTAG TGGCTAACCC TAAAGATTG CTAGACACTG ATAAATCTT TTTTGAAAAA      360
ATCGCTCCCT TACTCCCCAC AAACGCTAAA GAATACACGC CCCAAAGAAT TTCAGCCATG      420
CTCATTAAAC GCTATTCGGT CGCAGTAGAT GCTTTAGCGG AAAAATATCA TGTGAATATC      480
ACGCAAAATT TTAGCGCTCC TAAGGGAGTA ACTTTGTAA AGGTGGTTAT TTATATTTTG      540
TTATTGACGC TTTTGGGCGC GTTTTGGGG CTTTATTTT TTAATAATC T      591

```

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293

```

ATGTGTTCTA AAAAAATAAG AAATCTCATT TTATGCTTTG GTTTTATTTT AAGCTTGTGC      60
GCTGAAGAAA ATATCACCAA AGAAAACATG ACTGAAACGA ACACGACTGA AGAAAACACC      120
CCTAAGACG CTCCATTCT TTGGAAGAA AAACGCGCCC AAACCTAGA GCTTAAAGAA      180
GAAATGAAG TGGCAAAAAA GATT      204

```

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294

274

GTGCTAAAGA CATTATCCAT ACGATTAGTC ATACTTTTAA ATTGCTCCCT AGCGACAAAC	60
GCTTGCACTG GGGTGCAAAA ATTGCGCGAT GAAAGCCACC GGTATGCGAT AAACCTCCAT	120
AGATCCACTA AACTTAAAAA CATGAAACAA ATCGCTCTTT TAAAAGAAAA GGGCATAGGA	180
GAAGCCAGCG TGAAAAAATT GTTGGATTAT TTTGGGAGTT TTGAAGCGAT AGAAAAAGCG	240
ACGCATCAGG AAAAAAACGC CGTTTTAAAA AAACGAAAA	279

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295

GTGGGCATTA TTAGGGGGAT TATCCACAGG CCAGAACTCA TTTTATTAGA TGAGCCTTTT	60
AGCGCTTTAG ATAGTTTGAA TCGTAAGAAT TTACAGGATC TCATCAAAGA AATACACCAA	120
AATTCTTGCG CTACTTTTCAT TATGTAACG CATGATGAAA ACGAGGCGCA AAAGTTAGCC	180
ACAAAAACCC TAGAAATCAA AGCCCTTAAA CAAGAGCAG	219

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296

GTGATTTTAA TCGCTACCGC TAATAATATT GACAGGATCC CAGCTCCTTT AAGAGACAGA	60
ATGGAATTTA TCAGCGTGTC CAGCTACACG CCTAGCGAAA AAGAAGAGAT CGCTAAAAAC	120
TACCTCATCC CCAAGAATT AGAAAAGCAC GCCTTAAAGC CTAGCGAAGT GGATATTAGC	180
CATGAATGTT TGAAACTCAT TATTGAAAAA TACACCAGAG AAGCGGGCGT TAGGGATTTA	240
CGAAGACAGA TCGCAACGAT TATGCGTAAA GCGGCTTTAA AATACCTAGA AGATAACCCG	300

275

CACAAAAAAG	GGCGGACCAA	AAAAAGCGAA	GACAAAGATA	AAAAAGGCGG	AAATGAAGAA	360
AACGAAAAAA	GAGGTGAGAG	TAAAGATTTT	TGCGTCTCTA	TCACGCCTGA	TAACCTTAAA	420
GAGTATTTAG	AACGCATGGT	GTTTGAAATT	GRCCCATAG	ATGAAGAAAA	TAAAATCGGT	480
ATCGTCAATG	GCTTGGCATG	GACTCCAGTG	GGCGGTGATG	TGCTTAAAT	TGAAGCGGTT	540
AAGATTAGAG	GCAAGGGGGA	ATTGAACTC	ACCGGGAGTT	TGGGCGACGT	GATGAAAGAA	600
TCCGCCATTA	TTGCCTTTTC	TGTTGTCAA	GTCTTGTGG	ATAACGAAAC	CTTAAAAGTG	660
CCTAAAATCC	CTAGCGAGAC	CGATGCAGAG	AATWAGAAAA	AGAAAAAAGT	GCTGAAAGTT	720
TWWAACGCTT	ACGATTGCA	CTTGCATGTC	CCTAAGGGGC	TACGCCTAAA	GACGGCCCGA	780
GCGCTGGGAT	CGCTATGGCG	AGCG				804

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297

ATGGGGTGT	CGTTTATCT	TAAAAAGTT	AGGGTTTATT	CTAAATGTT	GGTTGCTTTG	60
GGGCTTTCAA	CGGTGTTGAT	CGGTGCGCG	ATGAATCCAA	GCGCTGAGAC	AAAAAACC	120
AATGACGCCA	AAAACCAACA	ACCAGTTCAA	ACTCATGAAA	GAATGACAAC	AAGTTCTGAA	180
CATGTTACGC	CACTAGATTT	TAATTACCCG	GTGCATATTG	TTCAAGCCCC	ACAAAACCAT	240
CATGTTGTAG	GTATTTTAAT	GCCACGCATT	CAAGTGAGCG	ATAATCTAAA	ACCCTATATT	300
GATAAGTTTC	AAGACGCTTT	AATTAATCAA	ATCCAAACTA	TTTTTGAAAA	AAGAGGCTAT	360
CAAGTGTTC	GTTTTCAAGA	TGAAAAAGCT	TTGAATGTGC	AAGATAAGAA	AAAGATTTTT	420
TCCGTTTGG	ATTTGAAAGG	GTGGGTAGGA	ATCTTAGAAG	ATTTGAAAA	GAATTTAAAA	480
GATTCCCAT	GTCCCAT					498

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...432

276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298

ATGGATAGAA AACTCTTAAG ATTATACCAG CCCTTAAACG CTTATTCTTA CAATAGCGAT	60
TCGCTTTTTT TATACGATTT TTCACGCCCT TTTATCAAAA ATAGCGGCGC GATTTTAGAC	120
ATAGGCTCAG GGTGTGGGGT TCTAGGCTTG CTCTGCGCTA GAGACAACCC GCTAGCGAGC	180
GTTCAATTTAG TGGAAGGGA TAGCAAAATG GCGTTTTGCT CCAAAAAA CGCCCTTAA	240
TTCCCTAACG CTCAAGTGT TGAGAGCGAT TTTTAGATT TTAACCTCC GATTGTAT	300
GATGCGATTG TGTGCAACCC TCCTTTTAT GCTTTAGGAT CTATTAAATC TCAAATTA	360
GGGCATGCCA GGCACCAGAG CGAATTAGAC TCGCTTCTT TGGTGGCTAA AGTGAAAAA	420
TGCCTGAAAC CC	432

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299

ATGTTGAGTG CGTTGGTGAT GCTGCCTTTT ATGGAGGTTT TTTATTATT CAATTTTCCG	60
TTGTGGCTCA ATCTTTTCTT AGGGCAAACC ATTGGAGCGG TGATTTTTT CAAGTTGGAT	120
AAGTTGATTT TTTCTAAAA A	141

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300

ATGAATACTA TTATAAGATA TGCGAGTTTA TGGGGCTTGT GTATTACTCT AACTCTAGCG	60
---	----

277

CAAACCCCCT	CTAAACCCCC	TGATGAAATC	AAGCAAATCC	TTAACAATTA	TAGCCATAAG	120
AATTTAAAGC	TCATTGATYC	GCCGACAAGT	TCTTTARRAG	CGACACCGGG	TTTTTWCCCC	180
TCGCCTAAAG	AAACAGCGAC	CACGATCAAT	CAAGAGATCG	CTAAATACCA	TGAAAAAAGC	240
GATAAAGCCG	CTTTGGGGCT	TTATGAATTG	CTAAAGGGGG	CTACCACCAA	TCTCAGTTTG	300
CAAGCGCAAG	AACTCAGTGT	CAAGCAAGCG	ATGGAAGAAC	CACACCATCG	CCAAAGCGAT	360
TTTTTGCCT	ACTTTGAACG	CGAGTTA				387

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301

ATGGTTTTGT	TTCTATCCAT	TTTTAAAAA	AGCTTTAATG	ATTTTTTAAG	CGCTAGAATG	60
CTTTTAATCA	ATCTTGGCCC	TATCCTTTTG	AGTTTGGCGT	TTTTTGGAGC	TATCTTTTAT	120
TACAATGGCG	GGAGTATTGT	GAATTATTGC	CAAACTTTAT	TACCGCAATC	TTTGAATGAT	180
TACGCTCATT	CTCAAGGCTT	TTTTGCCGGT	GTGTTCCGAT	GGGTTTTTAA	AGCGTTAGTG	240
TATTTTCTTA	TTTTTTGGAT	CGTAATTCTT	TTGAGTTTAG	TCATCAATAT	TTTTGCGTCT	300
ATTTTTTACA	CCCCTTTAGT	GGTCTCTTAT	TTGCACCAA	AATATTATCC	CCATGTCGTT	360
TTAGAAGAAT	TTGGCTCTAT	CCTTTTTTCT	ATTAAATATT	TTTTAAAATC	GCTCACTTTT	420
ATGCTTTTAT	TCTTAGCGGT	TTTAACGCC	CTTTATTTCA	TTCCCTTTAT	AGGGGTCTTT	480
GGGCTCTTTT	TTTCTATAGT	CCCGCATTTT	CYCTTTTTC	AAAACACCAT	GAGTTTGGAT	540
ATAGCCAGCA	TGATTTTCAA	CCATCAAAGC	TATCAAAATT	TACTCAAACA	GCACCGATTG	600
AAGCATTATC	GTTTTTCGTT	TTTTTGCTAT	CTTTTTTCCT	TGATTCCTTT	TTTTAATTTT	660
TTTGCCACCT	TGTTGCAAAC	CCTAAYGCTA	ACGCACTACY	TTTTTATCTT	TAAAGAGAAA	720
GAATGC						726

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

278

(B) LOCATION 1...378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302

ATGCAATACG CTAACGCTTA TCAAGCCTAC CAGCATAACC GAGTGAGTGT GGAATCCCCG	60
GCAAACTCA TTGAAATGCT TTATGAAGGG ATTTTAAGAT TTTCTTCGCA AGCCAAACGC	120
TGTATTGAGA ATGAAGACAT TGAAAAGAAG ATCTATTATA TTAATAGGT TACGGATATT	180
TTCACGGAGT TGTGAATAT TTAGACTAT GAAAAAGGGG GGRAAGTGGC GGTGTATCTT	240
ACAGGCTTAT ACACCCATCA AATCAAAGTT TTAACGCAAG CCAATGTGGA AAATGACGCG	300
AGTAAGATTG ATTTGGTGTT GAATGTGGCT AGGGGTTGT TAGAGGCATG GAGGGAAATC	360
CATTCAGATG AACTCGCC	378

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303

ATGATGTTTG ATAACACGCT TATCAATTTA TTTGAGACAG CGCCTCTTTT AACYTGCCTT	60
TTAGCTGGGA TTTTAACTTT TTTAAGCCCT TCGTGTTGC CTTTGATCCC GCGTATATG	120
TCTTATATTT CGCAATTTT TTTAGAGGAT ATTAAGATG GTAAGGCTAA AAGGGTTTCG	180
GTTTTTTTAA AATCCTTGAT GTTGTGGTG GGGTTTTTCGC TCGTGTTTT GGGCGTGGGC	240
ATGTCATATG CCAAGCTTAT CCATAGCTTT TCGTTTTCTT GGGTGAATTA TATCGCTGGG	300
GGGATTGTGA TCCTTTTGG TTTGCATTTT TTAGGCGTGT TTCGTTTGC ATTTTGTAT	360
AAAACCCAAA GCGTTGGTTT AGCGAGCAA TCTAACAGCA TGCAGCGCTT TACCCCTTTC	420
TTTTTGGCA	429

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304

GTGCTGGTGG TGGGCAAACC CAACGAAAGC TATGCAGATA CCCACGCCCG CATTGAGCAT	60
TTTATCAAGC TTGTAGATTT TAAGGGCGAA ATCGTTTTTA TCAATGAAGA TAATTCTAGC	120
GTAGAAGCTT ATGAAAATTT AGAGCATTTG GGTAAAGAAA ATAAGCGGAT CGCTACCAAA	180
GATGGCCGGT TAGACTCTTT GAGCGCTGTG AGGATTTTAG AGCGCTATTG CCAGCAGGTT	240
TTAAAAAAGG GC	252

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305

ATGCGGATAT TAATTCTCAA AAACAAGCCA CCAACGCTAC GATCAAAGGC TTTGACGCGC	60
TCTTGGGGTA TCAATTTTTT TTTGAAAAAC ACTTTGGCTT ACGCCTTTAT GGGGTTTTTT	120
GACTACGCTC ATGCCAATTC TATTAAGCTT AAAAACCCCTA ACTATAATAG CGAAGCGGCG	180
CAAGTGGCTA GTCAAATTCT TGGGAAACAA GAAATCAATC GTTTAACAAA CATTGCCGAT	240
CCCAGAACTT TTGAGCCGAA CATGCTCACT TATGGGGGGG CTATGGACGT GATGGTTAAT	300
GTCATCAATA ACGGCATCAT GAGTTTGGGG GCTTTTGGCG GGATACAATT GGCCGCAAT	360
TCATGGCTTA TGGCGASACC GAGCTTTGAG GGCATTTTAG GGAACAAGC CCTTGTGAGC	420
AGAAAGCCAC TTCCTTCCAA TTTTATTCA ATGTGGGGGC TCGCM	465

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...513

280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306

ATGAATGTCA	AAAAAAGGA	AAAGCCACAA	AGTGAAAGA	TTGATAGGGT	GGATTGTTTG	60
GAGAAACTTG	GGAAAGAAA	CACTACTTTT	TTAAGCAGTA	TAGCTATGGG	GAGCATTGGT	120
CAATTAGCGA	TCCCCATCC	TGGAGTTGGA	GTGCTCATTG	GGGGCTTTGT	GGGTGGGGTG	180
ATGAGTAAAA	CTTTTTATGA	TGTCTCGCTA	ACGATTTTCA	AAGAGGCTAA	ATTAGCGCGT	240
CAAAGGCGTA	TTGAGATTGA	AAAAGAATGC	CGTGAGAGTA	TCAGACAGTT	AGAGATGTAT	300
CAAAATCAAT	TTAATGAAGT	GTTTGAGCGG	TATTTTCATG	GGAATAAAA	ATTCTTTAAT	360
GAAAGTTTTG	ATGAGCTGGR	GAGGGCGCTT	TGTGCGGGCG	ATGCGGATTT	GGCTATAGCA	420
GTCAATAACA	AGATCCAAGA	GGGATGGGT	CAAGAGTTGC	TGTTTGACAA	TAAGCAAGAG	480
TGCTGGGAAT	TTATCACTAG	CCGTAAAGAG	GGT			513

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307

ATGTGGCCGT	RAAAGCTTTT	TCTAAAACCC	CTAAAAGAAA	CGAGCCTTGC	CCTTGTGGGA	60
GTGGCAAAAA	ATATAAGAT	TGTTGCGCTA	AAAGCGGGCC	TAAAAGGGC	TTATTTGCCA	120
AATAGATCCT	TAATCTTTT	CCTTATCAAG	CGTTATTTGC	GTTTTGATAA	AAGCCAGCCT	180
TTCATTAGTA	TCACTGCTTT	GTTAGCCTTT	TTTGCGGTGG	CGGTTGGCGT	GATGGTTTTA	240
ATTGTGGCTA	TGGCGATCAT	GAACGGCATG	AGTAAGGAAT	TTGAAAAAAA	GCTTTTTGTG	300
ATGAACCTAC	CCTTAACGCT	CTATACCACA	AGCCCTTATG	GGATCAGCGA	AGAAGTGGTT	360
CAAGCTTTAG	AAAAAAGTT	CCCTAATTG	CCTTTTTCAG	YCCCTATTTG	CAAACCCAAA	420
GCC						423

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

281

(B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308

ATGGTATCGT TGCTTGGCGC GCTTAAACGC ACCCCTTGCA CTAATCGCTT TTATCTTAAA	60
GCACTACTAT TTGCTATATT CTATCATGCA GTAAATAATT TTCTAACGCA ATGCCCGCCC	120
CATCAAGTCC GGGAGTTTTT TTCATCACGA CATGCACAGG GATGGAAGCG AGAAACGCTC	180
CCATGCGCCC TTTCGTTTCA AAACGCGCTC	210

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309

GTGCATCATT TGYAACGGCT TTTAGACTCA GGCTCTGAAA GGTGTATAGG CTGTGGGCTG	60
TGCGAAAAGA TTTGACAGAG CAACTGCATA AGGATCATCA CGCATAAGGG CGAAGACAAC	120
CGCAAAAAGA TCGATTCTTA CACGATCAAT TTGGGGCGTT GCATTTATTG CGGGTTGTGT	180
GCGGAAGTTT GCCCAGAATT GGCGATCGTT ATGGGGAATC GGTTTGAAA CGCCAGCACC	240
CAACGCTCCC AATACGCTC TAAAGCGAG TTCTAACGA GCGAACAAGA CGCTAAAAAC	300
TGCTCGCATG CCGAATTTTT AGGCTTTGGT GCGGTAAGCC CTAATTATAA CGAACGCATG	360
CAAGCCACCC CTTTAGATTA TGTCCAAGAA CCTTCAAAAG AAGAATCCAA AGAAGAGTTT	420
YCCACAAGCC CAGAAAGCCA TAAGGGAGAT GAAAATGTT	459

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310

282

ATGGCTATTT	GGGGGTGGTG	TTTTTTATTT	TTATCGTCCT	TGATGTGGGG	TTCAAGCATG	60
CATGAGTTGG	TTTTAAGATC	CCAAGCTTTA	GGGTTTGAAA	CGCGCTTAGT	CCAGTGCGAT	120
TTATCGTTTT	CTTATGAAAG	GTTTATTTCT	AAAACCAAAC	GCTCTTTAGC	GGTGTTAGAA	180
GAATTTGATT	GGTTAAATTC	TGGCTTTGAT	TTTTCACGCT	TGAACGTTGA	AAATGACACT	240
CTGGAATTAC	TCAAAGCGCT	GTATTTTAAA	TTAGAAAAAT	TAGAGAGCCT	GCTTTTAAAA	300
GAAAATTTAC	TTGAATTGGA	GCAAAAGGAT	CGCATCATCG	CTTTAGGGCA	TGGGCTAGTT	360
TGCCTAAAAA	AACAAAGCCT	GATAGCGCCT	CAAACTTACT	ATGGGCGTTG	CGTGTTAGAG	420
GGGAAAATCC	TAGCCTTTTT	TGGCGTGGCA	AGGGATAAAG	ATTTTTTTAGA	AATCACTCGC	480
ATGCACGCCCT	TAGACATTAA	GCGTTATGAT	TCCTTCATTG	TTGATAGCGA	AAGAAAAGGC	540
TTGAAATTA						549

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311

ATGCCGAAAA	ATTCTAAACT	ACAACCTGCT	AAGTTAGGGA	AAAATTTTGA	CCCTGTGGAT	60
CATTCTAACA	GGAATTTTTT	CTTTCTCTC	ATTCTGTCTG	TATTGTTACA	CTGGTTGATT	120
TATTTTTTAT	TTGAACACAG	AGAAGATTTT	TTTCCTTCAA	AACCCAAGCT	CGTTAAATTA	180
AATCCTGAAA	ATTTATTGGT	Y				201

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312

283

GTGTTTTTAG	TTCAATCGTG	GGCTTTGAGC	TTGAAAATAG	ACAGCCTGTT	TTCTCTTTTT	60
AGCGTGGGTA	AAATCCCTAG	CGGATCTAAA	GATCCCTTTG	CGTTAAGGCG	TTTGAGTTTT	120
GGGCTATTGA	AAATCATCGC	GCATTACGGG	TTAGAATTTG	ATTTGAAAGC	GGATTTAAAA	180
AACCTCTTTG	AAAAAGTGGG	CGTTTATCAA	AGCTTTGATT	TAGAGGTTTT	AGAAAAGTTT	240
TTACTGGAGC	GCTTTCATAA	TTTAATAGAT	TGTAACCTCT	CTATTATAAG	AAGTGTGTTA	300
AACACCAACG	AGCGAGACAT	TGTTAAAATC	ATTCAAAAAG	TCAAAGCCTT	AAAACGCTTT	360
TTAGACAATC	CTAAGAACGC	TCAAAAAAAA	GAGTTGCTTT	TTAGCGCTTT	CAAACGATTA	420
GCTAATATCA	ATAAAGACAG	AAACCCTAAC	GAATCAAGCG	GGTTTTCTAC	GAGTCTTTTC	480
AAAGAATTAC	AAGAGCATGC	CCTTTTGTAA	GCGTTCAAC			519

(2) INFORMATION FOR SEQ ID NO:313:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 777 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313

ATGAGTCTTG	CTCCAAGCGT	TATGGCGGGC	TTCTTGTTTT	GTGCCGGCTC	TTGCTCGCTT	60
CGCTTCCCTA	ATTATCTTAA	AATCATTTCC	ATAGATGTGG	ATACGGTGTT	TTTAGGCGAT	120
GTTGCAAGCG	CTTATTTTGC	GCTGGATAAT	GAACCCACTA	AATTGCTTGG	CATGGTGAGA	180
GACACTTTTT	CCCACCTTCC	TTTGAAGCC	TTTTGTGATT	TTTGCGAACG	CACATGCAAG	240
AATTTTAAAA	TTGATCTTTT	GCGCTTTAGC	CAAAACGAAT	TAAAACGCAT	CCATCAGGGC	300
TTTAACATGG	GCTTTTGGT	GGCGAATTTA	GATTTATGGC	GCGAAAATGG	GTTTGAAAAA	360
ATCGCTTTAG	AGTTTGTGAA	AACTAGGGGA	AAGGATCTTT	TCTACCCTGA	GCAGTGTTTA	420
ATCAATATGG	TGTTTTTAGA	GCGTATTTTA	GAATTGCCTA	TTCATTATAA	TTGCTATTCT	480
GATTTTTTCA	AAGAGCACTA	CCCTAAAAGT	ATCATCATGC	TCCATTTCAT	CAATACAAG	540
CCGTGGCGTT	CTGTCACTTC	TTGAACGGG	CGTTTGATTT	GCTATGAAGC	TGAAGCGAGT	600
TTTTGGCTCG	CCAACCTTTT	TTGCACCCCT	TTTAAAAACG	ATTTTTTTAA	AGAACGCCTT	660
GAAATGGCTA	AAGACCAACA	AATGCAATCT	TTTAAAACCC	ACATCCGATC	AAAAACGATT	720
AGGGATTATT	TTTATTTTAG	GATAAAAAAT	ATTTTGAAAA	AAGTTTTCGA	ACTCTCT	777

(2) INFORMATION FOR SEQ ID NO:314:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 582 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

284

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314

```

GTGATTGTTT GCAGCGCGGC GGGGTTGAGC CATTTTTTTG GGTTCCTAT GTCTTTGGGG      60
GCGTTTCATTG TGGGCATGGC GATTTCCTAAA TCGCGCTATA AAATCAATGT CCAAGAAGAA      120
TTCGCGCAAT TAAAAACCT CTTTTTGGCC CTTTTTTTCA TTACGATAGG GATGCAGATT      180
AATGTGAGTT TCTTCATGGA GAAATTCCTT GTCGTCATCT TTTTACTCAT TTTAGTGATG      240
AGTTTTAAGA CTTTTATCAT TTATGCGCTA TTGCGTTTTT TTAGAGACGC TAAACCGGCC      300
ATCAAAACCG CTCCTTCTTT GCGCAAATT GGGGAGTTTT CTTTCGTGAT CTTTTTAAAT      360
TCAGGCTCGC ACCAGCTCTT TAATTGCAA GAAAAAAAG GGATTCCTGG TTTTTTACAC      420
CAAAAAATA TCTTAAATAT TGCTCAAAAT GACATCCACC AGCTCCTTAT TCTCATGGTG      480
GTCTTTTCTA TGTTAGCAAC CCCTTTTATT TAAAATACC TAGAATCTAT CGCTCAATTT      540
ATTTTGCACC AAAAGAGCCA AGAAAACGAG CCGGCTAAAA AA                          582

```

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315

```

ATGTTCTATC TTATCAATAC AGGAGTGCCT CATTTAGTGG GATTTGTGAA AAATAAAGGG      60
TTATTAAATT CTCTTAACAC ACTGGAATTA AGGGCTTTAA GGCATGAATT TAACGCTAAT      120
ATTAACATCG CTTTTATAGA AAATAAAGAG ACGATTTTTT TACAACTTA TGAGAGAGGG      180
GTTGAAGATT TCACGCTAGC TTGCGGGACA GGCATGGCAG CGGTTTTTAT CGCCGCGCGC      240
CTTTTTTATA ACACCCCTAA AAAAGCCACT CTCATCCCTA AAAGCAACGA ATTTTATAGAG      300
CTTCTTTTAA AAAATGATGG AATTTTTTAT AAAGGAGTCG CGCGTTATAT CGGCATGAGC      360
GTTTTAGGCA TGGGTGTTTT TAAAAATGGG TGTTTT                          396

```

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

285

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316

ATGATTAAAG CGATTGATAT TTCTCATGST TTTGAAAARC CTCTTTTRTRA TGGCGTGAAT	60
TTGCGCATT AACCCAAAGA AAGCYTGGYG ATTTTAGGCG TGAGCGGGAG CGGTAAAAGC	120
ACGCTTYTAA GCCATTTGGC CACCATGCTA AAACCGGATA GCGGAACAGT CAGTTTGTTA	180
GAACACCAAG ATATTTATGC CCTAAATCC AAAAAGCTTT TGAATTGCG GCGCTTAAAA	240
GTGGGCATCG TTTTCAATC GCATTACCTT TTTAAGGGTT TTAGCGCTTT AGAAAACCTG	300
CAAGTCGCTT CAATCCTAGC CAAGCAAGAA ATAAATCATT CCCTTTTAGA ACAATTAGGC	360
ATAGCCCCACA CCCTAAAACA AGGCGTGGGC GAATGAGCG GCGGCCAGCA ACAACGCTTA	420
AGCATCGCCA GAGTGCTTTC TAAAAAACC CAAATCATT TCGCTGATGA ACCCACC GGG	480
AATTTAGACA CCACTAGCGC TAATCAAGTC ATCAGCATGC TGCAAAATTA CATTACAGAA	540
AACGAAGGGG CGTTAGTCTT AGCCACGCAT GATGAGCATT TAGCCTTCAC TTGCTCTCAA	600
GTCTATCGCC TAGAAAAGA ATCTTTGATT AAGGAAAA	639

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317

ATGCTTGATA AACGCATTAA AACGCTTTTA CTTTTTTTG GTCTTAATAT GGTGTGTTG	60
AGCGTGAGTT TTACCAATAA GCCTCATTTG TGTTTTTGGT TTTTAGTGTT AGGTTGTAT	120
TTAGTTTATG AGTGGCAAAA GAAACAAAAA AAAGATTTTC AAAGCGCTAA AAGTTTGAAA	180
TTTGACAGCG TTAGCGAATT AGAAAAGGAT TTTGAACATG GAAGTAAC	228

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

286

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318

ATGAAAACAA TTA AAAATGG TATTATGATC GGCACACTCG GTGCGTTGTT ATTGAGCGGT	60
TGTTCTAGCT TTGATGCTCA GCGTTTCGCT TGTCTCCCTA AAGACCATTC TTCAAAAGAC	120
GCTTCTACCA AAAAAGAAGC GCAATACATT CCTAAGGGCT TTTTGGACCC TTATCTTCT	180
AACTTAAACC ATTGGGATTC TACATTC	207

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 570 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319

ATGGAGCTTA TTTTAGGCTC TCAATCCAGC GCTAGGGCGA ATCTTTTAAA AGAGCATGGG	60
ATTAAGTTTG AACAAAAAGC GCTCTATTTT GATGAAGAAA GCCTAAAAAC CACAGACCCT	120
AGGGAGTTTG TCTATTTGGC GTGCAAGGGG AAATTAGAAA AAGCTAAAGA GTTACTTGCG	180
AATAATTGCG CTATCGTGGT GGCTGATAGC GTGCTGAGCG TGGTAATCG CATGCAACGA	240
AAAGCTAAAA ACAAGCGAGA AGCCCTTGAA TTTTAAAAAC GCCAAAATGG CAATGAAATA	300
GAGGTTTTAA CTTGCTCTGC ATTGATTCTT CCTGTGTTGG AATGGCTGGA TCTATCGGTT	360
TTTAGAGCGC GTTTAAAGGC GTTGTATTGC AGCGAAATAG AAAAATATTT AGAGAGCGGT	420
TTATGGCAAG GAAGTGCGGG CTGTGTGCGT TTAGAGGACT TTCATAAGCC TTATATTAAA	480
AGCTCAAGCA AGAATTTAAG CGTGGGGTTG GGGCTGAATG TGAAGGCTT GTTAGGGGCA	540
CTAAAATTAG GGGTTAAACT TTCATTATTA	570

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 405 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

287

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320

ATGCTTATTT	TAGGACACCC	TTTAATCCCT	AGCGCTCGTT	TTGTTTTCAT	TAAAAACACC	60
GATGCTATTC	ATTCCAGCGC	CAATAACGAT	ATAGTGTTGTT	TTGAAGCAAA	CCCCAAAAAT	120
TTGGAATTAG	CCCAATATTG	CTGTGAAAAT	GCGGTCCATT	TTAGCGTGAT	CTTTTATCG	180
CACAAGATAG	AGACGGACAC	CTTTTTTTTA	TTCAACGCTT	TCAAACCGCT	CTATTGTATT	240
TTTAAGGATA	TTAAGCAAGC	CATACTCGCC	CAACAACACG	CCACTAATTA	CTTGTTAGAT	300
AGCAAAATCT	TGTTTTCTAT	GGATTTTAAC	GATACAGAGT	CATGGGAGAT	TTGCGCTAAA	360
AATCAAATAG	ATGGTGTTCAT	TTCTAAAGAT	TCACTCCTTT	TGAAA		405

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321

ATGAAAAAAA	GATTGAATAT	AGGGCTTGTG	GGTTTAGGGT	GCGTGGGGAG	CACGGTCGCT	60
AAAATCTTAC	AAGAAAATCA	AGAAATCATT	AAAGACAGAG	CCGGCGTGGA	AATTAAAATT	120
AAAAAGCGG	TGGTGCGAGA	CGTGAAAAAA	CACAAGGGCT	ATGCTTTTGA	AATCAGTGAT	180
GATTTAGAAA	GCCTGATAGA	AGATAAAGGG	ATTGATATTG	TCGTGGAGCT	TATGGGTGGG	240
GTGGAAGCGC	CTTATCTTTT	AGCTAAAAAA	ACTTTAGCCA	AACAAAARGC	CTTCGTTACA	300
GCCAATAAAG	CCATGTTAGC	GTACCACCGC	TATGAATTAG	AACAAATCGC	TAAAAACACC	360
CCCATAGGCT	TTGAAGCGAG	CGTGTGTGGG	GGTATCCCCA	TTATCAAGGC	TTTAAAAGAC	420
GGCTTGAGCG	CTAATCACAT	CCTTTCCTTT	AAAGGGATT	TAAACGGCAC	GAGCAATTAC	480
ATTTTAAGCC	AGATGTTTAA	AAATCAAGCG	AGCTTTAAGG	ACGCTTTGAA	AGACGCGCAC	540
CATTTAGGCT	ATGCCGAATT	GAACCTGAA	TTTGACATTA	AGGGCATTGA	TGCGGCGCAC	600
AAATTATTGA	TTTAGCGTC	TTAGCGTAT	GGCATTGATG	CGAAATTAGA	AGAAATCTTG	660
ATTGAAGGCA	TTGAAAAGAT	AGAGCCAGAT	GACATGGAAT	TTGCAAAAGA	GTTTGTTTAT	720
AGCATCAAAC	TTTAGGCAT	CGCTAAAAAA	CACCAGGGAT	TGCAT		765

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

288

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322

ATGCAAGAAA	AACGACTTAA	AGCCATTCAA	AACAAAATCG	CTTCTTGGAT	CAAGGAAATT	60
GAAAGCGGCT	TTATAGATGC	ATTGTTTTCT	AAGATTGGCC	CTTCAAAGAT	GCTGCGCTCC	120
AAACTCATGC	TCGCTTGTG	AGACGAAAAA	ACAGACGCTA	TTTTATTAGA	TAAAGCGCTC	180
AATTTGTGTG	CGATTGTGGA	AATGATACAG	ACCGCTTCTT	TATTGCATGA	TGATGTGATT	240
GACAAGGCGA	CCATGCGCCG	AAAGCTCCCT	AGCATTAAACG	CTCTTTTTCG	GAATTTTAAC	300
GCCGTGATGC	TTGGGGATGT	GTTTTATTCT	AAAGCCTTTT	TTGAGTTGTC	TAAAATGGGC	360
GAATCCATCG	CTCAAGCCCT	CTCTAATGCG	GTTTTAAGGC	TCTCTAGGGG	CGAGATTGAA	420
GACGTGTTTG	TGGGGGAATG	TTTAAATAGC	GACAAACAAA	AATACTGGCG	TATTTTAGAA	480
GACAAGACCG	CCCATTTTCAT	AGAAGCGAGC	TTAAAAAGCA	TGGCGATTCT	TTTAAATAAA	540
GACGCCAAAA	TGTATGCGGA	TTTGGGTTG	CATTTTGGCA	TGGCGTTTCA	AATCATTGAT	600
GATTTGTTAG	ACATCACTCA	AGACGCCAAC	ACTCTAGGTA	AGCCCAATTT	TAGCGATTTT	660
AAAGAGGGCA	AGACCACTCT	ACCCTACTTG	CTTTTATATG	AAAAATTGAA	TCAGCATGAA	720
CAGGGCTTT						729

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 756 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323

ATTGTTAGGA	AAAAAAACGA	AGAAATCTTG	ATTGATGAAA	ATTGTTGTTG	GGGTGTGATA	60
GCCCTTGATA	GATTGGCAAA	ACTCAATAAG	GCCCAATAGGA	CTTTCAAAAG	GGCTTTTTAT	120
CTCTCTATGG	TGCTCAATGT	CGCCGCTGTA	ACGAGTATTG	TGATGATGAT	GCCTTTGAAG	180
AAAACAGATA	TATTTGTTTA	TGGCAATTGAT	CGATACACAG	GAGAATTTAA	AATCGTCAAA	240
CGCTCCGATG	CTAGGCAAAAT	CGTCAATTCT	GAAGCCGTTG	TGGATAGTGC	AACTTCAAAA	300
TTTGTCTCAT	TGCTGTTTGG	TTATAGCAAA	AATTCTTTGA	GGGATCGCAA	GGATCAACTA	360
ATGCAGTATT	GCGATGTGAG	TTTCCAAACC	CAAGCAATGA	GAATGTTCAA	TGAAAAATATC	420
AGACAATTCC	TAGATAAAGT	CCGAGCAGAA	GCTATCATTG	GCTCCAACAT	ACAAAGAGAA	480
AAAGTCAAAA	ATAGTCCCTT	AACGAGATTA	ACATTTTTC	TTACCATCAA	AATCAGCGCT	540
GATACAATGG	AAAATTATGA	ATATATCACT	AAAAAACAAG	TAATATTTTA	TTATGATTTT	600
GCTAGAGGTA	ACTCTTCTCA	AGAAAATCTT	ATCATCAACC	CTTTTGGCTT	CAAAGTGTTT	660
GACATTCAAA	TCACGGATT	ACAAAACGAA	CAGACAGTAA	GCGAAATTTT	GAGAAAAGATT	720
AAAGAAGTGG	AATCAAAAAA	TAAGGCATTA	AATAAA			756

SUBSTITUTE SHEET (RULE 26)

289

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324

ATGAGAGCGA	TCGCTATTGT	TTTAGCCAGA	AGTTCCAGTA	AAAGGATTAA	GAATAAAAAT	60
ATGATTGATT	TTTTCAATAA	ACCCATGCTC	GCTTACCCTA	TTGAAACAGC	ACTAAATTCC	120
AAGCTCTTTG	AAAAAGTGTT	TATCTCTAGC	GATAGCATGG	AGTATGTCAA	TTTAGCCAAA	180
AATTATGGGG	CGAGTTTTTT	GAATTTACGC	CCTAAAAATT	TAGCAGACGA	CAGGGCCACG	240
ACTTTAGAAG	TGATGGCCTA	TCACATGAAA	GAATTAGAAT	TAAAAGATGA	AGACATTGCG	300
TGTTGTTTGT	ATGGCGTTTC	AGTATTTTTA	CAAGAAAAGC	ATTTACAAAA	CGCTTTTGAA	360
ACTTTAAAAC	AAAATCAAAA	TACGGATTAT	GTTTTTCACAT	GCTCTCCCTT	TAGCGCTTCG	420
CCTATCGTTC	TTTAGCCTT	GAAAACGGCG	TTCAATGGC	TTTTAAAGAG	CATTCAAACA	480
CGCGCAGCA	AGATC					495

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325

ATGAGTAATC	AAGCGAGCCA	TTTGATAAT	TTTATGAACG	CTAAAAATCC	CAAAAGTTTT	60
TTTGATAATA	AGGGGAATAC	CAAATTCATC	GCTATCACAA	GCGGTAAGGG	GGGCGTGGGG	120
AAATCCAACA	TTAGCGCTAA	TTTAGCTTAC	TCTTTATACA	AGAAAGGTTA	TAAGGTAGGG	180
GTATTGTATG	CGRATATTGG	TTTAGCGAAT	TTAGATGTCA	TTTTTGGGGT	GAAAACCCAY	240
AAAAATATCT	TGCATGYCTT	AAAAGGCCGAA	GYCAAATGY	AAGAAATCAT	TTGCGAGATT	300
GAACCCGGGG	TTTGCTTAAT	CCCTGGGGAT	AGCGGCGAAG	AAATTTTAAA	ATACATCAGC	360
GSSGCGGAAG	YTTTCGATT	ATTCTTAGAT	GAAGAGGGGG	TTCTAAGCGC	TTTAATTTAT	420

290

ATTTTAATTA ATACATTTTC TAAAAATTTG GGTCCACTAT CTCAAACTTT TCTTAATTTT 480
 CAGTCATTTT TTTTATTTT TATTCAATCT CCC 513

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326

ATGCAGCATT TAGTCTTAAT CGGTTTATG GGGAGCGGTA AAAGCTCTCT AGCACAAGAA 60
 TTGGGGCTGG CTTTGAAATT AGAAGTGCTG GATACGGATA TGATCATTAG CGAGAGGGTG 120
 GGCTTGAGCG TGAGAGGGAT TTTTGAAGAG CTTGGCGAAG ACAATTTTCAG GATGTTTGAA 180
 AAAATT 186

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327

ATGAGCATTAG AGGAAAATTT AGAGCAAGTT AGAAACGAAT TTAAAAGCGA TGAAAAGCTT 60
 TTAGAAGGAG CGTTTAGATT AGAAAAGTTT TTCAAACGCT ACAAGTGGGT GTTGTTGTTT 120
 ATCGTGGTGG CTTTATCGC TTATTTAGGG GATACAAAAT TACAAGATTA TAAGCATGAG 180
 CAAACGAGAG AGCGGATCAC TCAAATTTAT AATGAAGTGC TAGAGAGTCC TAATAATATA 240
 GCCTTGCAAA AAAGATTGAA AGAAGTCGCC CCAGAGTTGT ATGACTTGTA TCAGTTCGCC 300
 AGAGCGAGTG AGAGGAACGA TGCAAACGAG TTAAAAGGC TTTCGCAATC TTCTAATGAA 360
 ATCGTTAAAG CGTTCGCCAA ATATTCTTAC GCATCGCTCT CTAGAGATAA AAACCTGCTT 420
 GAAAAAAGCC CCATTCTTAA AGAAATGAGC GCTTTACAAG AAGTGAACCT GTTGATGAA 480
 GAAATTTCTA AAGACGCAAT CAAAAAGCG CATCAAAGTT TATCAACTAT CCTCTAAGT 540

291

TCTTCACTCT ATGCTATAAT CTCTGTTTAA AAACATTATG GAATGTTAGA AGATATTTCAG 600
 CAAAACCCCTT CCAAACCAAC CAATCTAAAG AAAGAAACCA TTCAAGGAAC GCAT 654

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328

GTGCATTTCA ATCAGGTTGT TCTCCCAAAA GCGGTGGGCG CGATTTTAGT CGCACCAAAA 60
 GGGCCCGGGA GCGCTTTAAG AGAAGAATAC CTTAAAAATA GGGGTTTATA CCATCTAATC 120
 GCCATAGAGC AAGAAAGCTC AATTCATAAC GCTAAAGCGG TGGCTTTAAG CTATGCTAAA 180
 GCGATGGGTG GGGGGAGAAT GGGGGTTTAA GAAACGAGTT TTAAAGAAGA ATGCGAGAGC 240
 GATTTATTCG GCGAGCAAGC GGTCTGTGTC GGGGGGTTAG AAGTCGATCG TAAGAATGGG 300
 GTT 303

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329

ATGAAAAAAT TTTTCTCTCA ATCTTTGTTA GCTCTTATTA TCTCTATGAA TGCGGTATCT 60
 GGCAATGGATG GTAATGGCGT TTTTGTAGGG GCGGTTTATT TGCAAGGACA GGCGCAAATG 120
 CATGCGGATA TTAATTCTCA AAAACAAGCC ACCAACGCTA CGATCAAAGG CTTTGACGCG 180
 CTCTTGGGCT ATCAATTTTT CTTTGAAAAA CACTTTGGCT TACGCCTTTA TGGGGTTTTT 240

(2) INFORMATION FOR SEQ ID NO:330:

292

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330

ATGCTAAAAA	AGATTTTTTA	TGGTTTTATC	GTTTTATTTT	TGATTATCGT	AGGGTTGTTG	60
GCCGTTCTTG	TCGCTCAAGT	TTGGGTAAGT	ACGGATAAGG	ATATTGCTAA	AATTAAAGAT	120
TATCGCCCCA	GTGTCGCTTC	ACAGATTTTA	GACAGAAAAG	GGCGTTTGAT	CGCTAATATT	180
TATGATAAGG	AATTTGCTTT	TTATGCGCGT	TTTGAAGAAA	TCCCCCACG	ATTTGTTGAA	240
AGCCTTCTAG	CGGTAGAAGA	CACCTCTTTT	TTTGAGCATG	GGGGGATCAA	TTTAGACGCT	300
GTCATGCGCG	CTATGATTAA	AAACGCTAAA	AGTGGTCGTT	ACACTGAAGG	GGGTAGCACT	360
CTAACCCAAC	AACTCGTTAA	AAACATGGTG	CTCACACGGG	AAAAAACCTT	AACCAGAAAA	420
CTCAAAGAAG	CTATCATCTC	CATACGCATT	GAAAAAGTCT	TAAGCAAAGA	AGAAATTTTA	480
GAGCGTTATT	TGAACCAAAC	TTTTTTTGGG	CATGGGTATT	ATGGCGTGAA	AACCGCAAGT	540
TTAGGGTATT	TTAAAAAACC	CCTTGACAAA	CTCACGCTTA	AAGAAATCAC	CATGTTAGTC	600
GCCTTACCTA	GGGCTCCAAG	TTTTTATGAC	CCTACCAAAA	ATTTAGAATT	TTCACTCTCT	660
AGGGCTAATG	ATATTTTAAG	GCGGTTGTAT	TCTTTAGGCY	GGATTTCTTC	TAACGAGCTC	720
AAATCCGCTC	TCAATGAAGT	GCCAATCGTC	TATAACCAAA	CTTCCACGCA	AAATATCGCT	780
CCCTATGTCG	TGGATGAAGT	GTGAAGCAA	TTGGATCAAT	TAGACGGGTT	AAAAACTCAA	840
GGCTATACCA	TAAAACTCAC	GATAGATTTG	GATTACCAAC	GCTTAGCGTT	GGAGTCTTTG	900
CGTTTTGGGC	ATCAAAAAAT	CTTAGAAAAA	ATCGCTAAAG	AGAAGCCAAA	AACTAACGCT	960
TCTAATGATA	AAGATGAAGA	CAACTTAAAC	GCCAGCATGA	TAGTTACAGA	AACGAGCACC	1020
GGTAAGATTT	TAGCCTTAGT	GGGGGGGATT	GATTATAAAA	AAAGCGCTTT	CAATCGCGCC	1080
ACGCAAGCCA	AACGGCAGTT	TGGGAGCGCR	ATCAAGCCTT	TTGTGTATCA	AATCGCTTTT	1140
GATAATGGCT	ATTCCACCAC	TTCCAAAATC	CCTGATACCG	CGCGAAATTT	TGAAAATGGC	1200
AATTATAGTA	AAAACAGCGT	GCAAAACCAC	GCATGGCACC	CTAGCAATTA	TRCTCGCAAA	1260
TTTTTAGGGC	TTGTAACCTT	GCAAGAAGCC	TTGAGCCATT	CGTTAAATCT	GGCTACGATT	1320
AATTTAGCGA	TCGCTTGGCT	A				1341

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

293

(A) NAME/KEY: misc_feature
(B) LOCATION 1...654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331

ATGAACGATA	CAACAGAGCA	CCATGGATCC	AATCCGCTAA	ACGCCCCACC	ACCTAGCAAC	60
TCACAGAGCA	ACGATCTCTT	AAATTGCTA	GACTCGTTAT	ATCCTAAAGG	GAGTTTAGGG	120
GAACAAAGAT	TTCACGAAGC	TTTAAAGAAT	CAAGAAGAGT	TGAAAAATAT	CCTAATAGAA	180
ATAGAAAAGC	TACCGCAAGA	AAAAAGGTAT	GAACCTCTGA	TGCAGATAGG	ACAAGCCAAA	240
CAGAGAATAA	TGGAAGCATA	CGCTCATTCA	TTCTTAGGAT	ATATAGGGGG	ACTAGAGCAT	300
CTGTTAGGAT	TGTGTATGGG	TGGGATATTT	GTTTGTGTTG	CAATCTATTT	TGTATTTTTA	360
AGAACTAGCA	AAAACACAGA	GCTAGTGGA	AGTCTAAAAA	CAAAATTAAA	ACTTCAGTAT	420
TTTACTATG	CCTTTGGTGT	GGGTGCGGTT	TTGTTTTTTG	GATTAGAAAC	AATTAGATCG	480
ATTTATGAAC	TATATATCTT	AGGAATTGGT	AGCACTAACG	ACAAGGTGCT	CTTTGTTTTG	540
AAAAACATTT	GCTTCATAGG	TATGGGCTAT	TTGATTTATA	AAGTTATTAA	AGTTATTGGT	600
ATAAAAAATT	TTATCAATGG	TCTTTTCGCT	TCAAAGAAAC	AAGGCGGTGC	AGAA	654

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332

ATGATGGATA	AGGTGGGTTT	TAAATCTCAA	GGCATCTTTG	TGATGGACGC	TAGCAAGAGG	60
GATGGGCGTT	TGAACGCGTA	TTTGGAGGC	TTGGGTAAAA	ACAAGCGGGT	GGTGTGTTT	120
GACACTTTGA	TCTCTAAAGT	TGGACAGAA	SGGCTTTTAG	CCATTTTAGG	GCATGAGTTA	180
GGGCATTTTA	AAAATAAGGA	TTTGTGAAA	AATTTAGGGA	TTATGGGAGG	CTTGCTCGCT	240
CTTGTTTTTG	CTTTGATCGC	TCATTTGCCG	CCGTTGGTTT	TTGAAGGCTT	TAATGTCTCG	300
CAAACGCCAG	CGAGTTTGAT	CACGATTCTA	CTCTTGTTTT	TGCCGGTGTT	TTCTTTTAC	360
GCCATGCCTT	TGATTGGGTT	TTTAGCCGC	AAGAACGAAT	ACAATGCCGA	CAAGTTTGGG	420
GCGAGTTTAA	GCTCTAAAGA	GACTTTAGCC	AAAGCGTTAG	TGTCCATTGT	GAATGAAAT	480
AAAGCGTTCC	CCTATTCGCA	CCCTTTTAT	GTTTCTTGC	ATTTACGCA	CCC GCCGCTA	540
TTAGAACGCC	TAAAGCTTT	GGATTATGAA	ATTGAA			576

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 603 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

294

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333

ATGAATATTT	ATCAAAAAA	CTTGCAAGCT	CTTTTCAAAA	AAGACCCTCT	TTTGTTTCGCA	60
AAGCTCAAAG	CCATTAAAGA	AAACAAAAA	TACGAAGTGT	TTTTAGGGAA	TGATAGCGCG	120
AATTTCAACC	TCTTAGATAA	AGAAACAAAC	ACGCCCTTAT	TTGAAAAAAG	CCCGCTAGAT	180
TCAAGCTTAG	AGCTATATAA	AAATAGCGAA	ATTCACATGC	TCTATCCTTA	TTTGTATTAT	240
TTTGGCTTGG	GTAATGGGGT	GTTTATCGC	TTGCTTTTAG	GCAATGAAAA	TTTAAAACGC	300
TTGGTGGTCA	TTGAGCCTGA	AATAGAGGTG	ATTTTCATTG	TGCTGAATCT	TTTGGATTTT	360
TCCACTGAGA	TTTTAGAAAA	TCGTTTGATT	TTATTGCATG	CAAGTTTTTG	CAATTACAAC	420
ATGATTGCTT	CATTATTIGA	TATGGATAAA	AAGTCTCGTT	TATACGCAAG	AATGTATGAT	480
TTAAAACTTT	TTAACGCTTA	TTATGAACGA	TACTCTCATC	AAATGATAGA	AATCAACCAG	540
CATTTACGCG	GCGCTTTAGA	GCATGGCGCT	ATTAGCGTAG	GCAATGACGC	TAAAGCGCAC	600
TCA						603

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 390 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334

ATGAAAAAGA	TTATTCTTGC	ATGCCTTGTC	GCTTTTGTGG	GTGCCAATTT	AAGCGCAGAG	60
CCTAAGTGGT	ATAGCAAGGC	CTATAACAAA	ACAAACGCCC	AAAAAGGCTA	TCTTTATGGG	120
AGTGGTTCAG	CACTTCTTAA	AGAGGCTTCT	AAACAAAAAG	CGTTAGCGGA	TTTAGTGGCG	180
TCTATTAGCG	TGGTGGTCAA	TTCACAAATC	CACATTCAAA	AAAGTCGTGT	GGATAATAAG	240
TTAAAATCCA	GCGATTACAC	AACGATCAAC	TTAAAACCG	ATGACTTGGA	ATTGAATAAT	300
GTAGAAATTG	TCAATCAAGA	AGCGCAAAAA	GGGATCTACT	ACACCAGACT	GAGGAATCAA	360
TCAAAACTTG	TTTTTGCAGG	GTTTAAGGGA				390

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 432 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

295

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335

ATGAAAATCC	AAACAATTTTC	AACACTTGTC	CTTACAATAA	TAATGGTAAT	ACAAAAAATG	60
ATTGTTGGCA	AAATTTTCACC	CCACAAAACC	GCAGAAGAAT	TCACYAATTT	AATGTTGAAC	120
ATGATCGCTG	TTTTAGACTC	CCAATCTTGG	GGCGATGCGA	TCTTAAACGC	TCCTTTTGAG	180
TTCACTAACA	GCCCAACAGA	TTGCGATAAT	GATCCTTCAA	AATGCGTAAA	TCCTGGGACA	240
AACGGGCTTG	TCAATTCTAA	AGTCGATCAA	AAATATGTGT	TAAACAAACA	AGACATTGTC	300
AATAAATTTA	AAAACAAAGC	RGATCTTGAT	GTAATTGTTT	TAAAGGATTC	AGGGGTTGTA	360
GGGTTTSGCA	ATGGATATGG	CAATGATGGT	GAATATGGCA	CATTAGGGGT	AGWAGCCTAT	420
GCTTTAGGAT	CC					432

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 927 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336

GTGGTAATAA	GGTTAGTCCT	AAACATGCTA	ACATGTCAAA	TTAGCTATAT	AAGGATAAGT	60
TATCTTGTCT	CTGTTAGCGA	TTTTGTGATT	TGCAAGGAAA	GATTTATGGA	TGAAATTAA	120
ACGCTGTTAG	TGGATTTTTT	CCCGCAGGCA	AAGCATTTTG	GGATAATCTT	AATCAAGGCT	180
ATTGTTGTCT	TTTGTATAGG	TTTTTATTTT	TCGTTTTTCT	TACGGAACAA	AACCATGAAA	240
CTCTTATCCA	AAAAGGATGA	GATTTTGGCG	AATTTTGTCT	CGCAGGTTAC	TTTTATCTTA	300
ATCCTTATCA	TTACTACAAT	CATCGCGCTC	AGCACGCTAG	GCGTCCAAAC	CACCTCTATT	360
ATCACTGTTT	TAGGAACGGT	GGGGATTGCG	GTGGCGTTGG	CTTTAAAAGA	TTATCTTTCA	420
AGCATTGCTG	GAGGGATAAT	CCTTATTATT	TTACACCCTT	TCAAAAAAGG	AGACATCATT	480
GAAATCTCTG	GCCTAGAGGG	CAAAGTAGAA	GCGCTTAATT	TTTTTAATAC	TTCTTTACGC	540
TTGCATGACG	GGCGCTTGGC	GGTTTTGCCT	AATAGAAGTG	TCGCTAATTC	TAATATTATC	600
AATAGCAATA	ACACTGCGTG	TCGGCGCATT	GAATGGGTCT	GTGGGGTAGG	GTATGGGAGC	660
GATATTGAAC	TGGTGCATAA	GACTATAAAA	GATGTTATG	ACGGGATGGA	AAAAATTGAT	720
AAAAACATGC	CCACTTTCAT	TGGAATCAGC	GATTTTGGAC	AAAGTTCGCT	GAACCTCACC	780
ATTAGGGTTT	GGGCAAAGAT	TGAAGACGGG	ATCTTTAATG	TGAGGAGCGA	ACTCATTGAA	840
CGCATCAAAA	ACGCCCTGGA	CGCTAATCGT	ATTGAAATCC	CTTTCAACAA	GCTAGATATT	900
TCTATCAACA	AACAAGACTC	TTCTAAG				927

296

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337

ATGAAAACT TTTCCCACT CTATTGTCTT AAAARGCTCA AAAAACGCCA TTTAATCGCT	60
CTGAGTCTGC CCTTGCTTTC TTATGCGAAT GGCTTTAAAA TCCAAGAGCA AAGCTTGAAT	120
GGCAGCGCTT TAGGCTCGGC GTATGTCGCT GGGGCTAGGG GTGCTGACGC TTCTTTTAC	180
AACCCGGCTA ACATGGGCTT TACTAACGAT TGGGGCGAAA ACAGAAGCGA ATTGAAATG	240
ACCACCACCG TGATCAATAT CCCGACCTTT AGCTTTAAAG TCCCTACGAC CAATCAAGRC	300
TTATATTCGG TAACAAGTTT AGAAATTGAT AAAAGCCAAC AAAATATTTT AGGCATCATC	360
AACACTATAG GGTTAGGCAA TATCCTTAAA GCGCTTGGCA ATACGGCCGC TACCAATGGC	420
TTATCACAAG CTATCAATCG GTTCAAGGG CTTATGAACT TAACCAATCA AAAAGTCGTA	480
ACCTCGCTT C	491

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338

ATGTGTTTAG CGATCCCTC TAAAGTCATA GCCATTAACG ATAATGTGGC ACTCTTAGAG	60
ACTTTGGGCG TTCAAAGAGA AGCGAGCTTG GATTTAATGG GCGAGTCCGT TAAAGTGGGC	120
GATTATGTGC TACTACACAT CGGCTATGTG ATGAGTAAAG AT	162

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

297

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339

```

ATGAAATATT TATGGCTTTT TTTAATATAC GCTATAGGGC TTTTTCGAAC AGATAAAACG      60
CTAGATATTA TTAAAACCAT TCAAAAACCTT CCTAAGATTG AAGTGCGCTA CTCCATAGAT      120
AACGATGCCA ATTACGCTTT AAAATTGCAT GAAGTCTTAG CGAACGATTT AAAGACTAGC      180
CAGCATTTTG ATGTTTCTCA AAACAAAGAG CAAGGTGCTA TCAATTACGC AGAACTCAAG      240
GATAAAAAAG TCCATCTTGT AGCGCTTGTG AGCGTGCGG TAGAAAACGG CAATAAAATT      300
TCACGATTAA AACTTTATGA TGTGGATACA GGAACGCTCA AAAAGACTTT TGACTACCCC      360
ATTGTAAGTT TAGATCTATA CCTTTTGCA GCGCACACA TGGCCATTGT GGTGAATGAT      420
TATTTAAAAG CCCCTTCTAT CGCTTGGATG AAGCGCCTGA TTGTTTTTTC TAAATACATT      480
GGACCAGGAA TCACAAACAT CGCACTAGCG AATTATACGA TCGCTTATCA AAAAGAAATC      540
ATCAAAAACA ACCGACTCAA TATTTTCCCC AAATGGGCGA ACGCTGAGCA AACGGAGTTT      600
TATTAC

```

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340

```

GTGGTGAGCG GGGTGGTGAT CATTATTGTG TTTTGTGTC CGATTCTAAC CTTACAGGGG      60
TTAGAGGGCA AGATGTTTAG GCCTTTAGCG CAAAGCATTG TGTATGCGCT TTAGGCACT      120
TTAGTTCTAT CCATCACTAT CATTCTGTGA GTGAGCTCTC TTGTCTTAA AGCCACGCCC      180
CATAGCGAAA CCTTTTAAAC GAGGTTTTTA AACAGAATCT ACGCCCTTT ATTGGAATTT      240
TTTGTGCATA ACCCTAAAAA AGTGATTTTA GGAGCGTTTG TTTTTTTAAAT CGCAAGCCTT      300
TCTTTATTCC CTTTGTGGG GAAGAATTTC ATGCCTGCTT TAGATGAGGG CGATGTGGTT      360
TTGAGCGTGG AAACCACCCC CTCTATTTC TTAGATCAAT CTAAAGATCT CATGTTAAAC      420
ATTGAAAGCG CGATTAAAAA GCATGTCAAA GAAGTAAAA GCATTGTGCG GCGCACAGGG      480
AGCGATGAAT TGGGGCTGGA TTTAGGGGGT TTGAATCAAA CCGATACTTT TATTTCTTTC      540

```

298

ATCCCTAAAA AAGAATGGAG CGTTAAAACC AAAGATGAAT TGGTTAGAAA AAATCATGGA 600
 TTCTTTAAAA GACTT 615

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341

GTGGGATATA TCCCTARGGA AAAGATTGTA GGCATTAGCG CGATCGCTAA ACTCATTGAA 60
 ATTTATAGCA AACGCCTGCA AATCCAAGAA AGGCTGACCA CTCAAATTGC AGAACTTTT 120
 GATGAAATCA TAGAGCCAAG GGGCGTGATC GTGTTTGTG AAGCCAAGCC ACTTGTGCAT 180
 GAGCATGCAA GGGGTGCAA AGCAAAATGC GATCAT 216

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342

GTGGCTCTTG TGTITGATAG TTTGATAGAG AACAAGAAG 39

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

299

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343

ATGAAAAAAA TTGTTTGTAG CTGTGTGTTG GTTTTGAGTT TGGGTTTTTTT AAAAGCCCAT	60
GAAGTGAGCG CTGAAGAGAT TGCGGATATT TTCTACAAAC TCAACGCCAA AGAGCCTAAA	120
ATGAAAATCA ACCACACGAA GGGGTTTTGC GCTAAAGGCG TGTTCCTCCC TAACCCGCAA	180
GCAAGAGAGG ATTTAGAGGT GCCACTACTC AATGAAAAAG AAATCCCTGC GTCTGTAAGG	240
TATTCTTTAG GGGGCGTGGT CGATTGGACG ATAAAGCAA GGTAGGGGA ATGGCGT	297

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344

GTGATCAAAC CTCATAGCGT GGGATTGGTA AGGATTGGGA TTGTTTGTC TTTAGAAGTG	60
GGGTATGAAC TGCAGGTACG CACCCGTAGC GGCTTGGCTT TGAATCATCA GGTGATGCTG	120
TTAAATTYCC CTGGCACGGT GGATAATGAT TATAGGGGCG AAATTAAGGT CATTTTAGCG	180
AATTTGAGCG ATAAAGATTT TAAAGTTCAA GTAGGGGATA GGATCGCTCA AGGGGTGTT	240
CAAAAACTT ATAAAGCCGA ATTTATAGAA TGCGAACAAT TAGATGAAAC CTTCAAGGGG	300

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 765 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

300

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345

ATGGAAATCA	TTTTATTAAT	TGTTGCGGCG	GTTGTGTTGT	TTTATTTTTA	CAACACCCTC	60
AAAGAATATT	TGAAAAACCC	CCTAAACCCCT	AAAACCAAAA	CCGAAGAATA	CGACTTGAAA	120
AATGACCCCT	ATTTGCTGGT	GCAATCTAGC	CCCCTAGACA	AATTCAAGCA	AACCCAAATA	180
GGCGCGTATA	TGCGTCTTTT	AAAATTTTTA	GACATTCAAA	AAAACGCCTT	GGATAACGCT	240
TTAAGAACGC	TTTTTATCCA	TGAATTGGAG	CAGCCCTTAA	ACAGCGAACA	GCAAAATTTA	300
GCCAAAGAGC	TTCTCAATGA	GCCSGTGGAT	AAAAAAGAAA	ATTTTGAATC	CTTATGCCAA	360
GAAATCGCCG	ACCACACGCA	TGGAGAATAC	ACCAAACGCC	TGAAATTAGT	GGAATTTCTT	420
ATGCTATTAG	CCTATGCTGA	TGGGATTTTG	GACAGCAAAG	AAAAAGAATT	GTTTTTAGAT	480
GTGGGGGCGT	TTTTGCAGAT	AGACAATCAA	GATTTTAACG	AGCTTTATGA	CAATTTTGAA	540
CACTTCAATT	CAATAGAAAT	CCCTATGTCT	TTAGAAGAAG	CAAAAAATCT	TTTTGAAATC	600
CAAACCCACA	CCACCATGCA	AGATTTAGAA	AAAAAAGCTT	TGGATTTAAG	CGCCCCCTAT	660
TACCATAAAA	TGAATGACAA	CAAACGCTAC	AGCGAACAAG	ATTTTATCTC	TTTGAAAAAA	720
ATCGCCCTCG	CTTCCCAACT	TTTAGAAAAT	GATTTAAAAG	ACTCA		765

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346

ATGGAAGTAG	AGCATGGCAA	GATTGAAACC	ACTTTAAGCT	TGGGGGCGTC	TCATTTGGA	60
GTCATTAAAA	TGATGCTTTT	AGAGAGCCTG	CCTTCTTTAG	TGAATAATAT	CACCATCACT	120
TTAATTTCTC	TAATAGGCTA	TTCCGGCTAWG	GCYGGAGCGT	TAGGGGCTGG	GGGATTGGGG	180
GATTTAGCCA	TTAGGATTGG	CTATCAAAGT	TATAGGGGCG	ATGTGCTTTT	TTATGCGGTG	240
GTCGTGATCA	TCGTTTTAGT	GCAAATCATT	CAAAGCGCGG	GGGATTATGT	GGTGAAACGC	300
TTGAGAAAGA	ATAAGTAT					318

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1581 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

SUBSTITUTE SHEET (RULE 26)

301

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...1581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347

ATGAACGAAA	TTGACAAATC	CGTTGATATC	GGATTCTTAC	GGATTCTGGA	TGTTATTAAA	60
AAAGTTAAAA	CCCCAAAGGG	TGGTATTGAG	GTTTTAAGGA	CTTTAATTGA	TTTCACGCCC	120
AAAATTGAAA	ACGCCCTAAA	TTTAGCGACC	AAAAGCCATA	AGGGGCAATA	CAGAAAGAGC	180
GGTGAGCCCT	ATATTGTCCA	TCCTATTTCG	GTGCGGAGCG	TGGTGCGGCT	TTGTGGGGGC	240
GATGAGGCGA	TGGTGTGCGC	CGCGCTTTTG	CATGATGTGG	TAGAAGACAC	GCCTTGTGAG	300
ATTGAAACGA	TTGAGCGAGA	ATTTGGGCAA	GATGTGGCTA	ATTTAGTGGA	TGCGCTCACC	360
AAAATCACTG	AAATCAGGAA	AGAAGAGTTA	GGCGTGAGTT	CTCAAGATCC	CAGAATCGTG	420
GTTTCAGCCC	TCACTTTATG	AAAGATCCTT	ATTAGCGCGA	TACAAGATCC	AAGAGCCTTA	480
GTGGTAAAGA	TTAGCGACAG	GTTGCACAAC	ATGCTCACCT	TAGACGCCTT	GCCTCATGAC	540
AAGCAGGTGC	GTATTTCTAA	AGAAACTCTA	GCGGTGTATG	CCCCCATAGC	GAGTCGATTG	600
GGCATGTCTT	CAATCAAAAA	CGAATTAGAA	GACAAGAGCT	TTTATTATAT	TTATCCAGAA	660
GAGTATAAAA	ATATTAAAGG	GTATTTGCAC	AAAAACAAAC	AGTCTTTACT	CTTAAAACTC	720
AACGCTTTTG	CGAGCAAGTT	AGAAAAAAG	CTTTTGTACA	GCGGGTTTAG	CCATTCGGAT	780
TTTAAACTCG	TTACAAGGGT	GAAACGCCCT	TATTCTATTT	ATCTTAAGAT	GCAACGAAAA	840
GGGGCGGTTA	ATATTGATGA	AATTTTGGAC	TTGTTAGCCA	TTAGGATTTT	ATTGAAAAAC	900
CCGATTGATT	GCTACAAGGT	TTTAGGGATT	ATTCATTTGA	ATTTCAAACC	CATTGTTTCT	960
CGTTTTAAAG	ATTACATCGC	TTTGCCCAAA	GAAATGGCT	ATAAGACAAT	ACACACGACG	1020
ATTTTTGATG	AATCTTCTGT	TTATGAAGTG	CAGATCCGCA	CTTTTGATAT	GCACATGGGG	1080
GCGGAGTATG	GTAATTCAGC	CCATTGGAAG	TATAAAGCCG	GGGGCGTGGA	TCATGAAGAA	1140
CATCATGAGG	GCATGCGGTG	GTTGCAAAAT	TTTAAATACC	ATGACAGCGA	TTTGAAAAAC	1200
GACCCTAAGG	AAATTTACGA	ACTCGCTAAG	AACGATTTGT	ATCGTGAAGA	TATTGTCGTT	1260
TTTTCGCCCC	ATGGGGACAC	TTACACTTTA	CCGGTGGGCG	CGATCGCTTT	AGATTTTCGCT	1320
TACATGGTGC	ATAGTGATTT	GGGCGATAAA	GCCACGGACG	CTTATATCAA	TAGTAAAAAA	1380
GCCTTACTCA	ATCAAGAATT	AAGGAGTGGG	GATGTGGTTA	AAATCATTTA	AGGCGATAAA	1440
GTAATACCTC	GTTTCATTTG	GATGGATCAG	CTTAAACTT	CTAAGGCTAA	AAACCATTTG	1500
CGCATCCAAA	GAAGAAACCG	CTTGAAAGAA	ATTGACACTA	AGAGCATGAT	CAATATCTTA	1560
GCGACTTTTT	TTTGGGCGCT	C				1581

(2) INFORMATION FOR SEQ ID NO:348:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...372

SUBSTITUTE SHEET (RULE 26)

302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348

GTGGTGGTGC TTGAGAATAT AAAAGACGCT GTGCCTTTAG CGCAAAGCCT RATARAGGGG	60
GGTATTCCAA TCATAGAAGT AACTTTGCGA TCAAACGTG CTTTAGAGGC CATAGAGCTT	120
ATCGCTAAGA ATGTGCCAAA AATGCGCGTG GGTGCTGGCA CGATACTCAA TCTCACTCAA	180
TTAGAGCAGG CTCAAAATAG GGGGGCAGAG TTTTGTGATTA GCCCGGGTCT TACGATAAAG	240
CTTTTAGAAC ACGCAAAGAA AAAAGACATG CCTTTAATAC CTGGGGTTTC TAGCAGCAGT	300
GAAGTCATGC AAGCTTTAGA ATTGGGTTAT AACGCTTTGA AATTTTTCCTT GCGGAGTAT	360
TGCGGGGGCC GT	372

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349

GTGGAAAAA TCAAACCCTA TGCCCTAAA GATAGCCCTT TAATAGACTA TTCTAGCCTA	60
GTTAGAAACG TCCAATCCAC TTAAAAAGGC ACTTCTTTTG AAACGCTTAT CAATGGCGTT	120
TGGGAAAGCT TTGAAACGAA GGTTTTAGGG GAGTTTAACG CCTATAATAT CGCTTCAGCG	180
ATTTTAACCG CTAAGCATT T AGGCTTAGAG ACAGAAAGGA TCAAACGGCT TGTTTTTGAG	240
CTTAAGCCTA TTAACCATCG TTTGCAACTG TTGGAAGCGA ATCAAAAAAT CATTATAGAC	300
GATASCTTTA ATGGGAATTT AAAGGGCATG	330

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1791 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350

ATGTCTAATC	AAGAATACAC	CTTCCAAACT	GAAATCAACC	AGCTTTTGGA	TTTGATGATC	60
CACTCTTTGT	ATTCTAATAA	AGAGATTTTT	TTAAGGGAGT	TGATTTCTAA	CGCGAGCGAC	120
GCTTTGGATA	AGCTGAATTA	TTTGATGCTA	ACCGATGAGA	AATTAAAAGG	GCTGAATACC	180
ACGCCTAGCA	TCCATTTGAG	TTTTGATAGC	CAAAAAA	CCTTAACGAT	TAAAGACAAT	240
GGTATAGGCA	TGGATAAAAG	CGATCTCATC	GAGCATTTAG	GCACGATCGC	TAAATCAGGC	300
ACGAAGAGTT	TTTTAAGCGC	TTTGAGTGGG	GATAAGAAAA	AAGATAGCGC	CTTAATTGGC	360
CAATTTGGCG	TGGGCTTTTA	TTCGGCGTTC	ATGGTAGCGA	GTAAGATTGT	CGTTCAAACC	420
AAAAAAGTTA	CCAGTCATCA	AGCTTATGCA	TGGGTGAGCG	ATGGTAAGGG	CAAGTTTGAA	480
ATCAGCGAAT	GCGTCAAAGA	GGAGCAAGGC	ACAGAAATCA	CCCTCTTTTT	AAAAGAAGAA	540
GATTCTCATT	TTGCGAGCCG	TTGGGAGATT	GATAGCGTTG	TTAAAAAGTA	TTCTGAGCAT	600
ATCCCTTTCC	CTATTTTITT	AACTTACACC	GATACGAAAT	TTGAGGGCGA	AGGGGATAAT	660
AAAAAAGAAG	TTAAGAAGA	AAAATGCGAT	CAGATCAATC	AAGCGAGCGC	TTTATGGAAA	720
ATGAATAAGA	GCGAATTGAA	AGAAAAGGAT	TACAAAGACT	TTTACCAATC	GTTTGCGCAT	780
GATAACAGCG	AGCCTTTGAG	CTATATCCAT	AATAAAGTGG	AAGGCTCTTT	AGAATACACG	840
ACGCTTTTTT	ATATCCCTAG	CAAAGCGCCC	TTTGATTTGT	TTAGGGTGGA	TTATAAAAGC	900
GGGGTCAAAC	TTTATGTTAA	ACGGGTGTTT	ATCACTGATG	ATGACAAAGA	ATTGTTGCCG	960
TCTTATTTGA	GGTTTGTTAA	AGGCGTGATT	GACAGCGAAG	ATTTGCCCTT	GAACGTGAGT	1020
CGTGAAATCT	TACAGCAGAA	TAAGATTTTA	GCCAATATCC	GTTTCGGCTT	AGTGAAAAAG	1080
ATTTTAAGCG	AGATTGAAAG	GCTGAGCAAG	GATAACAAGA	ATTACCATAA	ATTCTATGAG	1140
CCTTTTGGA	AAGTGTTAAA	AGAAGGCTTG	TATGGGGATT	TTGAAAACAA	AGAAAACTT	1200
TTAGAATTGT	TGAGATTCTA	TTCTAAAGAC	AAAGGAGAAT	GGATTTCTTT	AAAAGAATAC	1260
AAAGAAAATT	TAAAAGAAAA	TCAAAAAAGC	ATTTACTACC	TTTTAGGCGA	AAATTTAGAC	1320
TTATTAAAAG	CGTCCCCCTT	TTTAGAAAAA	TACGCTCAAA	AAGGCTATGA	TGTTTTGTTA	1380
TTGAGCGATG	AAATTGATGC	GTTTGTGATG	CCAGGCGTGA	ATGAATACGA	TAAAACGCCC	1440
TTTAGAGACG	CTAGCCATAG	TGAGAGTTTG	AAAGAGCTTG	GTTTGGCAGA	AATCCATGAT	1500
GAGGTAAAAG	ATCAGTTTAA	AGATTTAATC	AAAGCGTTTG	AAGAAAATCT	TAAAGATGAG	1560
ATTAAGGGCG	TAGAGCTTTC	TGGTCATCTC	ACTTCAGCGG	TGGCTTTAAT	AGGCGATGAA	1620
CCAAATGCCA	TTGATGGCTA	TTGGATGCGT	CAATGGGGCG	AAAGCGTGCC	TGAAAGCAAG	1680
AAAACCTTAG	AATTAAACCC	TAACCATGCG	ATTTTGCAAA	AACTCTTAAA	ATGCGAAGAT	1740
AAAGAGCAGT	TGAGCGCTTT	TATCTGGTTG	CTTTATGATG	GGCGAAGCTT	T	1791

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351

GTGAATTTAG	GGGCTTACTA	CACGCCCCCT	TATTTAGTGG	ATTGCGCTTA	CAAGCTTTTA	60
AAAAAGCATG	TTGGTATTGA	AAACTACACG	CTTTTAGACA	CCGCATGTGG	TAATAAAGAG	120
TTTTTAAAGC	TCCACCACCC	TAAAAAATA	GGAGCGGATA	TTGACCCTAA	GTGTGATGCT	180
TTAATAATAA	ACGCTCTAGC	CAATCCTAAA	AGAGAAAATT	ATGGCATTAG	CCAAGATGAA	240
CCTTTAATCA	TCGTGGGCAA	TCCCCCTAT	AACGATAGAA	CTTCCTTTAT	CAAACAAGAT	300
ATTAAAAATA	AAGATTTTAT	TTTTGAGATA	GACAACGATT	TGAAATCCCG	AGATTTAGGG	360
ATAAGTTTTT	TAAAACTTTT	TGCAATTTTA	AAGCCGGCGT	TTATTTGCGT	GCTACACCCT	420
TTATCTTATC	TCATCAAAGA	AGCTAATTTT	AAGCAATTTA	AAGCTATT		468

304

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352

ATGAAAAGCA	TTTTGCTCTT	TATAATTTT	GTAGTTTGTG	AGTTAGAAGG	CAAAAAATTT	60
TCACAAGATA	ATTTTAAGGT	GGATTATAAC	TACTATTTGC	GCAAACAGGA	TTTGCACATC	120
ATTAAACGC	AAAACGATTT	GTCCAATGCC	TGGTATCTCC	CTCCACAAA	AGCCCCCAA	180
GAACATTCTT	GGGTGGATTT	TGCTAAAAA	TATTTAAACA	TGATGGATTA	TCTAGGCACT	240
TATTTTGTG	CTTTTATCA	TAGTTTCACC	CCCATTTTTC	AATGGTACCA	CCCTAATATC	300
AACCCCTACY	AACGCAATGA	GTTTAAGTTC	CAAATCAGTT	TTAGAGTGCC	TGTATTTAGG	360
CATATTCTTT	GGACTAAAGG	CACGCTTTAT	CTGGYTTATA	CCCAAATAA	CTGGTTTCAA	420
ATTTATAATG	ACCCTCAATC	CGCCCCCATG	CGAATGATTA	AATTTTCATG	C	471

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353

ATGGGCTTGA	TGGGCGTGTC	GCAAGGCTTA	CCAAACACCA	CTAGCAAGTT	TGGTATTGAA	60
TTTGACTCTT	TAGCTGATGT	GGTCGCTTTT	GGAGTCGCCC	CAAGCCTTAT	TACTTACTTT	120
TATGTGGGGT	ATAACTTTTG	GCGTATAGGC	ATGGCGGTGA	GCGCGTTGTT	TGTGATTTTT	180
GGAGCGATAC	GATTAGCGCG	ATTCAATATC	AGCACCAACA	CAAGCGATCC	CTATTCTTTC	240
ATCGGTATCC	CCATTCTTGC	GCGGCGGTA	TTGGTGGTGC	TTTGCCTGTT	ATTAGATAAT	300
AAATACCATT	TCTTAGAAGG	CAATACCGAA	AAGTTATTTT	TAGGCTTTAT	TGTCCTTATTA	360
GGGGTGCTTA	TGGTGAGCAA	TATCCGCTAC	CCTAATTTTA	AAAAAGTCAA	GTGGAATCTC	420
AAGCTTTTCA	TCTTAGTGTT	GATCTTTTTA	TCGTTAGTGT	TTGTGCGCCC	TTTAGAGGCT	480

305

TTGAGCGTGT TTATGGGGTT GTATTTGATC TATGGCATCA TTCGGTGGAT CTTTTTAATG 540
GTAAAAATTA CTTTAAATAA AAATAAAAGC GCA 573

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354

ATGATAGGAG TTTACCCCAA TTATTCCAAA AAGCAACTAA AACGCCCTT AGTCATATTT	60
GTAAGTAGGG AGTTAGCGCT GGCTAATGGT ATTCTTACAG ACGCCTATGA CATTGAAGCA	120
AATCTTTACA TGAATGCTCG TATCGTTATG AARAATAATA AAAGGAAACA TTATGAGCAG	180
CGGGTTAATT TACATTTTCT TAGAAGTCTT GGTARCGTGT TTGATCACCG CTCTAATCAT	240
GTATTATGTG ATGAAAAAGA TCTATTACGC	270

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355

GTGAAAATAA CCATAATGAT TAAAGATTTT AACCACTATT GTAGAAAAAT AACGAGAGGG	60
TTTGTAAGAAA TTCCCACCAA AAAACAAGGA GCAAAAAAGA TGAAAAAAGC GGGTTTTCTT	120
TTTTTGGCGG CGATGGCTAT CATTGTTGTG AGTTTAAACG CCAAAGATCC GAATGTGTTG	180
CGTAAGATTG TTTTGTAGAA ATGTTTGCCT AATTATGAGA AAAATCAAAA TCCTTCACCA	240
TGCATAGAAG TCAAACCCGA CGCCGGCTAT GTGGTTTAA AAGATATTAA CGGTCCGTTG	300
CAATATTTGT TGATGCCAAC GACTCACATT AGTGGCATTG AAAACCCCTT GTTGCTTGAT	360
CCTTCTACGC CTAACCTTTT TACTTGTCA TGGCAAGCGC GCGATTTTAT GAGTWAAAAA	420
TACGGAAAAC CCATTCCTGA TTATGCGATC TCTTTGACGA TCAATTCTAA AAAAGGGCGA	480

306

TCGCAAAACC	ATTTTCACAT	CCATATTTCT	TGCATTAGCC	TTGATGTGCG	CAAACAGCTG	540
GATAATAATC	TAAAAAATAT	CAACAGCCGT	TGGTCGCCAT	TATCAGGTGG	CTTGAACGGG	600
CATAAATATT	TGGCGCGTCG	GGTAACAGAG	AGCGAATTAG	CGCAAAAAAG	CCCGTTTGTC	660
ATGCTTGCTA	AAGAAGTGCC	TAACGCGCAC	AAACGCATGG	GAGACTATGG	CTTGGCGGTG	720
GTGCAACAGA	GCGATAACTC	CTTGTCTTG	TTAGCGACAC	AATTTAACCC	ATTGACTTTA	780
AATCGCGCTT	CAGCCGAAGA	GATTCAAGAT	CATGAATGCG	CGATTTTGCG	T	831

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356

GTGCTAACGA	GTGGGGACAT	GATCACTTGT	CCGTATTGCG	GGCGTATTTT	RTACGCTGAG	60
AGTACGCATG	AAAGTAACGC	TCAACCTCCA	AAAGAAAGCC	AACCAAAAGA	AAGCCAAGAA	120
GAAAGCCAAG	AAGAAAGCCA	AGAAGAAAGC	CAAGAAGCCG	TCCGTTTGAT	TGTT	174

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357

ATGAAATTGA	ATGACCCTTT	CACAAGCCCT	AATAAAGCCA	AAAAAGAATT	ATCGCCAAAA	60
GGCTTTAGGG	GGGGGTTAGA	GTCTGAAATT	TTATTAGGCT	TTGTCTTGCA	AAAAGAAAGG	120
GTTTTTTTGC	ACACGCATGA	GCAATTTGGAA	TTAAGCCACG	AAGAAGAAAC	ACGCTTTTTT	180
GAATTGCTAG	GAAAGCGTTT	GAATGACTGC	CCCATAGAGT	ATTTATTAGG	AAGCTGTGAT	240
TTTTATGGGC	GCTCTTTTTT	CGTGAATGAG	CATGTTTTAA	TCCCACGGCC	TGAAACCGAG	300
ATTTTAGTCC	AAAAAGCCCT	TAATATTATT	TCTCAATACC	ATTTAAAAGA	AATAGGCGAA	360

307

ATCGGCATAG	GGAGCGGATG	CGTGTCCGTG	AGTTTGGCTT	TAGAAAACCC	TAATCTCTCT	420
ATTTATGCGA	GCGATATTC	ACCAAAAGCT	TTAGAAGTGG	CGTTAAAAAA	TATTGAACGC	480
TTTTGTCTAA	AAGAGCGTGT	TTTTTTAAAA	CAAACGCGCC	TTTGGGATCA	TATGCCAACG	540
ATAGAAATGC	TTGTCTCTAA	CCCGCCCTAT	ATCGCTAGAA	ATTATCCTTT	GGAAAAATCC	600
GTTCTCAAAG	AACCGCACGA	AGCCCTTTTT	GGGGGGGTTA	AAGGCGATGA	AATCTTAAAA	660
GAAATCGTTT	TTTGTAGCCG	TAAATTAAAA	ATCCCTTTTT	TGGTTTGTGA	AATGGGGTAT	720
GACCAGTTAA	AGAGCTTGAA	AGAATGCTTG	GAGTTTTGCG	GTTATGATGC	AGAGTTTTAC	780
AAGGATTTGA	GCGGCTTTGA	TAGAGGGTTT	GTGGGCGTTT	TAAAAAGTTT	TTTAAGA	837

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358

ATGATTTCCTT	TCATTGGGTT	TGAATGCTCC	GCATTAAAAG	TTTTTTTAAAC	TTTGGTTAC	60
ATAGTTTTTAA	AAAGYTGGA	CTATAGCGCT	ATAAGACTAA	TTGTTATA		108

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359

GTGATCCAGT	CTCACCTTAA	ACAAACTCTA	ATTGAAGATG	AAAATTATTT	TTATGCTAAC	60
AAGGGTCTTT	ATAAAACCAA	CAAAGAAGCC	TTTTTAAGGG	TTTATAAAAT	CCCAGAGAGC	120
ATGCCCATAG	AAAAACGAGA	AAGTTTAAGC	AAGGTTTCTA	AAATCTTTTT	AGCGTTGCTT	180
TTTTTCATTT	CTAGCATGCT	TTTTGGGATC	TTTTGGCGTT	TGCCCAAACG	ATTGGACACT	240
AAAATGAGTT	TAGAGAGCGC	GCACAAAAC	GAATTAGAAA	ATGCATTCCA	ACGATACGAT	300

308

CGCGTAGGGG TGCCTTTTGA AGACATTGCA GGGGTGAATG AAGTCAAAGA AGAATTACTA 360
GAAGTGATRG ATTWTTTWAA AAAACCC 387

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360

ATGTTTGTAG TAAAAATGGT GTTAGGGTTT TTGATCCTTT TAAGCCCTTT GTGCGCTACT 60
GGATTGGATA TTTCACAAAC AGACATTATA GAGCGTTCTT TAAATTTTCCT CTTGTTTGTG 120
GGGATTTTGT GGTATTTTGT GGCTAAAAGA TTGCGTTCAT TTTTGCAATC CAAAAGCCTT 180
GAAATCTCCA AACGCTTAGA AGAGATTCAA GCCCAACTTA AAGTGAGTAA AGAACATAAG 240
AAAAAACTCC TTAAAGAATT AGAGCAAGCC AAAGAAAAAG CTGAATTGAT TATTTCTGAT 300
GCGAATAAAG AAGCCCTACA CGATCACGCA AAAATACGAA TTACAAACCA AAATGGATGT 360
GGAAAATTTG ATCAAAAATT C 381

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361

ATGAGGGTTT TAGAGTGGAA ATATTGGTTA AATACTGATA AGTGGGATAC GCCCACCAC 60
AAACCGCCTC AAACTTTAA AATACAAATT TTTAAGATAC AAATAGGTAT AATCAATAAC 120
TTCAATCATT TAATCAAAGG GAGTTCTATG AAAAACGCTT TCAAAGCGTT TGCCTTGTTA 180
ATCGTATTTT TCTCAAACGC TCTATTAGCG CAGGATTTAA AAATCGCTGC TGCTGCTAAT 240
CTCACGCGCG CTTTAAAGC CCTTGTTAAA GAATTTCAA AAGAACACCC AAAAGACGCT 300
ATTAACATTA GCTTTAATTC TTCAGGCAAA CTCTACGCTC AAATCGCTCA AAACGCCCTT 360

309

TTTGATTTAT	TCATTTTCAGC	GGATATTGCT	AGACCCAAAA	AACTTTATGA	TGAAAAAATA	420
ACCCCTTTTA	AAGAAGAAGT	CTATGCTAAA	GGCGTGTGG	TTTTATGGAG	TGAAAATCTA	480
AAAATGGATT	CTTTAGAAAT	TCTTAAAGAC	CCTAAAATTA	AACGTATCGC	TATGGCTAAT	540
CCTAAACTAG	CCCCTTATGG	AAAAGCCAGC	ATGGAAGTCT	TGGATCGTTT	AAAACCTCACT	600
CCTAGTCTTA	AATCTAAAAT	CATTTATGGC	GCTTCTATTT	CTCAAGCCCA	TCAATTCATC	660
GCCACCAAAA	ACGCTCAAAT	AGGCTTTGGA	GCGTTATCTT	TGATCGATAA	AAAAGACAAA	720
AACCTCTCTT	ATTTTCATCAT	TGATAAAACC	CTTTATAACC	CTATTGAACA	AGCCTTAATC	780
ATCACTAAAA	ATGGGGCTAA	TAACCCTTTA	GCCAAAGTTT	TTAAAGATTT	TTTATTCAGC	840
CCTAAAGCTA	GAGCTATCTT	TAAAGAATAC	GGCTATATTG	TGGAT		885

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362

GTGGCTTTAT	TAGAGCCAAG	CGTGATGTAT	CTTACCGAAA	AGTATCAATA	CTCTCGTTTT	60
AAGGTTACTT	GGGTCTTGT	AGCGTTAATC	TTTGTGGTAG	GCGTGGTGTT	GATTTTCTCG	120
CTCCATAAGG	ATTATAAAGA	CTATCTCACT	TTCTTTGAAA	AAAGTCTTTT	TGATTGGTTG	180
GATTTTGCAT	CAAGCACCAT	TATCATSCCT	TTAGGCGGGA	TGRCAACCTT	TATTTTATG	240
GGCTGGGTTT	TGAAAAAGA	AAAATTGCGT	CTTTTGAGCG	CGCACTTTT	AGGCCCTAAA	300
TTGTTTGCAA	CTTGGTATTT	CTTGCTTAAA	TACATCACCC	CTTTAATTGT	GTTTTCATT	360
TGGTTGAGCA	AGATTTAT					378

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363

310

GTGGGGCTTA	TGAAAATAAG	ATTTATGGGG	CGGAGTGT	TTGTGGGGGA	TTTGAACGC	60
ATTGAAGAAG	TGGCTAGATT	TGAAGAATTT	TGGCTTTTAG	GGGGGCAAAA	AGCGATCAAA	120
GAGCCTAGAA	GATTGGTTTT	AGAAATCGCT	TTAAAACACC	AGCTCAACAA	GCTTTTAAAA	180
CGCGTTCAAA	AGCATTTC	AGAAGACGAA	TTAGGAATTT	TTAAACAAAT	GCATGACAAA	240
AAAATTCAAA	GCGTCGCCAC	CAATTCCATA	GGGCGTTTGT	TTGATATAGT	GGCGTTTAGT	300
TTGGGCGTGG	TGGGAACGAT	TAGTTTTGAA	GCCGAGAGCG	GGCAGGTTTT	AGAAAATCTA	360
GCCCTACAAA	GCGATGAGAT	CGCTTTTAC	CCTTTTGAAA	TCAAAAACAG	CGTGGTGCGT	420
TTGAAGGAAT	TTTATCAAGC	GTTTGAAAAG	GATTTGGGCG	TTTTAGAACC	CAAACGCATC	480
GCTAAGAAAT	TTTTTAACAG	CTTAGTAGAA	ATCATTACCG	CCTTGATTGC	GCCTTTTAAA	540
GGGCATGTCG	TGGTGTGCAG	TGGGGGCGTG	TTTTGCAACC	AATTGTGTGT	CGAACAATTA	600
GCCAAGCGAT	TGAAAAAGCT	TCAAAGGGAG	TATTTTTTCC	ACAAGCATTT	CCCCCCTAAT	660
GACAGYAGTA	TCCCTGTCGG	TCAAGCCTTA	ATGGCGTATT	TCAACCCTAC	AATCATCAAA	720
AAAGGA						726

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364

GTGAGCGATT	CTAACGCTTT	AAAGGAAGTG	TTTTTAAACA	TCAGCGCTAA	AGAAGATCAT	60
TGCGACGTTT	TGATCAATTC	CGCCGGTTAT	GGGGTGT	GGAGCGTGGA	AGACACGCC	120
ATTGAAGAGG	TTAAAAAGCA	ATTTAGCGTG	AATTTTTTCG	CCCTTTGTGA	AGTGGTGCAA	180
CTTTGTTTGC	CCTTATTAAA	AAACAAGCCT	TATTCTAAGA	TTTTCAATCT	TTCTTCCATA	240
GCGGGGCGTG	TGAGCATGCT	CTTTT	TAGGC	CATTACAGCG	CGAGTAAGCA	300
GCATTATAGCG	ATGCCCTTGCG	TTTAGAGCTT	AAGCCCTTTA	ACGTTCAAGT	GTGTTTGATT	360
GAGCCAGGCC	CGGTGAAAAG	CAATTGGGAA	AAAACCGCTT	TTGAAAATGA	TGAGCGGAAA	420
GATAGCGTTT	ATGCTTTTGA	AGTGAATGCG	GCT			453

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

311

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365

GTGATAGTGG CGTGGCTTTT TAGGTTTAAA AGCATTGCGT TTTCTATTTT AATCACTCTG	60
TTGGTTATTT TAGTGGATAT TTGGGTGTAT AGCGATGTGC GCCAGTTTTT ATTGGACACT	120
TCTAGCTCTT TTATTTGGCT TTTAATCGCT TTTACTAATCA AGTGGGGCGT GATTGTTATA	180
AGTGCGCGCA AATGCTACCA ATTCAGCCAA AAAATGTTTG CGTTAATCCA AAGAAAAAGG	240
CAAATCAGAG AGAATTTAAA AAACCGCTCC AATCGCAAAG ATGCTAAAAA TTTTGAAAAA	300
CTCTCTAACA TCGCTGAAGA AATCATTTC AAAAAACAAG AAGAGTCCCA CCACAAAGAA	360
GATTCTAATG ATGAAAACCA CAAAGACAAG CTTTCTAACA TTACCGAAGA AATGATTCTC	420
AAAAACAAG AGGAACTGAA AGCTAGAAAG GATAAGGGGG AT	462

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...537

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366

ATGAACTACC CTAATCTACC TAACAGCGCT TTAGRGATAA GCGAACAGCC AGAAGTGAAA	60
GAAATCACTA ACGAGCTTTT AAAGCAATTA CAAAACGCTT TAAGGAGCAA CGCGCATTTT	120
AGCGAGCAAG TGGAAATTAAG CCTTAAATGC ATCGTTAGGA TTTTAGAAGT GCTTTTGAGT	180
TTGGATTTT TTAAGAATGC GAATGAGATT GATAGCAGTT TAAGAAATTC CATTGAGTGG	240
CTGACTAAG CCGCGGAGAG CTTGAAATTA AAAATGAAAG AATACGAGCG CTTTTTTAGC	300
GAGTTTAATA CGAGCATGCA TGCCAACGAG CAGGAAGTAA CCAATACCTT AAACGCTAAC	360
GCCGAGAAC TTTAAAGCGR AATTAAAARG CTAGAAAATC AATTGATAGA AACCACGACA	420
AGACTTTTAA CGAGCTATCA AATCTTTTAA AACCAAGCCA GAGATAACGC TAACAACCAA	480
ATCACAAAA ACAAAACCCR AAGCCTTGAA GCGATTACAC AAGCTAAAA CAACAGC	537

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

312

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...480

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:367

GTGTTTGCCA CTGACAGCAG TAGCTTTTCT ATGGGGCTTA CCATGGCGAG TGCTTATGAY	60
CCCATTTCAG GATCGCAAAA ACCCATTGTG GGGCAAGCCC TTTTATTGTT AGCGATTTTA	120
ATTTTATTGG ATTTATCGTT CCACCATCAA ATCATTTTAT TTGTGGATCA CAGCTTAAAA	180
GCCGTCCCTT TAGGGCGATT TGTCTTTGAG CCAGAATTAG CTAAAAACAT TGTCAAAGCC	240
TTTTCACACT TGTTTGTCTAT AGGGTTTCT ATGGCGTTCC CTATTTTATG CTTGGTGTTA	300
TTGAGCGATA TTATTTTGG CATGATCATG AAAACCCACC CTCAATTCAA CCTGCTCGCT	360
ATCGGGTTTC CGGTTAAAT TCGATCGGG TTTGTGGGCA TTATTTTAAT CGCTTCGGCT	420
ATCATGGGCG GTTTTAAAGA AGAAATCAGC CTGGCCTTA GCGTTATTTRG TAAAATCTTT	480

- (2) INFORMATION FOR SEQ ID NO:368:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 282 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...282

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:368

ATGTATGGCG TGAAGAGAT TAAAGATAAA ATTGACAAGC AACTCCACAA TAACGATCAT	60
TTGTTTGAAG GGCTTTTGG GAAAAAGAA GATTTGAAAA AATTGGTGAG CATGTTTGGG	120
CAGTTGCGTT TCCAAAGCG CTGGAGCCAA ACCCAAGAG TGCCACAAAC CAGTGTCTA	180
GGGCATACTT TATGCGTGCG GATTATGGGG TATTATTGA GTTTGACTT GAAAGCTTGT	240
AAAAGCATGC GGATCAATCA TTTTTTGGGC GGGCTTTTTC CA	282

- (2) INFORMATION FOR SEQ ID NO:369:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 438 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

313

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369

ATGACTTTAG	ATGACTTATT	AGGGGGGAGT	TTGGACCCGC	ATTGTTTTTG	CAAACCCTTA	60
ATCAAAACCA	AAAAAGACCA	AGAAAGGCTC	TTATCCCTTG	CTTTAAAAGC	CCACCCTAAA	120
ATCTCTTTTG	GAWWGGACAG	TGCCCCGCAT	TTCATTTCTA	AAAAGCATAG	CGCTAACATC	180
CCGGCGGGCA	TCTTTTCTGC	CCCTATTTTG	TTGCCTGCGT	TGTGCGAACT	TTTTGAAAAA	240
CACAACGCTT	TAGAAAATTT	GCAAGCCTTT	ATCAGTGATA	ACGCTAAAAA	AATCTACGCG	300
CTAGACAATT	TACCCAGTAA	AAAAGCGCAT	TTGTCTAAAA	AACCCTTTAT	AGTCCCTACG	360
CACACGCTTT	GCTTGAATGA	AAAAATCGCT	ATCTTAAGAG	GGGGCGAAAC	GCTATCTTGG	420
AACCTTCAAG	AAATCGCC					438

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370

ATGGGCGTTT	TGGGCATGTT	CGCTTTTTTT	TCATGGGTTT	TTTTATTCAA	GCACAATCTC	60
AGCCATAAAA	TCCGCTTATA	CCATGAAAAA	AAGGATTTTG	ACAAATTGCT	CAAACAAATC	120
CTATCCCAAG	ACACCCAAAA	GACTTTTTTA	AAAACAAAAT	TTAAAGCGA	TCTCGCTAAA	180
AACCTCTCTC	AAATCTTAGC	CCGCTATGAT	TTAAAGCTG	ATTTAAACAC	GCCAAATAGC	240
GGTGCGAA	AAGTGGATAA	CCTTTTFAAA	CATTACCACA	ATATAGAAAA	TAACACCCTT	300
GAGCCTAAAG	ATCACGCTAA	ACATTCCCTA	GCTTATGAGC	ATGCTTATTT	TTCTAAACGC	360
TTGAAGGCTT	TCATTCTATA	CGATTTGAAA	AACGCCTTTG	AAGTTTTAAC	AAACGCGCAA	420
ATCCCTTTGG	AATTACGCCG	CTACGCTTAT	AGAAATCGCC	CAAAAAGGCA	GCAAAAAAGA	480
GGTTTTAAAG	GCTGTGAATG	CGATGCAAGA	GGATTTGGA			519

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

SUBSTITUTE SHEET (RULE 26)

314

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371

```

GTGAGTGTTC CTGCAACGAG TGCGAATTTA GGCCCCGGTT TTGATTGCTT GGGTTTGACT      60
TTGAATTTAC GCAATCGTTT TTTTATTGAG CCTAGTAATA TCCATGCGGT GAAATTGGTT      120
GGGGAGGGTG AAGGGATCCC TAAATTTTAA ACCAACAATA TTTTCACCAA AGTGTTTTAT      180
GAGATTTTAA AAAAGCATGG GAATGACGGC TCGTTTAAAT TTTTATTGCA TAATAAAGTC      240
CCTATTACAA GGGGCATGGG GTCTAGCTCA GCGATGATTG TGGGGGCGGT CGCTTCAGCG      300
TTTGCGTTT TAGGGTTTGC TTTTGATAGA GAAAACATTC TCAATACTGC TCTAATTTAT      360
GAAAACCACC CGGATAATAT CACCCCGGCG GTGTTTGGGG GGTATAATGC AGCGTTTGTC      420
GAAAAAAGA AAGTGATAAG TTTAAAAACC AAAATCCCTT CTTTTTTAAA AGCGGTGATG      480
GTGATCCCTA ATAGGTCAT TTCTACCAAG CAATCGCGCC ATCTCTGCCC AAGCGTTACA      540
GCGTGCAAGA AAGCGTGTTC AACCTTTCGC ATGCGAGTT      579

```

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 312 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372

```

GTGGCTAAAA ATTTGCTAGC GAGCGGGGTT TGCGATAAAG CGACCGTGCA GCTTGCTTAT      60
GCGATTGGGG TGATAGAGCC TGTGTCTATT TATGTGAACA CGCATAACAC GAGCAAGCAT      120
TCAAGCGCGG AGTTGGAAAA ATGCGTGAAA TCGGTTTTCA AACTCAGGCC AAAAGGCATC      180
ATTGAAAGCT TGGATTTGTT AAGACCCATT TATTGCTCA CTTCAGCTTA TGGGCATTTT      240
GGGCGCGAGT TAGAAGAATT CACTTGGGAA AAGACTAACA AGGTGAAGA GATTAAAGCG      300
TTCTTTAAGC GT      312

```

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1065 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

315

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373

```

GTGCGTTTGT TTAGATTIGT GGGGTGGTAT TATTTCAAAT ACTTTTAAAT CGTGCTTTTA 60
GCTTTGGAAT TGTTTTTTGT AGGCATTGAC AGCCTGAAAT ACGCCGATAA AATGCCTGAT 120
TCTGCCAACA TGATCATTTT ATTTTTCACC TATGATATTT TATTCGCTCT CAATTACACC 180
TTGCCCATTT CCTTGCTTTT AGCGATGGTT TTATTTTATA TCACCTTCAT TAAATCCAAC 240
CAATACACCG CCCTGCTCTC TATTGGATTT TCCAAATGCC AGATTTTAAG CCCTATTTTT 300
TTGATTAGCC TGTTTTTCAC GGCTGTTTAT GTGGGGTTGA ACGCGACTCC TTTGTGTAT 360
ATGGAAGAAA AAACGCAAAA TTTAATTTAT AAAGACAATT CTTTGAGCGT TTCAGAGCAT 420
TTGTTAGTGA AATACAACGA TGATTACGTG TATTTTGATA AGATTAATCC CTTATTGCAA 480
AAAGCCCAAA ATATCAAGGT TTTTCGCCTA AAAGATAAAA CTTTAGAATC TTATGCTGAA 540
GCTAAAGAAG CTTTTTTTGA AGACAAATAT TGGATTTTAC ATGACACTAC TATCTATGAG 600
ATGCCCTTGA GTTTTGAACT GGGCGCGAAC GCTTTAAACA CCACGCATTT AGAAACCTTT 660
AAAACGCTCA AAAATTTCCG CCTTAAAGTT TTAGACACCA TTTATCAAAA CAAGCCTGCG 720
GTTTCTATCA CAGACGCTCT TTTATCCTTG CATGCTTTAG TGCGCCAAAA CGCGGACACG 780
AAAAAAGTGC GCTCGTTTTT GTATGTGTTT GCGATTTTGC CCTTTTTTGT GCCGTTTTTA 840
AGCGTTTTTA TCGCTTATTT TTCGCCCAGT CTCGCCCGCT ATGAAACCTT GGCTCTTTTA 900
GGGCTAAAGT TTATCATTAT CACGCTCGTT GTTGGGGGCG TATTCTTTGC TTTAGGGAAG 960
TTCAGCATTT CAGGGATACT CATTCCTGAA ATAGGCGTTC TATCGCCCTT TTTCGTATTT 1020
CTAGCTCTCA GTCPTTGGTA TTTTAAAAAA CTTAATAAGA GATTG 1065

```

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 717 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374

```

ATGATTTATG GCGTTTATGA CGGCTTGTTT TTGGCTATTT TACAGGCTCA AAATTACCGC 60
TTCCATTGCG TTTATTTGTT TGAAGAAAAT TTAGACTTGT TTAAATCAG TTGCTATTTT 120
GCGCGTTATG AAGATTTGAT TAAAAAAGGG GCTAAACTTT TTATTCAAGG GTTTTTTAAC 180
CCTAATGAAT TGAAAAATGA TTTTITGAAA CGCCCTATCA CGCATTCTTT TTTAAAGCTA 240
GAAATCATGC CCTATAAAAG CGCTTTTAAT TTGCGCATGC GAGAAAACAT TCAAAGCTAT 300
TACAAACAAG CCTTAAGGGG TTGGGGGAGT TTGAAGACG AATTGCTAGG GTTAAAGAAC 360
ACGCTTAAAA ACTTACCCCT ATACCAAAACC CTAAAAACCA AACCCAAAAA AATTAACGCC 420
CCCATTGCGG TGGTGGGTAA TGGGCCAAGC CTGGATTAT TGTAGATTT TTTAAAGAA 480
AATGAAGAAA AATTCATCAT TTTTCATGCG GGAACCGCTT TAAAGCCTTT AAAAGCGCAT 540
GGCGTTAAAG TGGATTTTCA AATAGAAGTG GAGCGCATAG ACTATCTTAA GGAGGTTTTA 600
GAAAGAGCCC CCCTAGAAGA CACCCCTTA ATGGGCGCTA ACATGCTCAA TCCTAACGCT 660
TTTGATTTAG CCAAAGAAGC GTTGATGTTT ATGCGTGGGG GGAGCGCTTG CGCAGTA 717

```

SUBSTITUTE SHEET (RULE 26)

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 867 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375

```

ATGCTGGCGT TTTTAAAAAC CCCTAGAAAC AGCGCTTTTG CTTGGGTYT TTTCGTGGGG      60
GCGTTATTGT TTTACTGGTG CGCTTTAAGG CTTTCGCATT CGGATTTTAC YTATTTATTG      120
CCCTTAATCA TTGTTTTAGT AGCGTTAGTT TATGGGGTTT TATTTTATTT GTTGCTCTAT      180
TTTGAAAACC CCTACTTCAG GCTTTTGAGT TTTTTAGGCT CTAGTTTAT CCACCCTTTT      240
GGATTGATT GGTAGTCCC GGATAGCTTT TTTTCTTATA GCGTGTTTAG GGTGGATAAA      300
TTATCTTTAG GGCTTATTTT TTAGCTTGC ATTTTITTGA GCGCTCAAAA TCTTAAAAAA      360
TACAGAATGA TAGGGGTTTT ATTGCTGCTT GCGCGTTTGG ATTTTCATTT TTTTAAAAATA      420
AGCGATTAA AAGAGGTTGG AAATATTGAA TTAGTCTCTA CAAGAACGCC CCAAGATTG      480
AAATTGACT CAAATTACCT TAATAATATT GAAAACAACA TTCTTAAAGA AATCAAACCTC      540
GCTCAAAGCA AGCAAAAAAC CTTGATTGTT TTTCCAGAGA CCGCTTACCC TATCGCTTTA      600
GAAAACCTCC CTTTAAAAAC CCAACTAGAA GATTTAAGCG ACAAGATCGC CATTTTAATA      660
GGGACATTGC GCGCTCARGG CTATAGCCTT TATAACAGCT CGTTTTTATT TTCTAAAAAA      720
AGCGTTCAAA TCGCTGATAA AGTGATCTTA GCCCCCTTTG GCGAGATAAT GCCTTTACCG      780
GAGTTTCTTC AAAAACCCCT TGAAAAGCTC TTTTITGCGA GAGCGCTTAT TTATACCGCA      840
ACGCTCCCCA TTTCAGCGAT TTTACAT

```

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376

317

ATGAACGATC	CTAAGCATGT	GGTGTATGTT	TGGCTGGACG	CTTTATTGAA	TTATGCGAGC	60
GCGTTAGGGT	ATTTGAACGG	TTTAGACAAT	AAAATGGCGC	ATTTTGAACG	CGCTAGGCAT	120
ATTGTGGGTA	AGGATATTTT	ACGCTTCCAT	GCCATTTATT	GGCCAGCCTT	TTTGATGAGT	180
TTGAATTTGC	CCTTATTCAA	ACAGCTCTGT	GTGCATGGGT	GGTGGACGAT	AGAGGGCGTG	240
AAAATGAGTA	AGAGCTTGGG	TAATGTTTTA	GACGCTCAAA	AGCTCGCCAT	GGAGTATGGG	300
ATTGAAGAAT	TACGCTATTT	TTTATTGCGT	GAGGTGCCTT	TTGGGCAAGA	TGGGGATTTT	360
TCTAAAAAAG	CGTTAGTAGA	ACGGATTAAT	GCGAATTTGA	ATAACGATTT	GGGGAATTTG	420
TTGAATCGTT	TGCTAGGCAT	GGCTAAAAAG	TATTTCAATT	ATTCTCTAAA	AAGCACCAAA	480
ATCACTGCGT	ATTATCCTAA	AGAGCTAGAA	AAAGCACATC	AAATTTTAGA	TAACGCTAAT	540
TCTTTTGTGC	CTAAAATGCA	ATTGCATAAG	GCTTTAGAGG	AATTGTTTAA	TATTTATGAT	600
TTTTTTGAATA	AATCATCGC	TAAAGAAGAG	CCGTGGGTCT	TGCACAAAAA	CAACGAATCA	660
GAAAAATTAG	AAGCCTTATT	GAGTTTGATC	GCAAACACGC	TACTACAATC	AAGCTTCTTG	720
CTCTATGCGT	TCATGCCAAA	GAGCGCTATG	AAATTAGCGA	GCGCTTTTCG	TGTAGAAATC	780
ACGCCCAATA	ATTACGAACG	CTTTTTTAAG	GCTAAAAAAT	TACAAGATAT	GTTTTTACAA	840
GACACCGAGC	CTTTATTTTC	CAAAATTGAG	AAAATTGAAA	AGATTGAAAA	GATTGAAAAG	900
ATTGAAAAGA	TTGAAAAAGG	GGAGGAAGCC	CTAGCAGAAA	AAGCAGAAAA	AAAAGAAAAA	960
GAAAAAGCCC	CACCAACACA	AGAAAATTAT	ATTAGTATTG	AGGATTTCAA	GAAAGTAGAG	1020
ATTAAAGTGG	GGCTTATCAA	AGAAGCTCAA	AGGATTGAAA	AATCCAATAA	ATTACTGCGC	1080
TTAAAGTGG	ATTTAGGCGA	AAATCGTTTG	AGGCAGATCA	TCTCAGGGAT	CGCTTTGGAT	1140
TATGAGCCTG	AAAGCTTGGT	GGGTCAAATG	GTGTGCGTGG	TGGCTAATTT	AAAACCCGCA	1200
AAGCTTATGG	GTGAAATGAG	TGAGGGCATG	ATTTTAGCGG	TGCAGATAA	TGATAATCTG	1260
GCTTTAATCA	GCCCTACCAG	AGAAAAAATT	GCAGGAAGTT	TGATCAGC		1308

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377

ATGAACGAC	CGATCAGCAA	ATTGAAACAA	AACTTTTITAC	AATTCAAACA	TTCTTTCAAC	60
AAACATTTAG	ATAAGTACAG	CCTTTATTAT	AGGCTGTTCA	ATATCAGCTC	TATCGTTATA	120
GGTTTTTTAA	TAGCGCTTTT	TTCTTATGGG	GCAGGGGTGA	TTTTAGTTTA	TCCAATATTA	180
TTCTTGTTTG	CTCTTATAAT	AAAACCTAGC	TTTTTTTATT	ACACTACTTA	TCTTTTGCTA	240
CTCGTTTCTC	TCAGCATAAT	AAGCAAATAC	TATCTCCTAA	GCCACGCAAA	TTTCACAATG	300
AAGCTAATCA	TGCTTATGAC	TCAATGGCAA	AATTGGTTCT	TA		342

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

318

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...5
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:378

ATGGG

5

(2) INFORMATION FOR SEQ ID NO:379:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...381
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:379

GTGTTCACTT ATTCCTTGGG GCAGGTTTTC TTTTCTCTAA GTATCGGTTT AGGGATCAAT	60
ATCACTTATG CTGCCGTTAC GGATAAAACG CAGAATTTGC TTAAAGCAC GATTGGGTG	120
GTTTTATCAG GRATTTTAAAT TTCTCTTG TG RCAGGGCTTA TGATTTTCAC TTTTGTGTTT	180
GAATATGGGG CTAATGTCTC ACAAGGCACA GGGTTAATCT TCACTTCITT ACCGGTGGTT	240
TTTGCCCAA TGGGAGCGAT AGGCGTTCCT TGTTTCAATT CTTTCTTGC TCGCGCTCGC	300
TTTGCTGGC ATCACTTCTA CCGTGCTTT ATTAGAGCCA AGCGTGATGT ATCTTACCGA	360
AAAGTATCAA TACTCTCGTT T	381

(2) INFORMATION FOR SEQ ID NO:380:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 537 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

319

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...537

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380

ATGAAACCAT	TGCATTTTTC	ACACCTGGAC	AGAGAGCAAT	CAGGCGATGT	GGGTTTTATC	60
ATTAAAAACC	TTATTTTTTT	AGGGGTTTTT	TCCTTATTGG	GTTGGTTGAA	TACCGAGTAT	120
TTTCTATGGC	CTAGCATGCT	GGAATTAAAA	AAAATCCTTT	TAGAAGAAAA	TCGTAAAAAA	180
AGCGTTTTAG	AATACGCGCA	AAGGCATTTT	GAAACAGCCC	TAGCAAACTA	CCGCAATCAA	240
AAAGAAACCA	GCGAATCTTT	GTTAAAGATT	TTTAATGATG	AAGAGTCCAG	GCGGATTTTA	300
GAAGAGATCT	TAAAAAAATG	TTTTGACGCC	TATAAAATCA	AACCCTTGCT	CTCTCAAAAC	360
CCCTCCCAAA	AAACCCAATT	TTTTATCATG	GCTAGAGCGA	GCGAATTGGA	AAAAACTTAT	420
CTTTTTTTCA	CCTTAATCAA	CAAGTATTTA	CCGAGCGCTC	AAAGCCAATT	GCCCTTAAAG	480
ATTTCTAAAG	ATAGCGACGG	GTTGTTGGTG	CAATTTGGCG	TGAGTATTGA	TCTCCAA	537

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381

ATGAATGCAT	TGAAGCGTGC	GTGTTTAAGA	TGATGGGCG	AAACCAATAC	CGATGATTTA	60
ASCCCARYGA	GCGACGCTTT	CACACGGAGC	GATATTCCTT	TACACGCCAA	AGCCATGCTA	120
AAAAACCGGA	TTGAAAATTA	CGAACAACGC	ATTGAAGCCA	TTAAACTAA	AGGCGTTCCT	180
GTAGCGTATG	TGGGCGATGT	GGTTGGCACA	GGAAGCTCTA	GAAAAAGCGC	GACTAACTCT	240
ATCATGTGGC	ATTTTGTGTA	GGACATTCCCT	TTTGTGCCTA	ATAAAAGGAG	TGGAGGCATT	300
GTGATTGGGG	GGGTGATCGC	TCCGATTTTC	TTTGC GACTT	GTGAAGATAG	CGGGGCGTTA	360
CCCATTGTGG	CTGATGTTAA	GGATTTGAAA	GAGGGCGATA	TCATTAAAT	CTACCCTTAT	420
AAAGGCGAAA	TCACGCTGAA	CGATAAGGTG	GTTAGCACCT	TTAAGCTAGA	GCCTGAAACT	480
TTATTAGATG	AAGTCAGGGC	TTCTGGGCGT	ATCCCTTAA	TCATTGGTAG	GGGTTTGACC	540
AATAAAGCGC	GTAAATTTTT	GGGCCGGCGA	ATCGGAAGCG	TTCAAAAAAC	CTTCCGCCCC	600
TCAAGCGCGC	TAAGGCTACA	CTTTGCC				627

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

320

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382

ATGCTTTCAG	CCCACCAACC	TTTTAAAAAT	TACCCTGATC	TGATTAAAAA	AGAGTTGCAA	60
GAGCATAACG	CCTATGCGAG	CGTCGCTAGT	GGGGTGCCAG	CGATGTGTGA	TGGTATCAGC	120
CAAGGTTATG	AGGGAATGGA	ATTGAGCTTG	TTTAGTAGAG	ATGTGATCGC	ATTAAGCACC	180
SCCGTAGGGT	TAAGCCATAA	TGTTTTTGAC	GGGGCGTTTT	TTTTGGGCGT	GTGCGATAAA	240
ATTGTGCCAG	GCTTGCTCAT	AGGAGCGTTA	AGCTTTGGGA	ATTTAGCGAG	CGTGTTTGTG	300
CCAAGCGGGC	CTATGGTGAG	CGGGATAGAA	AATTATAAAA	AAGCCAAAGC	GCGCCAAGAT	360
TTTGCAATGG	GAAAGATCAA	CAGAGAAGAG	CTTTTAAAAG	TGGAAATGCA	AAGCTATCAT	420
GATGTGGGCA	CTTGCACTTT	TTATGGCAGC	GCTAATTCTA	ATCAAATGAT	GATGGAGTTT	480
ATGGGGTTGC	ATGTGGGCCAA	TTCTAGCTTT	ATCAACCCTA	ACAACCCCTT	ACGAAAGGTT	540
TTAGTAGAAG	AGAGCGCTAA	AAGATTAGCG	AGCGGGAAAG	TCCTGCCTTT	AGCCAAACTC	600
ATTGATGAAA	AAAGCATCTT	TAACGCTCTT	ATAGGCTTAA	TGGCAACAGG	GGGTTCTACT	660
AACCACACTT	TGCATTTGAT	CGCTATCGCA	GATCTTGTGG	GG		702

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 795 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383

ATGAAATTTT	TAAAAATCTT	TGCCAGTAGC	GTAACCTAG	ATGAAAAATT	TTTAATGTTT	60
CTTCTTTGCA	ACGCTCTTTC	TAACGCTTAC	AAAAATAGCG	ATTGTTTTTC	TTTCTCTAAA	120
GGCTTTTATG	GCGCTTTTTT	AATCGGGTTT	GTGGTGTATT	ATGGTTGCGC	GCTAATCCCT	180
AAAAAACGCT	TGAAATATTC	ATTAGAATGG	CTGTTTATAG	GAAGCGGTAT	TATTTTTAGC	240
GTGGCAGAAA	TTTTTACGCT	GTTTATGTTT	AAAATGCCTT	TTTCCAAAGG	CTTGATTGAC	300
ACGCTTTTAT	CCACAAACAG	CTCTGAAACG	ATGGCGTTTA	TAAAAAGCTA	TAAAAATTAT	360
TTGCTTTACT	ACGCTTTGAT	TTTGATCGCT	TTGTTGATCG	CCATTAAAAT	CATTGCTTTT	420
AGAGCGCTTG	TGCCTGGTGT	GATAGCGAGC	GTTTTAGGGC	TTTCTATCCT	TACAATAGGG	480
AGCGTTTCGT	ACATTAAACA	CCTTACAAAG	AACGATGCGA	TTTTAAAAAG	ATCACTCTTT	540
TCTCTTTCTT	TAGCTAGGGG	GTTTTATTCC	GCTTATTTGA	GTTTGTTTGA	TCGCCAACAA	600
GCCATAAAAT	TTATAGCTTT	TTTAAATAAT	CTTTATTTAC	CAAGCGATTA	TCTTTCTAGC	660
ACGGGCGATA	TTTCAAATGT	CGTCTTAGTC	ATCGCGAAAG	CGCGAGCAGA	AATTTTCATGC	720
AACCTATATG	CTATAGCGTT	CCTAATAATC	CCTTATSCGA	GCGAACTCGC	CAACGAGAGA	780
GAGAGAGAGA	GAGAG					795

(2) INFORMATION FOR SEQ ID NO:384:

321

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384

```

Met Cys Ser Gln Glu Ile Leu Ser Ser Leu Gln Thr Ile Ile Ala Glu
1      5      10      15
Gln Phe Ser Ile Asn Ile Ile Thr Gln Leu Ala Asn Lys Leu Thr Gln
      20      25      30
Val Lys Asn Leu Asn Phe Phe Glu Asn Lys Asp His Thr Ile Lys Leu
      35      40      45
Asn Thr Ile His Asn Gly Leu His Ile Arg Pro Leu Asn Tyr Val Ser
      50      55      60
Asn Leu Phe Phe Asn Leu Gln Arg Ile Ile Gly Leu Ile Ser Leu Phe
      65      70      75      80
Gly Ile Leu Phe Ser Ile Ser Ile Tyr Leu Pro Phe Ile Met Ile Phe
      85      90      95
Ala Thr Val Pro Cys Ile Leu Ile Ser Asn His Ile Ala Lys Lys His
      100     105     110
Ser Ala Ser Ile Asp Lys Leu Gln Asp Gln Lys Glu Ser Met Gln Asn
      115     120     125
Tyr Leu Tyr Ser Gly Leu Asp Asn Gln Lys Asn Lys Asp Asn Leu Leu
      130     135     140
Phe Asn Phe Met Leu Asn Phe His His Lys Phe Ile Glu Thr Lys Glu
      145     150     155     160
Leu Tyr Leu Asn Asn Phe Val Lys Val Ala Gln Lys Asn Leu Ile Phe
      165     170     175
Thr Ile Tyr Ala Asp Val Leu Ile Thr Thr Leu Ser Ile Ala Leu Phe
      180     185     190
Phe Leu Met Val Phe Ile Ile Leu Ser Lys Leu Ile Gly Val Gly Ala
      195     200     205
Ile Ala Gly Tyr Ile Gln Ala Phe Ser Ser Thr Gln Gln Gln Leu Gln
      210     215     220
Asp Leu Ser Phe Tyr Gly Lys Trp Phe Phe Ala Ile Asn Lys Tyr Phe
      225     230     235     240
Glu Asn Tyr Phe Cys Ile Leu Asp Tyr Lys Ile Pro Lys Pro Glu Thr
      245     250     255
Gln Ile Lys Leu Glu Glu Lys Ile His Ser Ile Thr Phe Glu Asn Ile
      260     265     270
Ser Phe Ser Tyr Pro Asn Ser Lys Leu Ile Phe Glu Asn Phe Asn Leu
      275     280     285
Ser Leu His Ser Asn Lys Ile Tyr Ala Leu Val Gly Lys Asn Ala Ser
      290     295     300
Gly Lys Ser Thr Leu Ile Asn Leu Leu Leu Gly Phe Tyr Thr Pro Asn
      305     310     315     320
Ser Gly Gln Ile Ile Ile Asn Asn Lys Tyr Pro Leu Gln Asp Leu Glu
      325     330     335
Leu Asn Ser Tyr His Gln Gln Met Ser Ala Ile Phe Gln Asp Phe Ser
      340     345     350
Leu Tyr Ala Gly Tyr Ser Ile Asp Asp Asn Leu Phe Met Gln Asn Asn
      355     360     365

```

322

```

Ile Thr Lys Glu Gln Leu Lys Gln Lys Arg Glu Ile Leu Lys Ser Phe
  370                      375                      380
Asp Glu Asn Phe Gln Asn Cys Leu Asn Asp Cys Asn Asn Thr Leu Phe
385                      390                      395                      400
Gly Ala Gln Tyr Asn Gly Val Asp Phe Ser Leu Gly Gln Lys Gln Arg
                      405                      410                      415
Ile Ala Thr Met Arg Ala Phe Leu Lys Pro Ser Asn Cys Ile Val Leu
                      420                      425                      430
Asp Glu Pro Ser Ser Ala Ile Asp Pro Ile Met Glu Lys Glu Phe Leu
                      435                      440                      445
Asp Phe Ile Phe Lys Lys Ser Gln Ser Lys Met Ala Leu Ile Ile Thr
                      450                      455                      460
His Arg Met Asn Ser Val Lys Gln Ala Asn Glu Ile Ile Val Leu Asp
465                      470                      475                      480
Gln Gly Lys Leu Ile Glu Gln Gly Asn Phe Glu Thr Leu Met Lys Lys
                      485                      490                      495
Gln Gly Leu Phe Cys Glu Leu Phe Leu Lys Gln Gln Tyr
                      500                      505

```

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385

```

Met Lys Gly Pro Ile Leu Trp Pro Ala Phe Ser Gln Phe Ser Asp Gln
  1                      5                      10                      15
Asp Leu Ser Asp Ile Val Ala Tyr Leu Thr Ser Ile Leu Pro Lys Asn
                      20                      25                      30
Leu Ser Asp Lys Glu Val Phe Ala Gln Ser Cys Gln Arg Cys His Ser
                      35                      40                      45
Leu Asp Tyr Ala Lys Asp Lys Ala Phe Ser Asp Pro Lys Asp Leu Ala
50                      55                      60
Asn Tyr Leu Gly Ser His Ala Pro Asp Leu Ser Met Met Ile Arg Ala
65                      70                      75                      80
Lys Gly Glu His Gly Leu Asn Val Phe Ile Asn Asp Pro Gln Lys Leu
                      85                      90                      95
Leu Pro Gly Thr Ala Met Pro Arg Val Gly Leu Asn Glu Lys Ala Gln
100                      105                      110
Lys Gln Val Ile Ser Tyr Leu Glu Lys Ala Gly Asp Arg Lys Lys His
115                      120                      125
Glu Arg Asn Thr Leu Gly Ile Lys Ile Met Ile Phe Ala Val Leu
130                      135                      140
Ser Phe Leu Ala Tyr Ala Gly Lys Glu Lys Phe Gly Ala Lys Cys Ile
145                      150                      155                      160
Lys Phe Lys Lys Gly Gly Thr Trp Phe Tyr Asp Phe
                      165                      170

```

(2) INFORMATION FOR SEQ ID NO:385:

SUBSTITUTE SHEET (RULE 26)

323

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385

```

Met Lys Gly Pro Ile Leu Trp Pro Ala Phe Ser Gln Phe Ser Asp Gln
1           5           10           15
Asp Leu Ser Asp Ile Val Ala Tyr Leu Thr Ser Ile Leu Pro Lys Asn
20           25           30
Leu Ser Asp Lys Glu Val Phe Ala Gln Ser Cys Gln Arg Cys His Ser
35           40           45
Leu Asp Tyr Ala Lys Asp Lys Ala Phe Ser Asp Pro Lys Asp Leu Ala
50           55           60
Asn Tyr Leu Gly Ser His Ala Pro Asp Leu Ser Met Met Ile Arg Ala
65           70           75           80
Lys Gly Glu His Gly Leu Asn Val Phe Ile Asn Asp Pro Gln Lys Leu
85           90           95
Leu Pro Gly Thr Ala Met Pro Arg Val Gly Leu Asn Glu Lys Ala Gln
100          105          110
Lys Gln Val Ile Ser Tyr Leu Glu Lys Ala Gly Asp Arg Lys Lys His
115          120          125
Glu Arg Asn Thr Leu Gly Ile Lys Ile Met Ile Phe Phe Ala Val Leu
130          135          140
Ser Phe Leu Ala Tyr Ala Gly Lys Glu Lys Phe Gly Ala Lys Cys Ile
145          150          155          160
Lys Phe Lys Lys Gly Gly Thr Trp Phe Tyr Asp Phe
165          170

```

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386

```

Met Glu Arg Lys Thr Leu Gln Ser Ile Leu Cys Leu Ile Lys Lys Glu
1           5           10           15

```

324

```

Met Met Arg Pro Lys Gly Ile Leu Met Asn Cys Cys Arg Thr Trp Lys
      20      25      30
His Gln Val Leu Lys Gln Ser Thr Thr Gly Leu Val Val Leu Ser Ile
      35      40      45
Ile Ser Ser Thr Ala Pro Phe Ile Gly Leu Phe Gly Thr Val Val Glu
      50      55      60
Ile Leu Glu Ala Phe Asn Asn Leu Gly Ala Leu Gly Gln Ala Ser Phe
      65      70      75      80
Gly Val Ile Ala Pro Ile Ile Ser Lys Ala Leu Ile Ala Thr Ala Ala
      85      90      95
Gly Ile Leu Ala Ala Ile Pro Ala Tyr Ser Phe Tyr Leu Ile Leu Lys
      100      105      110
Arg Lys Val Tyr Asp Leu Ser Val Tyr Val Gln Met Gln Val Asp Ile
      115      120      125
Leu Ser Ser Lys Lys
      130

```

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387

```

Met His Glu Arg Ile Glu Arg Gly Ile Unk Asn Asn Glu Cys Lys Glu
1      5      10      15
Ile Phe Gly Asn Glu Leu Lys Gln Arg Lys Thr Lys Leu Ile Glu Asp
      20      25      30
Ile Glu Arg Arg Phe Lys Glu Cys Glu Glu Gln Phe Arg Gly Ser Val
      35      40      45
Gly Lys Asn Ile Glu Gln Leu Glu Glu Arg Val Lys Asp Ser Leu Ala
      50      55      60
Ile Ile Lys Arg Ile Asn Asn Leu Gly Leu Asn Pro Asn Ser Asn Phe
      65      70      75      80
Asn Met Asp Ser Gly Ile Asp Thr Ile Gly Leu Phe Ser Ser Ile Gly
      85      90      95
Gly Leu Val Leu Leu Leu Leu Thr Pro Val Val Gly Glu Phe Ala Leu
      100      105      110
Ile Ala Gly Val Gly Leu Ala Leu Val Gly Val Gly Lys Ser Ile Trp
      115      120      125
Ser Phe Phe Asp Ser Asp Tyr Lys Lys Ser Gln Gln Arg Lys Glu Val
      130      135      140
Asp Lys Asn Leu His Gln Ile Cys Glu Lys Leu Cys Arg Met
      145      150      155

```

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid

325

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388

```

Met Pro Gly Val Tyr Gln Met Ser Ile Glu Pro Leu Leu Lys Glu Cys
1          5          10          15
Glu Glu Leu Val Gly Leu Gly Ile Lys Ala Val Leu Leu Phe Gly Ile
20          25          30
Pro Lys His Lys Asp Ala Thr Gly Ser His Ala Leu Asn Lys Asp His
35          40          45
Ile Val Ala Lys Ala Thr Arg Glu Ile Lys Lys Arg Phe Lys Asp Leu
50          55          60
Ile Val Ile Ala Asp Leu Cys Phe Cys Glu Tyr Thr Asp His Gly His
65          70          75          80
Cys Gly Ile Leu Glu Asn Ala Ser Val Ser Asn Asp Lys Thr Leu Lys
85          90          95
Ile Leu Asn Leu Gln Gly Leu Ile Leu Leu Lys Ala Val Trp Ile Phe
100          105          110

```

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389

```

Val Glu Asn Asn Lys Ser Leu Lys His Ala Asn Glu Leu Arg Asp Lys
1          5          10          15
Arg Asp Glu Leu Glu Phe His Leu Arg Glu Leu Phe Gly Gly Asn Val
20          25          30
Phe Lys Ser Ser Ile Lys Thr His Ser Leu Thr Asp Lys Asp Ser Ala
35          40          45
Asp Phe Asp Glu Ser Tyr Asn Leu Asn Ile Gly His Gly Unk Asn Unk
50          55          60
Ile
65

```

(2) INFORMATION FOR SEQ ID NO:390:

SUBSTITUTE SHEET (RULE 26)

326

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390

```

Met Gln Glu Phe Ser Leu Trp Cys Asp Phe Ile Glu Arg Asp Phe Leu
1           5           10           15
Glu Asn Asp Phe Leu Lys Leu Ile Asn Lys Gly Ala Ile Cys Gly Unk
          20           25           30
Thr Ser Asn Pro Ser Leu Phe Cys Glu Ala Ile Thr Lys Ser Ala Phe
        35           40           45
Tyr Gln Asp Glu Ile Ala Lys Unk Gln Arg Gln Lys Ser
50           55           60
  
```

(2) INFORMATION FOR SEQ ID NO:390:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390

```

Met Gln Glu Phe Ser Leu Trp Cys Asp Phe Ile Glu Arg Asp Phe Leu
1           5           10           15
Glu Asn Asp Phe Leu Lys Leu Ile Asn Lys Gly Ala Ile Cys Gly Unk
          20           25           30
Thr Ser Asn Pro Ser Leu Phe Cys Glu Ala Ile Thr Lys Ser Ala Phe
        35           40           45
Tyr Gln Asp Glu Ile Ala Lys Unk Gln Arg Gln Lys Ser
50           55           60
  
```

(2) INFORMATION FOR SEQ ID NO:391:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 619 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

327

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391

```

Val Phe Val Ala Ser Lys Gln Ala Asp Glu Gln Lys Lys Leu Val Ile
1      5      10      15
Glu Gln Glu Val Gln Lys Arg Gln Phe Gln Lys Ile Glu Glu Leu Lys
20      25      30
Ala Asp Met Gln Lys Gly Val Asn Pro Phe Phe Lys Val Leu Phe Asp
35      40      45
Gly Gly Asn Arg Leu Phe Gly Phe Pro Glu Thr Phe Ile Tyr Ser Ser
50      55      60
Ile Phe Ile Leu Phe Val Thr Ile Val Leu Ser Val Ile Leu Phe Gln
65      70      75      80
Ala Tyr Glu Pro Val Leu Ile Val Ala Ile Val Ile Val Leu Val Ala
85      90      95
Leu Gly Phe Lys Lys Asp Tyr Arg Leu Tyr Gln Arg Met Glu Arg Ala
100     105     110
Met Lys Phe Lys Lys Pro Phe Leu Phe Lys Gly Val Lys Asn Lys Ala
115     120     125
Phe Met Ser Ile Phe Ser Met Lys Pro Ser Lys Glu Met Ala Asn Asp
130     135     140
Ile His Leu Asn Pro Asn Arg Glu Asp Arg Leu Val Ser Ala Ala Asn
145     150     155     160
Ser Tyr Leu Ala Asn Asn Tyr Glu Cys Phe Leu Asp Asp Gly Val Ile
165     170     175
Leu Thr Asn Asn Tyr Ser Leu Leu Gly Thr Ile Lys Leu Gly Gly Ile
180     185     190
Asp Phe Leu Thr Thr Ser Lys Lys Asp Leu Ile Glu Leu His Ala Ser
195     200     205
Ile Tyr Ser Val Phe Arg Asn Phe Val Thr Pro Glu Phe Lys Phe Tyr
210     215     220
Phe His Thr Val Lys Lys Lys Ile Val Ile Asp Glu Thr Asn Arg Asp
225     230     235     240
Tyr Gly Leu Ile Phe Ser Asn Asp Phe Met Arg Ala Tyr Asn Glu Lys
245     250     255
Gln Lys Arg Glu Ser Phe Tyr Asp Ile Ser Phe Tyr Leu Thr Ile Glu
260     265     270
Gln Asp Leu Leu Asp Thr Leu Asn Glu Pro Val Met Asn Lys Lys His
275     280     285
Phe Ala Asp Asn Asn Phe Glu Phe Gln Arg Ile Ile Arg Ala Lys
290     295     300
Leu Glu Asn Phe Lys Asp Arg Ile Glu Leu Ile Glu Glu Leu Leu Ser
305     310     315     320
Lys Tyr His Pro Thr Arg Leu Lys Glu Tyr Thr Lys Asp Gly Ile Ile
325     330     335
Tyr Ser Lys Gln Cys Glu Phe Tyr Asn Phe Leu Val Gly Met Asn Glu
340     345     350
Ala Pro Phe Ile Cys Asn Arg Lys Asp Leu Tyr Leu Lys Glu Lys Met
355     360     365
His Gly Gly Val Lys Glu Val Tyr Phe Ala Asn Lys His Gly Lys Ile
370     375     380
Leu Asn Asp Asp Leu Ser Glu Lys Tyr Phe Ser Ala Ile Glu Ile Ser
385     390     395     400
Glu Tyr Ala Pro Lys Ser Gln Ser Asp Leu Phe Asp Lys Ile Asn Ala
405     410     415

```

328

```

Leu Asp Ser Glu Phe Ile Phe Met His Ala Tyr Ser Pro Lys Asn Ser
      420      425      430
Gln Val Leu Lys Asp Lys Leu Ala Phe Thr Ser Arg Arg Ile Ile Ile
      435      440      445
Ser Gly Gly Ser Lys Glu Gln Gly Met Thr Leu Gly Cys Leu Ser Glu
      450      455      460
Leu Val Gly Asn Gly Asp Ile Thr Leu Gly Ser Tyr Gly Asn Ser Leu
465      470      475      480
Val Leu Phe Ala Asp Ser Phe Glu Lys Met Lys Gln Ser Val Lys Glu
      485      490      495
Cys Val Ser Ser Leu Asn Ala Lys Gly Phe Leu Ala Asn Ala Ala Thr
      500      505      510
Phe Ser Met Glu Asn Tyr Phe Phe Ala Lys His Cys Ser Phe Ile Thr
      515      520      525
Leu Pro Phe Ile Phe Asp Val Thr Ser Asn Asn Phe Ala Asp Phe Ile
      530      535      540
Ala Met Arg Ala Met Ser Phe Asp Gly Lys Glu Asp Asn Asn Ala Trp
545      550      555      560
Gly Asn Ser Val Met Thr Leu Lys Ser Glu Ile Asn Ser Pro Phe Tyr
      565      570      575
Leu Asn Phe His Met Pro Thr Asp Phe Gly Ser Ala Ser Ala Gly His
      580      585      590
Thr Leu Ile Leu Gly Ser Thr Gly Ser Gly Lys Asn Ser Val Tyr Val
      595      600      605
His Asp Ser Lys Arg Tyr Gly Ala Ile Cys Leu
      610      615

```

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392

```

Val Lys Thr Ser Cys Leu Val Thr Ile Gly Arg Ile Arg Gly Val Phe
1      5      10      15
Ile Ile Lys Ala Gln Leu Leu Leu Arg Glu Gly Gly Phe Met Asn Phe
      20      25      30
Thr Ala Tyr Asn Thr Lys Thr Pro Gly His Leu His Leu Tyr Val His
      35      40      45
Lys Gly His Thr Glu Leu Gly Glu Gly Glu Arg Leu Ile Lys Thr Leu
      50      55      60
Ser Met Lys Leu Ala Gln Gly Leu Pro Lys Glu Trp Arg Val Phe Pro
65      70      75      80
Ser Asn Glu Trp Pro Lys Glu Phe Asn Ile Leu Ala Leu Pro Tyr Glu
      85      90      95
Val Phe Ala Lys Glu Arg Gly Ser Ser Trp Ala Lys His Leu
      100      105      110

```

(2) INFORMATION FOR SEQ ID NO:393:

329

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...68

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393

```

Val Ala Lys Asp Ile Ile Ser Glu Ser Gln Asn Leu Cys Ala Arg Lys
1          5          10          15
Phe Arg Arg Leu Tyr Ala Leu Leu Lys Glu Asn Glu Met Leu Ile Arg
          20          25          30
Ile Gly Ser Tyr Gln Met Gly Asn Asp Lys Glu Leu Asp Glu Ala Ile
          35          40          45
Lys Lys Lys Ala Leu Met Glu Gln Phe Leu Val Gln Asp Glu Asn Ala
50          55          60
Leu Unk Ala Phe
65

```

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394

```

Met Lys Ser Arg Pro Ile Leu Ala Gln Ala Tyr Ala Leu Gln Met Met
1          5          10          15
Val Lys Gln Ile Ala Phe Leu Glu Thr Ile Leu Val Glu Asn Glu Gln
          20          25          30
Asp Ala Leu Ile Leu Glu Asn Ser Leu Ile Lys Gln Leu Lys Pro Lys
          35          40          45
Tyr Asn Ile Leu Leu Arg Asp Asp Lys Thr Tyr Pro Tyr Ile Tyr Met
50          55          60
Asp Phe Ser Ile Asp Phe Pro Ile Pro Leu Ile Thr Arg Lys Ile Leu
65          70          75          80
Lys Gln Pro Gly Val Lys Tyr Phe Gly Pro Phe Thr Ser Gly Ala Lys
          85          90          95
Asp Ile Leu Asp Ser Leu Tyr Glu Leu Leu Pro Leu Val Gln Lys Lys
100          105          110

```

330

```

Asn Cys Ile Lys Asp Lys Lys Ala Cys Met Phe Tyr Gln Ile Glu Arg
  115      120      125
Cys Lys Ala Pro Cys Glu Asp Lys Ile Thr Lys Glu Glu Tyr Leu Lys
  130      135      140
Ile Ala Lys Glu Cys Leu Glu Met Ile Glu Asn Lys Asp Arg Leu Ile
  145      150      155      160
Lys Glu Leu Glu Leu Lys Met Glu Arg Leu Ser Ser Asn Leu Arg Phe
      165      170      175
Glu Glu Ala Leu Ile Tyr Arg Asp Arg Ile Ala Lys Ile Gln Lys Ile
      180      185      190
Ala Pro Phe Thr Cys Met Asp Leu Ala Lys Leu Tyr Asp Leu Asp Ile
      195      200      205
Phe Ala Phe Tyr Gly Gly Asn Asn Lys Ala Val Leu Val Lys Met Phe
  210      215      220
Met Arg Gly Gly Lys Ile Ser Ser Ala Phe Glu Lys Ile His Ser
  225      230      235      240
Leu Asn Gly Phe Asp Thr Asp Glu Ala Met Lys Gln Ala Ile Ile Asn
      245      250      255
His Tyr Gln Ser His Leu Pro Leu Met Pro Glu Gln Ile Leu Leu Ser
      260      265      270
Ala Cys Ser Asn Glu Thr Leu Lys Glu Leu Gln Glu Phe Ile Ser His
      275      280      285
Gln Tyr Ser Lys Lys Ile Ala Leu Ser Ile Pro Lys Lys Gly Asp Lys
  290      295      300
Leu Ala Leu Ile Glu Ile Ala Met Lys Asn Ala Gln Glu Ile Phe Ser
  305      310      315      320
Gln Glu Lys Thr Ser Asn Glu Asp Arg Ile Leu Glu Glu Ala Arg Ser
      325      330      335
Leu Phe Asn Leu Glu Cys Val Pro Tyr Arg Val Glu Ile Phe Asp Thr
      340      345      350
Ser His His Ser Asn Ser Gln Cys Val Gly Gly Met Val Val Tyr Glu
      355      360      365
Asn Asn Ala Phe Gln Lys Asp Ser Tyr Arg Arg Tyr His Leu Lys Gly
  370      375      380
Ser Asn Glu Tyr Asp Gln Met Ser Glu Leu Leu Thr Arg Arg Ala Leu
  385      390      395      400
Asp Phe Ala Lys Glu Pro Pro Pro Asn Leu Trp Val Ile Asp Gly Gly
      405      410      415
Arg Ala Gln Leu Asn Ile Ala Leu Glu Ile Leu Lys Ser Ser Gly Ser
      420      425      430
Phe Val Glu Val Ile Ala Ile Ser Lys Glu Lys Arg Gly Phe
      435      440      445

```

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395

Val Ser Leu Gly Ala Phe Gln Gly Tyr Tyr Gly Gly Leu Val Asp Leu

331

```

1           5           10           15
Val Gly Gln Arg Leu Ser Glu Ile Trp Ser Ala Ile Pro Met Leu Phe
                20           25           30
Leu Leu Ile Val Ile Ser Ser Ala Phe Asn Ser Asn Phe Trp Ile Ile
                35           40           45
Leu Phe Leu Val Leu Leu Phe Ser Trp Met Gly Leu Ser Gln Val Val
                50           55           60
Arg Thr Glu Phe Leu Lys Ala Arg Asn Met Asp Tyr Thr Lys Ala Ala
65           70           75           80
Arg Ala Leu Gly

```

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396

```

Met Ser Glu Ala Tyr Phe Leu His His Lys Asn Ala Ser Gln Val Ser
1           5           10           15
Leu Asn Glu Gln Val Leu Asn Val Met Lys Gln Val Gln Leu Asp Glu
                20           25           30
Asn Phe Trp Asn Val Ser Leu Met
                35           40

```

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397

```

Val Ile Leu Ile Phe Ile Ile Val Val Glu Asp Gln Lys Gly Ile Phe
1           5           10           15
Pro Ile Ala Ala Ser Lys Arg Lys Ser Gln Ser Ser Val Ile Ile Glu
                20           25           30

```

SUBSTITUTE SHEET (RULE 26)

332

```

Asp Val Cys Phe Ser Lys Glu Asp Phe Val Glu Gly Ala Lys Ala Ile
   35           40           45
Glu Gly Leu Leu Lys Lys His Gly Phe Lys Asp Asn Gly Ile Ile Phe
   50           55           60
Gly His Ala Leu Ser Gly Asn Leu His Phe Val Val Thr Pro Ile Leu
   65           70           75           80
Glu Asn Glu Ala Glu Arg Lys Ala Phe Glu Asn Leu Val Ser Glu Met
           85           90           95
Phe Leu Met Val Ser Lys Ser Ser Gly Ser Ile Lys Ala Glu His Gly
           100          105          110
Thr Gly Arg Met Val Ala Pro Phe Val Glu Met Glu Trp Gly Glu Lys
           115          120          125
Ala Tyr Lys Ile His Lys Gln Ile Lys Glu Leu Phe Asp Pro Asn Gly
           130          135          140
Leu Leu Asn Pro Asp Val Ile Ile Thr Asn Asp Lys Glu Ile His Thr
           145          150          155          160
Lys Asn Leu Lys Ser Ile Tyr Pro Ile Glu Glu His Leu Asp Met Cys
           165          170          175
Met Glu Cys Gly Phe Cys Glu Arg Ile Cys Pro Ser Lys Asp Leu Ser
           180          185          190
Leu Thr Pro Arg Gln Arg Ile Val Ile His Arg Glu Val Glu Arg Leu
           195          200          205
Lys Glu Arg Val Ser His Gly His Asp Glu Asp Gln Val Leu Leu Asp
           210          215          220
Glu Leu Leu Lys Glu Ser Glu Tyr Leu Ala His Ala Thr Cys Ala Val
           225          230          235          240
Cys His Met Cys Ser Thr Leu Cys Pro Leu Gly Ile Asp Thr Gly Unk
           245          250          255
Ile Ala Leu Asn His Tyr Gln Lys Asn Pro Lys Gly Glu Lys Ile Ala
           260          265          270
Ser Lys Ile Leu Lys Ser His Ala Asn Asp His Lys Arg Gly Ser Phe
           275          280          285
Phe Phe Lys Unk Arg Phe Arg Gly Phe Lys Asn Ser
           290          295          300

```

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398

```

Met Lys Glu Lys Asn Phe Trp Pro Leu Gly Ile Met Ser Val Leu Ile
1           5           10           15
Phe Gly Leu Gly Ile Val Val Phe Leu Val Val Phe Ala Leu Lys Asn
           20           25           30
Ser Pro Lys Asn Asp Leu Val Tyr Phe Lys Gly His Asn Glu Val Asp
           35           40           45
Leu Asn Phe Asn Ala Met Leu Lys Thr Tyr Glu Asn Phe Lys Ser Asn
           50           55           60
Tyr Arg Phe Ser Val Gly Leu Lys Pro Leu Thr Glu Ser Pro Lys Thr

```

333

```

65          70          75          80
Pro Ile Leu Pro Tyr Phe Ser Lys Gly Thr His Gly Asp Lys Lys Ile
      85          90          95
Gln Glu Asn Leu Leu Asn Asn Ala Leu Ile Leu Glu Lys Ser Asn Thr
      100          105          110
Leu Tyr Ala Gln Leu Gln Pro Leu Lys Pro Ala Leu Asp Ser Pro Asn
      115          120          125
Ile Gln Val Tyr Leu Ala Phe Tyr Pro Ser Gln Ser Gln Pro Arg Leu
      130          135          140
Leu Gly Thr Leu Asp Cys Lys Asn Ala Cys Glu Pro Leu Lys Phe Asp
145          150          155          160
Leu Leu Glu Gly Asp Lys Val Gly Arg Tyr Lys Ile Leu Phe Lys Phe
      165          170          175
Val Phe Lys Asn Lys Glu Glu Leu Ile Leu Glu Gln Leu Leu Phe Leu
      180          185          190
Ser Ser Met Ala Cys Met Gly Ile Ser Ile Leu Lys Asn Ala Lys Ala
      195          200          205
Phe Phe Lys Tyr Lys Ile
210

```

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399

```

Met Pro Ile Lys Gly Ser Phe Leu Ala Arg Asn Arg Leu Val Ile Ala
1          5          10          15
Leu Thr Asp Ala Val Ile Ile Pro Gln Ala Asp Leu Lys Ser Gly Ser
      20          25          30
Met Ser Ser Ala Arg Leu Ala Gln Lys Tyr Gln Lys Pro Leu Phe Val
      35          40          45
Leu Pro Gln Arg Leu Asn Glu Ser Asp Gly Thr Asn Glu Leu Leu Glu
      50          55          60
Lys Gly Gln Ala Gln Gly Ile Phe Asn Ile Gln Asn Phe Ile Asn Thr
65          70          75          80
Leu Leu Lys Asp Tyr His Leu Lys Glu Met Pro Glu Met Lys Asp Glu
      85          90          95
Phe Leu Glu Tyr Cys Ala Lys Asn Pro Ser Tyr Glu Glu Ala Tyr Leu
      100          105          110
Lys Phe Gly Asp Lys Leu Leu Glu Tyr Glu Leu Leu Gly Lys Ile Lys
      115          120          125
Arg Ile Asn His Leu Val Val Leu Ala
130          135

```

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids

334

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400

```

Met Val Val Glu Leu Lys Asn Ile Glu Lys Ile Tyr Glu Asn Gly Phe
 1              5              10              15
His Ala Leu Lys Gly Val Asn Leu Glu Leu Lys Lys Gly Asp Ile Leu
      20              25              30
Gly Val Ile Gly Tyr Ser Gly Ala Gly Lys Ser Thr Leu Ile Arg Leu
      35              40              45
Ile Asn Cys Leu Glu Arg Pro Ser Ser Gly Glu Val Leu Val Asn Gly
      50              55              60
Val Asn Leu Leu Asn Leu Lys Pro Lys Glu Leu Gln Lys Ala Arg Gln
      65              70              75              80
Lys Ile Gly Met Ile Phe Gln His Phe Asn Leu Leu Ser Ala Lys Asn
      85              90              95
Val Phe Glu Asn Val Ala Phe Ala Leu Glu Ile Ala Arg Trp Glu Lys
      100             105             110
Thr Lys Ile Lys Ser Arg Val His Glu Leu Leu Glu Leu Val Gly Leu
      115             120             125
Glu Asp Lys Val His Phe Tyr Pro Lys Gln Leu Ser Gly Gly Gln Lys
      130             135             140
Gln Arg Val Ala Ile Ala Arg Ser Leu Ala Asn Cys Pro Asn Leu Leu
      145             150             155             160
Leu Cys Asp Glu Ala Thr Ser Ala Leu Asp Ser Lys Thr Thr His Ser
      165             170             175
Ile Leu Thr Leu Leu Ser Gly Ile Gln Lys Lys Phe Asp Leu Ser Ile
      180             185             190
Val Phe Ile Thr His Gln Ile Glu Val Val Lys Glu Leu Cys Asn Gln
      195             200             205
Met Cys Val Ile Ser Ser Gly Glu Ile Val Glu Arg Gly Ser Val Glu
      210             215             220
Glu Ile Phe Ala Asn Pro Lys His Ala Val Thr Lys Glu Leu Leu Gly
      225             230             235             240
Ile Lys Asn Glu His Ala Asp Gln Lys Ser Gln Asp Ile Tyr Arg Ile
      245             250             255
Val Phe Leu Gly Glu His Leu Asp Glu Pro Ile Ile Ser Unk Phe Unk
      260             265             270

```

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

SUBSTITUTE SHEET (RULE 26)

335

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401

```

Leu Unk Pro Met Lys Val Ile Gln Val Phe Leu Phe Ser Asn Pro Phe
1      5      10      15
Cys Ala Ile Val Pro Asn Thr Glu Pro Glu His Leu Glu His Tyr Asp
      20      25      30
His Asp Leu Glu Arg Phe Phe Phe Ala Tyr Lys Tyr Phe Leu Asp His
      35      40      45
Ala Gln Lys Arg Val Ile Tyr Lys Glu Asp Pro Phe Leu Lys Asn Tyr
      50      55      60
Ser Lys Asp Ala Ile Val Leu Glu Lys Lys Asp Ile Tyr Asn Ile Gln
      65      70      75      80
Tyr Ile Leu Lys Asp Gly Glu Pro Tyr Thr Ser Phe Glu Leu Lys Asn
      85      90      95
Leu Gly Ala Phe Leu Val Trp Gly Leu Gly Glu His Asn Ala Thr Asn
      100      105      110
Ala Ser Leu Ala Ile Leu Ser Ala Leu Asp Glu Leu Asn Leu Glu Glu
      115      120      125
Ile Arg Asn Asn Unk Leu Asn Phe Lys Gly Ile Lys Lys Arg Phe Asp
      130      135      140
Ile Leu Gln Lys Asn Asn Leu Ile Leu Ile Asp Asp Tyr Ala His His
      145      150      155      160
Pro Thr Glu Ile Gly Unk Thr Leu Lys Ser Ala Arg Ile Tyr Ala Asn
      165      170      175
Leu Leu Asn Thr Gln Glu Lys Ile Ile Val Ile Trp Gln Ala His Lys
      180      185      190
Tyr Ser Arg Leu Met Asp Asn Leu Glu Glu Phe Lys Lys Cys Phe Leu
      195      200      205
Glu His Cys Asp Arg Leu Ile Ile Leu Pro Val Tyr Ser Ala Ser Glu
      210      215      220
Val Lys Arg Asp Ile Asp Leu Lys Ala His Phe Lys His Tyr Asn Pro
      225      230      235      240
Thr Phe Ile Asp Arg Val Arg Lys Lys Gly Asp Phe Leu Glu Leu Leu
      245      250      255
Val Asn Asp Asn Val Val Glu Thr Ile Glu Lys Gly Phe Val Ile Gly
      260      265      270
Phe Gly Ala Gly Asp Ile Thr Tyr Gln Leu Arg Gly Glu Met
      275      280      285

```

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401

336

```

Leu Unk Pro Met Lys Val Ile Gln Val Phe Leu Phe Ser Asn Pro Phe
1          5          10          15
Cys Ala Ile Val Pro Asn Thr Glu Pro Glu His Leu Glu His Tyr Asp
20          25          30
His Asp Leu Glu Arg Phe Phe Phe Ala Tyr Lys Tyr Phe Leu Asp His
35          40          45
Ala Gln Lys Arg Val Ile Tyr Lys Glu Asp Pro Phe Leu Lys Asn Tyr
50          55          60
Ser Lys Asp Ala Ile Val Leu Glu Lys Lys Asp Ile Tyr Asn Ile Gln
65          70          75          80
Tyr Ile Leu Lys Asp Gly Glu Pro Tyr Thr Ser Phe Glu Leu Lys Asn
85          90          95
Leu Gly Ala Phe Leu Val Trp Gly Leu Gly Glu His Asn Ala Thr Asn
100         105         110
Ala Ser Leu Ala Ile Leu Ser Ala Leu Asp Glu Leu Asn Leu Glu Glu
115         120         125
Ile Arg Asn Asn Unk Leu Asn Phe Lys Gly Ile Lys Lys Arg Phe Asp
130         135         140
Ile Leu Gln Lys Asn Asn Leu Ile Leu Ile Asp Tyr Ala His His
145         150         155         160
Pro Thr Glu Ile Gly Unk Thr Leu Lys Ser Ala Arg Ile Tyr Ala Asn
165         170         175
Leu Leu Asn Thr Gln Glu Lys Ile Ile Val Ile Trp Gln Ala His Lys
180         185         190
Tyr Ser Arg Leu Met Asp Asn Leu Glu Glu Phe Lys Lys Cys Phe Leu
195         200         205
Glu His Cys Asp Arg Leu Ile Ile Leu Pro Val Tyr Ser Ala Ser Glu
210         215         220
Val Lys Arg Asp Ile Asp Leu Lys Ala His Phe Lys His Tyr Asn Pro
225         230         235         240
Thr Phe Ile Asp Arg Val Arg Lys Lys Gly Asp Phe Leu Glu Leu Leu
245         250         255
Val Asn Asp Asn Val Val Glu Thr Ile Glu Lys Gly Phe Val Ile Gly
260         265         270
Phe Gly Ala Gly Asp Ile Thr Tyr Gln Leu Arg Gly Glu Met
275         280         285

```

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402

```

Met Gly Ala Leu Ile Ala Met Phe Phe Leu Met Leu Ile Lys Lys Thr
1          5          10          15
Ile Ala Tyr Lys Glu Asp Lys Lys Ser Ala Ala Leu Lys Val Val Pro
20          25          30
Tyr Leu Val Ala Leu Met Ser Leu Ala Phe Ser Trp Tyr Leu Ile Val
35          40          45
Lys Val Leu Lys Arg Leu Tyr Ala Val Ser Phe Glu Ile Gln Leu Ala

```

337

```

      50              55              60
Cys Gly Cys Val Leu Ala Leu Leu Ile Phe Ile Leu Phe Lys Arg Phe
65              70              75              80
Val Leu Lys Lys Ala Pro Gln Leu Glu Asn Ser His Glu Ser Val Asn
      85              90              95
Glu Leu Phe Asn Val Pro Leu Ile Phe Ala
      100              105

```

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403

```

Met Ile Lys Arg Ile Ala Cys Ile Leu Ser Leu Ser Ala Ser Leu Ala
1              5              10              15
Leu Ala Gly Glu Val Asn Gly Phe Phe Met Gly Ala Gly Tyr Gln Gln
      20              25              30
Gly Arg Tyr Gly Pro Tyr Asn Ser Asn Tyr Ser Asp Trp Arg His Gly
      35              40              45
Asn Asp Leu Tyr Gly Leu Asn Phe Lys Leu Gly Phe Val Gly Phe Ala
      50              55              60
Asn Lys Trp Phe Gly Ala Arg Val Tyr Gly Phe Leu Asp Trp Phe Asn
      65              70              75              80
Thr Ser Gly Thr Glu His Thr Lys Thr Asn Leu Leu Thr Tyr Gly Gly
      85              90              95
Gly Gly Asp Leu Ile Val Asn Leu Ile Pro Leu Asp Lys Phe Ala Leu
      100              105              110
Gly Leu Ile Gly Gly Val Gln Leu Ala Gly Asn Thr Trp Met Phe Pro
      115              120              125
Tyr Asp Val Asn Gln Thr Arg Phe Gln Phe Leu Trp Asn Leu Gly Gly
      130              135              140
Arg Met Arg Val Gly Asp Thr Val Arg Leu Lys Arg Ala
      145              150              155

```

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

338

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404

```

Met Tyr Arg His Val Leu Lys Asp Phe Ser Leu Asp Phe Ser Lys Glu
1      5      10      15
Ser Val Gln Glu Leu Phe Asn Gln Leu Ala Lys Asp Thr Phe Leu Leu
20     25     30
Leu Leu Pro Val Leu Ile Ile Leu Met Val Val Ala Phe Leu Ser Asn
35     40     45
Val Leu Gln Phe Gly Trp Leu Phe Ala Pro Lys Val Ile Glu Pro Lys
50     55     60
Phe Ser Lys Ile Asn Pro Ile Asn Gly Val Lys Asn Leu Phe Ser Leu
65     70     75     80
Lys Lys Ile Leu Asp Gly Ser Leu Ile Thr Leu Lys Val Phe Leu Ala
85     90     95
Phe Phe Leu Gly Phe Phe Ile Phe Ser Leu Phe Leu Gly Glu Leu Asn
100    105    110
His Ala Ala Leu Leu Asn Leu Gln Gly Gln Leu Leu Trp Phe Lys Ser
115    120    125
Lys Ala Leu Trp Leu Ile Ser Ser Leu Leu Phe Leu Phe Val Leu
130    135    140
Ala Phe Val Asp Leu Ile Ile Lys Arg Arg Gln Tyr Thr Asn Ser Leu
145    150    155    160
Lys Met Thr Lys Gln Glu Val Lys Asp Glu Tyr Lys Gln Gln Glu Gly
165    170    175
Asn Pro Glu Ile Lys Ala Lys Ile Arg Gln Met Met Val Lys Asn Ala
180    185    190
Thr Asn Lys Met Met Gln Glu Ile Pro Lys Ser Asn Val Val Val Thr
195    200    205
Asn Pro Thr His Tyr Ala Val Ala Leu Lys Phe Asp Glu Glu His Pro
210    215    220
Val Pro Val Val Val Ala Lys Gly Thr Asp Tyr Leu Ala Ile Arg Ile
225    230    235    240
Lys Gly Ile Ala Arg Glu His Asp Ile Glu Ile Ile Glu Asn Lys Thr
245    250    255
Leu Ala Arg Glu Leu Tyr Arg Asp Val Lys Leu Asn Ala Thr Ile Pro
260    265    270
Glu Glu Leu Phe Glu Arg
275

```

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405

Met Asn Thr Unk Pro Leu Ile Ala Thr Leu Leu Gln Ala Pro Leu His

339

```

1           5           10           15
Val Leu Gly Ile Arg Glu Pro Val Ser Phe Gln Pro Phe Tyr Pro Lys
                20           25           30
Thr Glu Lys Pro Asn Arg Pro Gln Lys Phe Ala His Val Ser Ser Met
                35           40           45
Pro Ser Leu Glu Phe Leu Glu Lys Leu Val Ile Arg Tyr Leu Leu Glu
                50           55           60
Asp Arg Ser Leu Leu Asp Leu Ala Val Gly Tyr Ile His Ser Gly Val
65           70           75           80
Phe Leu His Lys Lys Gln Glu Phe Asp Ala Leu Cys Gln Glu Lys Leu
                85           90           95
Asp Asp Pro Lys Leu Val Ala Leu Leu Asp Ala Asn Leu Pro Leu
                100           105           110
Lys Lys Gly Gly Phe Glu Lys Glu
                115           120

```

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406

```

Met Gly Gln Ala Phe Phe Lys Lys Ile Val Gly Cys Phe Cys Leu Gly
1           5           10           15
Tyr Leu Phe Leu Ser Ser Ala Ile Glu Ala Val Ala Leu Asp Ile Lys
                20           25           30
Asn Phe Asn Arg Gly Arg Val Lys Val Val Asn Lys Lys Ile Ala Tyr
                35           40           45
Leu Gly Asp Glu Lys Pro Ile Thr Ile Trp Thr Ser Leu Asp Asn Val
50           55           60
Thr Val Ile Gln Leu Glu Lys Asp Glu Thr Ile Ser Tyr Ile Thr Thr
65           70           75           80
Gly Phe Asn Lys Gly Trp Ser Ile Val Pro Asn Ser Asn His Ile Phe
                85           90           95
Ile Gln Pro Lys Ser Val Lys Ser Asn Leu Met Phe Glu Lys Glu Ala
                100           105           110
Val Asn Phe Ala Leu Met Thr Arg Asp Tyr Gln Glu Phe Leu Lys Thr
115           120           125
Lys Lys Leu Ile Val Asp Ala Pro Asp Pro Lys Glu Leu Glu Glu Gln
130           135           140
Lys Lys Ala Leu Glu Lys Glu Lys Glu Ala Lys Glu Gln Ala Gln Lys
145           150           155           160
Ala Gln Lys Asp Lys Arg Glu Lys Arg Lys Glu Glu Arg Ala Lys Asn
165           170           175
Arg Ala Asn Leu Glu Asn Leu Thr Asn Ala Met Ser Asn Pro Gln Asn
180           185           190
Leu Ser Asn Asn Lys Asn Leu Ser Glu Leu Ile Lys Gln Gln Arg Glu
195           200           205
Asn Glu Leu Asp Gln Met Glu Arg Thr Arg Gly His Ala Arg Ala Gly
210           215           220

```

SUBSTITUTE SHEET (RULE 26)

340

Ser Ser
225

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407

```

Leu Leu Leu Phe Phe Leu Leu Lys Gly Val Val Phe Ser Leu Gly Phe
1           5           10           15
Phe Ser Phe Phe Glu Glu Val Ser Gly Ser Phe Unk Ala Val Ser Leu
          20           25           30
Unk Val Leu Ala Leu Val Met Gly Ser Ser Unk Gly Leu Glu Glu Phe
          35           40           45
Cys Val Leu Glu Glu Leu Ile Asn Ser Gly Leu Ser Val
          50           55           60

```

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407

```

Leu Leu Leu Phe Phe Leu Leu Lys Gly Val Val Phe Ser Leu Gly Phe
1           5           10           15
Phe Ser Phe Phe Glu Glu Val Ser Gly Ser Phe Unk Ala Val Ser Leu
          20           25           30
Unk Val Leu Ala Leu Val Met Gly Ser Ser Unk Gly Leu Glu Glu Phe
          35           40           45
Cys Val Leu Glu Glu Leu Ile Asn Ser Gly Leu Ser Val
          50           55           60

```

(2) INFORMATION FOR SEQ ID NO:408:

341

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408

```

Met Asn Thr Glu Ile Leu Thr Ile Met Leu Val Val Ser Val Leu Met
1           5           10           15
Gly Leu Val Gly Leu Ile Ala Phe Leu Trp Gly Val Lys Ser Gly Gln
          20           25           30
Phe Asp Asp Glu Lys Arg Met Leu Glu Ser Val Leu Tyr Asp Ala Arg
          35           40           45
Ala Thr
50
  
```

(2) INFORMATION FOR SEQ ID NO:409:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 122 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409

```

Met Gly Phe Leu Lys Val Leu Lys His Asp Ala Leu Gly Gln Val Gly
1           5           10           15
Asn Ile Val Ile Gly Asn Phe Leu Ile Thr Leu Thr Val Leu Ala Val
          20           25           30
Cys Phe Ser Ser Gln Ser Ala Glu Thr Thr Met Leu Thr Leu Ser
          35           40           45
Tyr Thr Leu Phe Phe Ile Leu Gly Ala Phe Leu Leu Val Ala Ile Ser
          50           55           60
Val Gly Ala Ile Lys Asn Leu Asn Ala Leu Phe Ser Lys Arg Gly Val
          65           70           75           80
Leu Ser Phe Ser Leu Pro Ile Ser Leu Glu Ser Leu Leu Leu Pro Lys
          85           90           95
Ile Leu Leu Pro Unk Val Phe Phe Tyr Leu Gln Phe Val Leu Val Cys
          100          105          110
Gly Glu Arg Ala Phe Gly Leu Leu Pro Phe
          115          120
  
```

SUBSTITUTE SHEET (RULE 26)

342

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409

```

Met Gly Phe Leu Lys Val Leu Lys His Asp Ala Leu Gly Gln Val Gly
1          5          10          15
Asn Ile Val Ile Gly Asn Phe Leu Ile Thr Leu Thr Val Leu Ala Val
          20          25          30
Cys Phe Ser Ser Gln Ser Ala Glu Thr Thr Met Leu Thr Leu Ser
          35          40          45
Tyr Thr Leu Phe Phe Ile Leu Gly Ala Phe Leu Leu Val Ala Ile Ser
          50          55          60
Val Gly Ala Ile Lys Asn Leu Asn Ala Leu Phe Ser Lys Arg Gly Val
65          70          75          80
Leu Ser Phe Ser Leu Pro Ile Ser Leu Glu Ser Leu Leu Leu Pro Lys
          85          90          95
Ile Leu Leu Pro Unk Val Phe Phe Tyr Leu Gln Phe Val Leu Val Cys
          100          105          110
Gly Glu Arg Ala Phe Gly Leu Leu Pro Phe
          115          120

```

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410

```

Met Leu Lys Thr His Leu Ser Ser Ala Arg Gly Val Val Val Leu Ser
1          5          10          15
Lys Ile Leu Pro Val Asn Val Val Leu Met Val Ser Val Arg Leu Phe
          20          25          30
Glu Lys Glu Leu Lys Arg Lys Pro Tyr Tyr Ile Ile Ala Ser Ala His

```

343

```

      35          40          45
Ser Asp Glu Gly Leu Glu Lys Leu Lys Lys Unk Gly Unk Asp Met Val
 50          55          60
Unk Unk Pro Thr Lys Leu Met Ala Gln Arg Val Ser Ala Asn Unk Trp
 65          70          75          80
Cys Unk Leu Asp Met Glu Asn Ile Leu Glu Arg Phe Ile Asn Lys Lys
      85          90          95
Asp Thr Leu Leu Asp Leu Glu Glu Val Ile Val Pro Lys Thr Ser Trp
      100          105          110
Leu Val Leu Arg Lys Leu Lys Glu Ala His Phe Arg Glu Ile Ala Lys
      115          120          125
Ala Phe Val Ile Gly Ile Thr Gln Lys Asp Gly Lys Tyr Ile Pro Met
      130          135          140
Pro Asp Gly Glu Thr Ile Ile Ala Ser Glu Ser Lys Leu Leu Met Val
      145          150          155          160
Gly Thr Ser Glu Gly Val Ala Thr Cys Lys Gln Leu Ile Thr Ser His
      165          170          175
Gln Lys Pro Lys Glu Val Asp Tyr Ile Ser Leu
      180          185

```

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410

```

Met Leu Lys Thr His Leu Ser Ser Ala Arg Gly Val Val Val Leu Ser
 1          5          10          15
Lys Ile Leu Pro Val Asn Val Val Leu Met Val Ser Val Arg Leu Phe
      20          25          30
Glu Lys Glu Leu Lys Arg Lys Pro Tyr Tyr Ile Ile Ala Ser Ala His
      35          40          45
Ser Asp Glu Gly Leu Glu Lys Leu Lys Lys Unk Gly Unk Asp Met Val
 50          55          60
Unk Unk Pro Thr Lys Leu Met Ala Gln Arg Val Ser Ala Asn Unk Trp
 65          70          75          80
Cys Unk Leu Asp Met Glu Asn Ile Leu Glu Arg Phe Ile Asn Lys Lys
      85          90          95
Asp Thr Leu Leu Asp Leu Glu Glu Val Ile Val Pro Lys Thr Ser Trp
      100          105          110
Leu Val Leu Arg Lys Leu Lys Glu Ala His Phe Arg Glu Ile Ala Lys
      115          120          125
Ala Phe Val Ile Gly Ile Thr Gln Lys Asp Gly Lys Tyr Ile Pro Met
      130          135          140
Pro Asp Gly Glu Thr Ile Ile Ala Ser Glu Ser Lys Leu Leu Met Val
      145          150          155          160
Gly Thr Ser Glu Gly Val Ala Thr Cys Lys Gln Leu Ile Thr Ser His
      165          170          175
Gln Lys Pro Lys Glu Val Asp Tyr Ile Ser Leu
      180          185

```

SUBSTITUTE SHEET (RULE 26)

344

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411

```

Met Phe Val Ala Ala Gly Leu Gly Ala Tyr Ala Ile Ala Leu Phe His
1          5          10          15
Leu Phe Thr His Ala Phe Phe Lys Ser Leu Leu Phe Leu Gly Ser Gly
20          25          30
Asn Val Met His Ala Met Glu Asp Asn Leu Asp Ile Thr Lys Met Gly
35          40          45
Ala Leu Tyr Lys Pro Met Arg Ile Thr Ala Val Phe Met Ile Ile Gly
50          55          60
Ser Val Ala Leu Cys Gly Ile Tyr Pro Phe Ala Gly Tyr Phe Ser Lys
65          70          75          80
Asp Lys Ile Leu Glu Val Ala Phe Gly Met His His His Ile Leu Trp
85          90          95
Phe Val Leu Leu Ile Gly Ala Ile Phe Thr Ala Phe Tyr Ser Phe Arg
100         105         110
Leu Ile Met Leu Val Phe Phe Ala Pro Lys Gln His Glu Ile Asn His
115         120         125
Pro Pro
130

```

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412

```

Met Phe Ile Ser Ser Ser Tyr Thr Leu Ser Phe Val Trp Leu Phe Leu
1          5          10          15
Ile Phe Phe Phe Phe Lys Asn Lys Pro Leu Gly Leu Arg Phe Ser Leu

```

345

```

      20      25      30
Ser Leu Ile Ser Val Ile Leu Ser Asn Ile Ala Leu Lys Asp Ser Leu
  35      40      45
Ser Leu Asn Glu Phe Leu Ser Ser Phe Thr Ala Pro Leu Ser Pro Phe
  50      55      60
Ser Cys Leu Leu Ile Leu Ala Tyr Ala Ser Phe Ser Cys His Ile Leu
  65      70      75      80
Lys Lys Pro Pro Leu Glu Thr Leu Gln Ser Tyr Ser Val Met Leu Phe
      85      90      95
Phe Asn Leu Leu Leu Leu Thr Asp Ile Leu Gly Phe Leu Pro Phe Ser
      100      105      110
Ile Tyr His His Phe Met Ala Ser Leu Ile Phe Ser Ala Leu Phe Cys
      115      120      125
Ser Ser Leu Phe Leu Ser Ser Pro Leu Leu Gly Val Ile Ala Leu Val
      130      135      140
Ala Leu Ser Ser Ser Leu Leu Met Arg Ser Asn Phe Gln Ile Leu Asp
  145      150      155      160
Ser Leu Leu Asp Phe Pro Leu Phe Leu Phe Val Phe Phe Lys Thr Leu
      165      170      175
Tyr Leu Ala Lys Lys Arg Leu
      180

```

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413

```

Val Gly Ser Phe Leu Phe Val Gly Pro Ser Gly Val Gly Lys Thr Glu
  1      5      10      15
Leu Ala Lys Glu Leu Ala Leu Asn Leu Unk Leu His Phe Glu Arg Phe
  20      25      30
Asp Met Ser Glu Tyr Lys Glu Ala His Ser Val Ala Lys Leu Ile Gly
  35      40      45
Ser Pro Ser Gly Tyr Val Gly Phe Glu Gln Gly Gly Leu Leu Val Asn
  50      55      60
Ala Ile Lys Lys His Pro His Cys Leu Leu Leu Asp Glu Ile Glu
  65      70      75      80
Lys Ala His Pro Asn Val Tyr Asp Leu Leu Leu Gln Val Met Unk Asn
      85      90      95
Ala Thr Leu Ser Asp Asn Leu Gly Asn Lys Ala Ser Phe Lys His Val
      100      105      110
Ile Leu Ile Met Thr Unk Unk Val Gly Ser Lys Asp Lys Asp Thr Leu
      115      120      125
Gly Phe Phe Ser Thr Lys Asn Ala Lys Tyr Asp Arg Ala Val Lys Glu
      130      135      140
Leu Leu Thr Pro Glu Leu Arg Ser Arg Ile Asp Ala Ile Val Pro Phe
  145      150      155      160
Asn Ala Leu Ser Leu Glu Asp Phe Glu Thr His Cys Phe Cys Gly Ile
      165      170      175

```

SUBSTITUTE SHEET (RULE 26)

346

Gly Arg Val Lys Ser Pro Ser Thr Arg Ala Arg Arg Asp Leu Lys Ile
 180 185 190
 Pro

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413

Val Gly Ser Phe Leu Phe Val Gly Pro Ser Gly Val Gly Lys Thr Glu
 1 5 10 15
 Leu Ala Lys Glu Leu Ala Leu Asn Leu Unk Leu His Phe Glu Arg Phe
 20 25 30
 Asp Met Ser Glu Tyr Lys Glu Ala His Ser Val Ala Lys Leu Ile Gly
 35 40 45
 Ser Pro Ser Gly Tyr Val Gly Phe Glu Gln Gly Gly Leu Leu Val Asn
 50 55 60
 Ala Ile Lys Lys His Pro His Cys Leu Leu Leu Leu Asp Glu Ile Glu
 65 70 75 80
 Lys Ala His Pro Asn Val Tyr Asp Leu Leu Leu Gln Val Met Unk Asn
 85 90 95
 Ala Thr Leu Ser Asp Asn Leu Gly Asn Lys Ala Ser Phe Lys His Val
 100 105 110
 Ile Leu Ile Met Thr Unk Unk Val Gly Ser Lys Asp Lys Asp Thr Leu
 115 120 125
 Gly Phe Ser Thr Lys Asn Ala Lys Tyr Asp Arg Ala Val Lys Glu
 130 135 140
 Leu Leu Thr Pro Glu Leu Arg Ser Arg Ile Asp Ala Ile Val Pro Phe
 145 150 155 160
 Asn Ala Leu Ser Leu Glu Asp Phe Glu Thr His Cys Phe Cys Gly Ile
 165 170 175
 Gly Arg Val Lys Ser Pro Ser Thr Arg Ala Arg Arg Asp Leu Lys Ile
 180 185 190
 Pro

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

347

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414

```

Met Arg Leu Asp Tyr Ala Leu Phe Asn Gln His Leu Ala Asn Ser Arg
1      5      10      15
Glu Lys Ala Lys Ala Leu Val Leu Lys Lys Gln Val Leu Val Asn Lys
20      25      30
Met Val Val Ser Lys Pro Ser Phe Ile Val Lys Glu Gly Asp Gln Ile
35      40      45
Glu Leu Ile Ala Pro Asn Leu Phe Val Ser Arg Ala Gly Glu Lys Leu
50      55      60
Gly Ala Phe Leu Glu Asp His Phe Ile Asp Phe Lys Glu Lys Val Val
65      70      75      80
Leu Asp Val Gly Ala Ser Lys Gly Gly Phe Ser Gln Val Ala Leu Leu
85      90      95
Lys Gly Ala Lys Lys Val Leu Cys Val Asp Val Gly Lys Met Gln Leu
100     105     110
Asp Glu Ser Leu Lys Asn Asp Gln Arg Ile Glu Cys Tyr Glu Glu Cys
115     120     125
Asp Ile Arg Gly Phe Lys Thr Pro Glu Lys Ile Asp Leu Ala Leu Cys
130     135     140
Asp Val Ser Phe Ile Ser Leu Tyr Cys Ile Leu Glu Ala Ile Leu Pro
145     150     155     160
Leu Ser Gly Glu Phe Leu Thr Leu Phe Lys Pro Gln Phe Glu Val Gly
165     170     175
Arg Thr Ile Lys Arg Asn Lys Lys Gly Val Val Met Asp Lys Glu Ala
180     185     190
Ile Leu Asn Ala Leu Glu Asn Phe Lys Asn His Leu Lys Thr Lys Asp
195     200     205
Phe Gln Ile Leu Thr Ile Gln Glu Ser Leu Val Lys Gly Lys Asn Gly
210     215     220
Asn Val Glu Phe Phe Ile His Phe Lys Arg Ala
225     230     235

```

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415

```

Met Ser Leu Pro Pro Val Cys Ile Leu Lys Asp Val Asn His Leu Leu
1      5      10      15
Gln Val Leu His Ser Leu Val Ala Leu Gly Asn Ser Met Leu Val Ile
20      25      30

```

348

Glu His Asn Leu Asp Ile Ile Lys Asn Ala Asp Tyr Ile Ile Asp Met
 35 40 45
 Gly Pro Asp Gly Gly Asp Lys Gly Gly Lys Val Ile Ala Ser Gly Thr
 50 55 60
 Pro Leu Glu Val Ala Gln Asn Cys Glu Lys Thr Gln Ser Tyr Thr Gly
 65 70 75 80
 Lys Phe Leu Ala Leu Glu Leu Lys
 85

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416

Met Gln Asn Arg Ser His Glu Ile Gln Gly Val Ser His Ile Lys Asn
 1 5 10 15
 Asn Tyr Lys Phe Thr Lys Glu Leu Asp Asn Tyr Ile Ser Lys Gly
 20 25 30
 Tyr Arg Ile Glu Glu Ile Tyr Gly Ala Phe Leu Trp Leu Lys Ile Val
 35 40 45
 Ala Ile Gly Leu Glu Leu Gly Glu Asp Asp Pro Gln Val Val Phe Glu
 50 55 60
 Ser Ile Asn Ala Thr Gly Val Gln Leu Lys Gly Leu Asp Leu Ile Arg
 65 70 75 80
 Asn Tyr Leu Met Met Gly Glu Asn Unk Asp Asn Gln Asn Arg Leu Tyr
 85 90 95
 Asn Thr Tyr Trp Val Pro Leu Glu Asn Trp Leu Gly Glu
 100 105

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417

349

```

Met Asp Thr Ile Lys Ser Ile Pro Ile Arg Thr Phe Ile Leu Leu Tyr
1      5      10      15
Lys Ser Ser Pro Lys Cys Val Val Leu Ala Ser Ile Thr Val Leu Phe
20      25      30
Val Gly Ile Leu Unk Ser Leu Asn Ile Leu Val Met Ile Lys Leu Ile
35      40      45
Asp Ile Val Val Asn Leu Leu Gln Lys His Thr His Phe Glu Tyr Ser
50      55      60
Leu Leu Leu Pro Thr Leu Leu Leu Trp Gly Ala Leu Leu Phe Leu Thr
65      70      75      80
His Val Phe Ser Gly Asn Phe Ile Lys Leu Ala Asn His Tyr Cys Arg
85      90      95
Thr Ile Phe Tyr Lys Tyr His His Ser Ala Cys
100      105

```

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418

```

Met Ile Phe Tyr Thr Thr Ile Lys Glu Pro Leu Lys Asn Leu Gln Tyr
1      5      10      15
Arg Tyr Ala Gln Phe Phe Gly Lys Ile Lys Pro Cys Ser Phe Leu Glu
20      25      30
Ser Leu Lys Ser Cys Phe Phe Gln Thr Tyr Ser Phe Ser Leu Thr Arg
35      40      45
Lys Gln Asp Phe Lys Ser His Leu Arg His Phe Ile Asp Ser Ala His
50      55      60
Ser Asn Ala Leu Val Gly Asn Leu Tyr Arg Ala Leu Phe Ile Gly Asp
65      70      75      80
Ser Leu Asn Lys Asp Leu Arg Asp Arg Ala Asn Ala Leu Gly Ile Asn
85      90      95
His Leu Leu Ala Ile Ser Gly Phe His Leu Gly Ile Leu Ser Ala Ser
100      105      110
Val Tyr Phe Leu Phe Ser Leu Phe Tyr Thr Pro Leu Gln Lys Arg Tyr
115      120      125
Phe Pro Tyr Arg Asn Ala Phe Unk
130      135

```

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

SUBSTITUTE SHEET (RULE 26)

350

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419

```

Met Asn Lys Pro Phe Leu Ile Leu Leu Ile Ala Leu Ile Ala Phe Ser
 1              5              10              15
Gly Cys Asn Met Arg Lys Tyr Phe Lys Pro Ala Lys His Gln Ile Lys
      20              25              30
Ala Lys Arg Ile Ser Leu Thr Ile Cys Lys Lys Ala Ser Phe Arg Leu
      35              40              45
Ile Val Met Glu Pro Phe
 50

```

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420

```

Met Ala Ala Trp Asn Thr Leu Val Glu Lys Ile Ile Ala Pro Lys His
 1              5              10              15
Lys Val Lys Ile Gly Phe Val Gly Lys Tyr Leu Ser Leu Lys Glu Ser
      20              25              30
Tyr Lys Ser Leu Ile Glu Ala Leu Ile His Ala Gly Ala His Leu Asp
      35              40              45
Thr Gln Val Asn Ile Glu Trp Leu Asp Ser Glu Asn Phe Asn Glu Lys
      50              55              60
Thr Asp Leu Glu Gly Val Asp Ala Ile Leu Val Pro Gly Gly Phe Gly
      65              70              75              80
Glu Arg Gly Ile Glu Gly Lys Ile Cys Ala Ile Gln Arg Ala Arg Leu
      85              90              95
Glu Lys Leu Pro Phe Leu Gly Ile Cys Leu Gly Met Gln Leu Ala Ile
      100             105             110
Val Glu Phe Cys Arg Lys Cys Phe Arg Leu Glu Arg Gly
      115             120             125

```

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids

(B) TYPE: amino acid

SUBSTITUTE SHEET (RULE 26)

351

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421

```

Met Thr Lys Ala Phe Val Pro Leu Ser Leu Leu Val Ser Ala Ile Leu
1      5      10      15
Leu Ala Phe Ser Leu Ile Leu Ile Pro Thr Ser Lys Ser Ala Tyr Tyr
20      25      30
Gly Phe Leu Arg Gln Lys Lys Asp Lys Ile Asp Ile Asn Ile Arg Ala
35      40      45
Gly Glu Phe Gly Gln Lys Leu Gly Asp Trp Leu Val Tyr Val Asp Lys
50      55      60
Thr Glu Asn Asn Ser Tyr Asp Asn Leu Val Leu Phe Ser Asn Lys Ser
65      70      75      80
Leu Ser Gln Glu Ser Phe Ile Leu Ala Gln Lys Gly Asn Ile Asn Asn
85      90      95
Gln Asn Gly Val Phe Glu Leu Asn Leu Tyr Asn Gly His Ala Tyr Phe
100     105     110
Thr Gln Gly Asp Lys Met Arg Lys Val Asp Phe Glu Glu Leu His Leu
115     120     125
Arg Asn Lys Leu Lys Ser Phe Asn Ser Asn Asp Ala Ala Tyr Leu Gln
130     135     140
Gly Thr Asp Tyr Leu Gly Tyr Trp Lys Lys Ala Phe Gly Lys Asn Ala
145     150     155     160
Asn Lys Asn Gln Lys Arg Arg Phe Ser Gln Ala Ile Leu Val Ser Leu
165     170     175
Phe Pro Leu Ala Ser Val Phe Leu Ile Pro Leu Phe Gly Ile Ala Asn
180     185     190
Pro Arg Phe Lys Thr Asn Trp Ser Tyr Phe Unk Val Leu Gly Ala Val
195     200     205
Gly Val Tyr Phe Leu Met Val His Val Ile Ser Thr Asp Leu Phe Leu
210     215     220
Met Thr Phe Phe Phe Pro Phe Ile Trp Ala Phe Ile Ser Tyr Leu Leu
225     230     235     240
Phe Arg Lys Phe Ile Leu Lys Arg Tyr
245

```

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

352

(B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422

```

Met Ser Lys Ser Ala Ile Phe Val Leu Ser Gly Phe Leu Ala Phe Leu
1           5           10           15
Leu Tyr Ala Leu Leu Leu Tyr Gly Leu Leu Leu Glu Arg His Asn Lys
          20           25           30
Glu Ala Glu Lys Ile Leu Leu Asp Leu Asn Lys Lys Asp Glu Gln Ala
          35           40           45
Ile Asp Leu Asn Leu Glu Asp Leu Pro Ser Glu Lys Lys Asn Glu Lys
          50           55           60
Ile Lys Lys Val Thr Glu Lys Gln Asp Asp Phe Leu Glu Pro Lys Arg
          65           70           75           80
Arg Thr Gln Arg Gly Ala
          85

```

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423

```

Val Met Ala Gln Ser Leu Leu Val His Ala Phe Phe Ala Ala Leu Leu
1           5           10           15
Ala Leu Ala Phe Met Ile Asn Leu Tyr Thr Leu Phe Lys Glu Lys Asn
          20           25           30
Phe Ile Gln Leu Asn Arg Lys Ile Tyr Leu Val Met Pro Ala Ile Tyr
          35           40           45
Ile Leu Leu Ser Ile Ala Leu Leu Ser Gly Val Phe Ile Trp Ala Met
          50           55           60
Gln Gln Phe Glu Phe Ser Phe Ser Ala Val Val Met Leu Leu Gly Leu
          65           70           75           80
Leu Leu Met Leu Ile Ala Glu Ile Lys Arg His Lys Ser Val Lys Phe
          85           90           95
Ala Ile Thr Lys Lys Glu Arg Met Lys Ala Tyr Ile Lys Lys Ala Lys
          100          105          110
Ile Leu Tyr Phe Leu Glu Thr Ile Leu Ile Ile Val Leu Met Gly Ile
          115          120          125

```

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

353

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424

```

Val Arg Asn Val Val Leu Phe Ile Leu Thr Ala Ile Phe Leu Ala Phe
 1              5              10              15
Met Leu Leu Val Ser Tyr Cys Met Pro His Tyr Ser Val Ala Val Ile
      20              25              30
Ser Gly Val Glu Val Lys Arg Met Asn Glu Asn Glu Asn Thr Pro Asn
      35              40              45
Asn Lys Glu Val Lys Thr Leu Ala Arg Asp Val Tyr Phe Val Gln Thr
      50              55              60
Tyr Asp Pro Lys Asp Gln Lys Ser Val Thr Val Tyr Arg Asn Glu Asp
      65              70              75              80
Thr Arg Phe Gly Phe Pro Phe Tyr Phe Lys Phe Asn Ser
      85              90

```

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425

```

Met Phe Lys Lys Ile Ile Phe Leu Cys Val Phe Leu Ile Gly Gly Phe
 1              5              10              15
Val Ile Pro Pro Leu Glu Ala Met Pro Ile Leu Arg Asn Lys Thr Pro
      20              25              30
Lys Lys Asn Tyr Gln Glu Ala His Glu Lys Leu Tyr Arg Ser Ile Ile
      35              40              45
Asn Arg Gln Unk Unk Thr Arg Lys Lys Ser Gly Trp Tyr Phe Leu Gly
      50              55              60
Gly Val Gly Ala Val Glu Ala Ile Lys Asp Tyr Gln Gly Lys Glu Met
      65              70              75              80
Lys Asp Trp Met Pro Arg Ser Ile
      85

```

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

354

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...128
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:426

```

Val His Phe Thr Cys Ile Phe Leu Thr Leu Leu Lys Trp Ile Leu Pro
1           5           10           15
Ala Lys Asn Lys Gln Ala Cys Lys Lys Ala Thr Asn Gln Ile His Ser
          20           25           30
Arg Unk Ala Lys His Pro Ala Lys Tyr Pro Pro Ser Ser Ile Asn Pro
          35           40           45
Ser Ile Gln Ala Gly Ile Gln Gly Val Met Gln Gly Phe Gly Ala Leu
          50           55           60
Ser Ser Unk Leu Glu Unk Pro Unk Phe Val Unk Ala Lys Cys Gly
65           70           75           80
Trp Ile Gly Gly Phe Glu His Tyr Leu Ser Pro Leu Tyr Gly Trp Gly
          85           90           95
Lys Ile His Asp Gly Ala His Cys Asp Leu Met Gln Lys Asp Ala Asn
          100          105          110
Gly Arg Gly Ile Gly Leu Glu Lys Gly Leu Pro Pro Phe Lys Gly Leu
          115          120          125

```

(2) INFORMATION FOR SEQ ID NO:427:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...108
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:427

```

Met Gln Lys Phe Phe Ser Arg Phe Arg Arg Trp Ala Leu Pro Phe Tyr
1           5           10           15
Phe Val Ser Ala Leu Ala Ala Ile Asp Ile Asp Glu Val Thr Glu Ala
          20           25           30
Gln Ala Asn Ser Ile Lys Leu Ser Asp Gln Leu Val Ser Leu Ser Asp
          35           40           45
Lys Leu Leu Glu Lys Ala Val Asp Arg Gly Arg Asn Thr Asp His Leu
          50           55           60
Lys Asp Leu Asn Asp Leu His Glu Lys Ile Lys His Leu Arg Leu Ile
65           70           75           80
Leu Glu Pro Lys Pro Lys Gly Lys Glu Asp Ser Pro Asn Leu Gly Gly
          85           90           95
Asn Lys Asp Met Lys Thr Val Glu Ile Gly Ser Gly

```


355

100

105

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428

```

Val Ile Leu Ala Phe Ala Phe Gly Met Ser Leu Leu Gly Leu Ala Gly
1           5           10           15
Met Phe Ile Asp Ile Pro Phe Leu Ser Thr Gly Val His Ile Pro Arg
          20           25           30
Lys Glu Asp Ile Leu Trp Ile Ser Leu Ile Gly Ile Ser Gly Thr Leu
          35           40           45
Gly Gln Tyr Phe Leu Thr Tyr Ala Tyr Met Asn Ala Pro Ala Gly Ile
          50           55           60
Ile Ala Pro Ile Glu Tyr Thr Arg Ile Val Trp Gly Leu Leu Phe Gly
65           70           75           80
Leu Tyr Leu Gly Asp Thr Phe Leu Asp Leu Lys Ser Ser Leu Gly Val
          85           90           95
Ala Leu Ile Leu Cys Ser Gly Leu Leu Ile Ala Leu Pro Ala Leu Leu
          100          105          110
Lys Glu Leu Lys Lys Ile
          115

```

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429

```

Met Ile Tyr Leu Gly Lys Lys Asn Phe Asn Ala Leu Leu Lys Gly Ala
1           5           10           15
Tyr Leu Met Asp Glu His Phe Arg Asn Ala Pro Phe Glu Ser Asn Leu
          20           25           30

```

356

Pro Val Leu Met Gly Leu Ile Trp Arg Val Val Tyr Leu Thr Phe Phe
 35 40 45
 Pro Ile Gln Lys Ala Thr
 50

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430

Met Ala Ala Lys Ser Lys Ala Unk Thr Leu Lys Val Phe Ser Lys Phe
 1 5 10 15
 Phe Ser Asn Phe Lys Ile Thr Lys Leu Lys Asp Asn His Glu Glu Ala
 20 25 30
 His Lys Leu Phe Gly Glu Asn Ser Arg Lys Ala His Asp Thr Glu Ile
 35 40 45
 Ile Tyr Ser Thr Leu Gln Val Val Pro Arg Tyr Ser Ile Glu Thr Val
 50 55 60
 Gly Phe Ser Leu Leu Ile Leu Ala Val Ala Tyr Ile Leu Phe Lys Tyr
 65 70 75 80
 Gly Glu Ala Arg Met Val Leu Pro Thr Ile Ser Met Tyr Ala Leu Ala
 85 90 95
 Leu Tyr Arg Ile Leu Pro Ser Val Thr Gly Val Ile Ser Tyr Tyr Asn
 100 105 110
 Glu Ile Ala Tyr Asn Gln Leu Ala Thr Asn Val Val Phe Lys Ser Leu
 115 120 125
 Ser Lys Thr Ile Val Glu Glu Asp Leu Val Pro Leu Asp Phe Asn Glu
 130 135 140
 Lys Ile Thr Leu Gln Asn Ile Ser Phe Ala Tyr Lys Ser Lys His Pro
 145 150 155 160
 Val Leu Lys Asn Phe Asn Leu Thr Ile Gln Lys Gly Gln Lys Ile Ala
 165 170 175
 Leu Ile Gly His Ser Gly Cys Gly Lys Ser Thr Leu Ala Asp Ile Ile
 180 185 190
 Met Gly Leu Thr Tyr Pro Lys Ser Gly Glu Ile Phe Ile Asp Asn Thr
 195 200 205
 Leu Leu Thr Ser Glu Asn Arg Ser Trp Arg Lys Lys Ile Gly Tyr
 210 215 220
 Ile Pro Gln Asn Ile Tyr Leu Phe Asp Gly Thr Val Gly Asp Asn Ile
 225 230 235 240
 Ala Phe Gly Ser Ala Ile Asp Glu Lys Arg Leu Ile Lys Val Cys Lys
 245 250 255
 Met Ala His Ile Tyr Asp Phe Leu Cys Glu His Glu Gly Leu Lys Thr
 260 265 270
 Gln Val Gly Glu Gly Ala Leu Ser Leu Ala Ala Val Lys Asn Ser Ala
 275 280 285

(2) INFORMATION FOR SEQ ID NO:431:

357

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431

```

Met Ala Phe Gln Val Asn Thr Asn Ile Asn Ala Met Asn Ala His Val
1      5      10      15
Gln Ser Ala Leu Thr Gln Asn Ala Leu Lys Thr Ser Leu Glu Arg Leu
20      25      30
Ser Ser Gly Leu Arg Ile Asn Lys Ala Ala Asp Asp Ala Ser Gly Met
35      40      45
Thr Val Ala Asp Ser Leu Arg Ser Gln Ala Ser Ser Leu Gly Gln Ala
50      55      60
Ile Ala Asn Thr Asn Asp Gly Met Gly Ile Ile Gln Val Ala Asp Lys
65      70      75      80
Ala Met Asp Glu Gln Leu Lys Ile Leu Asp Thr Val Lys Val Lys Ala
85      90      95
Thr Gln Ala Ala Gln Asp Gly Gln Thr Thr Glu Ser Arg Lys Ala Ile
100     105     110
Gln Ser Asp Ile Val Arg Leu Ile Gln Gly Leu Asp Asn Ile Gly Asn
115     120     125
Thr Thr Thr Tyr Asn Gly Gln Ala Leu Leu Ser Gly Gln Phe Thr Asn
130     135     140
Lys Glu Phe Gln Val Gly Ala Tyr Ser Asn Gln Ser Ile Lys Ala Ser
145     150     155     160
Ile Gly Ser Thr Thr Ser Asp Lys Ile Gly Gln Val Arg Ile Ala Thr
165     170     175
Gly Ala Leu Ile Thr Ala Ser Gly Asp Ile Ser Leu Thr Phe Lys Gln
180     185     190
Val Asp Gly Val Asn Asp Val Thr Leu Glu Ser Val Lys Val Ser Ser
195     200     205
Ser Ala Gly Thr Gly Ile Gly Val Leu Ala Glu Val Ile Asn Lys Asn
210     215     220
Ser Asn Arg Thr Gly Val Lys Ala Tyr Ala Ser Val Ile Thr Thr Ser
225     230     235     240
Asp Val Ala Val Gln Ser Gly Ser Leu Ser Asn Leu Thr Leu Asn Gly
245     250     255
Ile His Leu Gly Asn Ile Ala Asp Ile Lys Unk Asn Asp Ser Asp Gly
260     265     270
Arg Leu Val Thr Ala Ile Asn Ala Val Thr Ser Glu Thr Gly Val Unk
275     280     285
Ala Tyr Thr Asp Gln Lys Gly Arg Leu Asn Leu Arg Ser Ile Gly
290     295     300

```

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

358

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431.

```

Met Ala Phe Gln Val Asn Thr Asn Ile Asn Ala Met Asn Ala His Val
1      5      10      15
Gln Ser Ala Leu Thr Gln Asn Ala Leu Lys Thr Ser Leu Glu Arg Leu
20     25     30
Ser Ser Gly Leu Arg Ile Asn Lys Ala Ala Asp Asp Ala Ser Gly Met
35     40     45
Thr Val Ala Asp Ser Leu Arg Ser Gln Ala Ser Ser Leu Gly Gln Ala
50     55     60
Ile Ala Asn Thr Asn Asp Gly Met Gly Ile Ile Gln Val Ala Asp Lys
65     70     75     80
Ala Met Asp Glu Gln Leu Lys Ile Leu Asp Thr Val Lys Val Lys Ala
85     90     95
Thr Gln Ala Ala Gln Asp Gly Gln Thr Glu Ser Arg Lys Ala Ile
100    105    110
Gln Ser Asp Ile Val Arg Leu Ile Gln Gly Leu Asp Asn Ile Gly Asn
115    120    125
Thr Thr Thr Tyr Asn Gly Gln Ala Leu Leu Ser Gly Gln Phe Thr Asn
130    135    140
Lys Glu Phe Gln Val Gly Ala Tyr Ser Asn Gln Ser Ile Lys Ala Ser
145    150    155    160
Ile Gly Ser Thr Thr Ser Asp Lys Ile Gly Gln Val Arg Ile Ala Thr
165    170    175
Gly Ala Leu Ile Thr Ala Ser Gly Asp Ile Ser Leu Thr Phe Lys Gln
180    185    190
Val Asp Gly Val Asn Asp Val Thr Leu Glu Ser Val Lys Val Ser Ser
195    200    205
Ser Ala Gly Thr Gly Ile Gly Val Leu Ala Glu Val Ile Asn Lys Asn
210    215    220
Ser Asn Arg Thr Gly Val Lys Ala Tyr Ala Ser Val Ile Thr Thr Ser
225    230    235    240
Asp Val Ala Val Gln Ser Gly Ser Leu Ser Asn Leu Thr Leu Asn Gly
245    250    255
Ile His Leu Gly Asn Ile Ala Asp Ile Lys Unk Asn Asp Ser Asp Gly
260    265    270
Arg Leu Val Thr Ala Ile Asn Ala Val Thr Ser Glu Thr Gly Val Unk
275    280    285
Ala Tyr Thr Asp Gln Lys Gly Arg Leu Asn Leu Arg Ser Ile Gly
290    295    300

```

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

359

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432

```

Met Leu Asp Ile Trp Ile Asp Met Ile Ile Cys Ile Phe Tyr Leu Leu
1           5           10           15
Phe Phe Thr Thr Pro Tyr Ile Val Gly Asp Ile Leu Gln Leu Lys Phe
           20           25           30
Ile Arg Gln Lys Leu Cys Glu Lys Pro Val Leu Leu Pro Gln Lys Asp
           35           40           45
Tyr Glu Glu Ala Gly Asn Tyr Ala Ile Arg Lys Met Gln Leu Ser Ile
50           55           60
Ile Ser Gln Ile Leu Asp Gly Val Ile Phe Ala Gly Trp Val Phe Phe
65           70           75           80
Gly Leu Thr His Leu Glu Asp Leu Thr His Tyr Leu Asn Leu Pro Glu
           85           90           95
Thr Leu Gly Tyr Leu Val Phe Ala Leu Leu Phe Leu Ala Ile Gln Ser
           100          105          110
Val Leu Ala Leu Pro Ile Ser Tyr Tyr Thr Thr Met His Leu Asp Lys
           115          120          125
Glu Phe Gly Phe Ser Lys Val Ser Leu Ser Leu Phe Phe Lys Asp Phe
130          135          140
Phe Lys Gly Leu Leu Leu Thr Leu Gly Val Gly Leu Leu Leu Ile Tyr
145          150          155          160
Thr Leu Ile Met Ile Ile Glu His Val Glu His Trp Glu Ile Ser Ser
           165          170          175
Phe Phe Val Val Phe Val Phe Met Ile Leu Ala Asn Leu Phe Leu Pro
           180          185          190

```

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433

```

Met Leu Lys Lys Ile Phe Leu Thr Asn Ser Leu Gly Ile Leu Cys Ser
1           5           10           15
Arg Ile Phe Gly Phe Leu Arg Asp Leu Met Met Ala Asn Ile Leu Gly
           20           25           30
Ala Gly Val Tyr Ser Asp Ile Phe Phe Val Ala Phe Lys Leu Pro Asn
           35           40           45
Leu Phe Arg Arg Ile Phe Ala Glu Gly Ser Phe Ser Gln Ser Phe Leu
50           55           60
Pro Ser Phe Ile Arg Ser Ser Ile Lys Gly Gly Phe Ala Ser Leu Val
65           70           75           80

```

360

Gly Leu Ile Phe Cys Gly Val Leu Phe Met Trp Cys Leu Leu Val Ala
 85 90 95
 Leu Asn Pro Leu Trp Leu Thr Lys Leu Leu Ala Tyr Gly Phe Asp Glu
 100 105 110
 Glu Thr Leu Lys Leu Cys Thr Pro Ile Val Ala Ile Asn Phe Trp Tyr
 115 120 125
 Leu Leu Leu Val Phe Ile Thr Thr Phe Leu Gly Ala Leu Leu Gln Tyr
 130 135 140
 Lys His Ser Phe Phe Ala Ala Leu Met Arg Lys Leu Thr Gln Phe Met
 145 150 155 160
 His Asp Phe Ser Pro Phe Asp Phe
 165

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434

Met Asn Leu Glu Val Ala Leu Lys Ala Phe Glu Thr Leu Leu Pro Cys
 1 5 10 15
 Asn Lys Gln Glu Val Leu Lys Asn Leu Lys Pro Leu Asp Leu Ile Gly
 20 25 30
 Arg Cys Glu Leu Leu Ser Pro Asn Ile Leu Ile Asp Val Gly His Asn
 35 40 45
 Pro His Ser Ala Lys Ala Leu Lys Glu Glu Ile Lys Arg Ile Phe Asn
 50 55 60
 Ala Pro Ile Val Leu Ile Tyr Asn Cys Tyr Gln Asp Lys Asp Ala Phe
 65 70 75 80
 Leu Val Leu Glu Ile Leu Lys Ser Val Val Lys Lys Val Leu Ile Leu
 85 90 95
 Glu Leu His Asn Glu Arg Ile Ile Gln Leu Glu Lys Leu Lys Gly Ile
 100 105 110
 Leu Glu Thr Leu Gly Leu Glu His Ala Leu Phe Glu Glu Leu Lys Glu
 115 120 125
 Asn Glu Asn Tyr Leu Val Tyr Gly Ser Phe Leu Val Ala Asn Ala Phe
 130 135 140
 Tyr Glu Arg Tyr Pro Lys Lys Arg Asp
 145 150

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

361

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435

```

Met Phe Phe Lys Thr Tyr Gln Lys Leu Leu Gly Ala Ser Cys Leu Ala
1      5      10      15
Leu Tyr Leu Val Gly Cys Gly Asn Gly Gly Gly Glu Ser Pro Val
20      25      30
Glu Met Ile Unk Asn Ser Glu Gly Thr Phe Gln Ile Asp Ser Lys Ala
35      40      45
Asp Ser Ile Thr Ile Gln Gly Val Lys Leu Asn Arg Gly Asn Cys Ala
50      55      60
Val Asn Phe Val Pro Val Ser Glu Thr Phe Gln Met Gly Val Leu Ser
65      70      75      80
Gln Val Thr Pro Ile Ser Ile Gln Asp Phe Lys Asp Met Ala Ser Thr
85      90      95
Tyr Lys Ile Phe Asp Gln Lys Lys Gly Leu Ala Asn Ile Ala Asn Lys
100     105     110
Ile Ser Gln Leu Glu Gln Lys Gly Val Met Met Lys Pro Unk Thr Leu
115     120     125
Asn Phe Gly Glu Ser Leu Lys Gly Ile Ser Gln Gly Cys Asn Ile Ile
130     135     140
Glu Ala Glu Ile Gln Thr Asp Lys Gly Ala Trp Thr Phe Asn Phe Asp
145     150     155     160
Lys

```

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435

```

Met Phe Phe Lys Thr Tyr Gln Lys Leu Leu Gly Ala Ser Cys Leu Ala
1      5      10      15
Leu Tyr Leu Val Gly Cys Gly Asn Gly Gly Gly Glu Ser Pro Val
20      25      30
Glu Met Ile Unk Asn Ser Glu Gly Thr Phe Gln Ile Asp Ser Lys Ala
35      40      45
Asp Ser Ile Thr Ile Gln Gly Val Lys Leu Asn Arg Gly Asn Cys Ala
50      55      60
Val Asn Phe Val Pro Val Ser Glu Thr Phe Gln Met Gly Val Leu Ser
65      70      75      80

```

362

Gln Val Thr Pro Ile Ser Ile Gln Asp Phe Lys Asp Met Ala Ser Thr
 85 90 95
 Tyr Lys Ile Phe Asp Gln Lys Lys Gly Leu Ala Asn Ile Ala Asn Lys
 100 105 110
 Ile Ser Gln Leu Glu Gln Lys Gly Val Met Met Lys Pro Unk Thr Leu
 115 120 125
 Asn Phe Gly Glu Ser Leu Lys Gly Ile Ser Gln Gly Cys Asn Ile Ile
 130 135 140
 Glu Ala Glu Ile Gln Thr Asp Lys Gly Ala Trp Thr Phe Asn Phe Asp
 145 150 155 160
 Lys

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...59

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436

Met Ala Ile Gly Phe Pro Leu Val Phe Gly Ile Leu Leu Thr Leu Phe
 1 5 10 15
 Ser Arg Ser Tyr Trp Arg Glu Phe Gly Gly Val Ser Gly Val Leu Trp
 20 25 30
 Arg Ala Ser Gly Phe Ser Gly Ala Lys Val Glu Arg Asn Leu Glu Arg
 35 40 45
 Asp Pro His Ala Phe Phe Thr His Cys Asp Phe
 50 55

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437

Met Lys Lys Lys Ala Lys Val Phe Trp Cys Cys Phe Lys Met Ile Arg

363

```

1           5           10           15
Trp Leu Tyr Leu Ala Val Phe Phe Leu Ser Val Ser Asp Ala Lys
      20           25           30
Glu Ile Ala Met Gln Arg Phe Asp Lys Gln Asn His Lys Ile Phe Glu
      35           40           45
Ile Leu Ala Asp Lys Val Ser Ala Lys Asp Asn Val Ile Thr Ala Ser
      50           55           60
Gly Asn Ala Ile Leu Leu Asn Tyr Asp Val Tyr Ile Leu Ala Asp Lys
      65           70           75           80
Val Arg Tyr Asp Thr Lys Thr Lys Glu Ala Leu Leu Glu Gly Asn Ile
      85           90           95
Lys Val Tyr Arg Gly Glu Gly Leu Leu Val Lys Thr Asp Tyr Val Lys
      100          105          110
Leu Ser Leu Asn Glu Lys Tyr Glu Ile Ile Phe Pro Phe Tyr Val Gln
      115          120          125
Asp Ser Val Ser Gly Ile Trp Val Ser Ala Asp Ile Ala Ser Gly Lys
      130          135          140
Asp Gln Lys Tyr Lys Ile Lys Asn Met Ser Ala Ser Gly Cys Ser Ile
      145          150          155          160
Asp Asn Pro Ile Trp His Val Asn Ala Thr Ser Gly Ser Phe Asn Met
      165          170          175
Gln Lys Ser His Leu Ser Met Trp Asn Pro Lys Ile Tyr Val Gly Asp
      180          185          190
Ile Pro Val Leu Tyr Leu Pro Tyr Ile Phe Met Ser Thr Ser Asn Lys
      195          200          205
Arg Thr Thr Gly Phe Leu Tyr Pro Glu Phe Gly Thr Ser Thr
      210          215          220

```

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...53

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438

```

Met Leu Asp Phe Asp Leu Val Leu Phe Gly Ala Thr Gly Asp Leu Ala
1           5           10           15
Met Arg Lys Leu Phe Val Ser Leu Tyr Glu Ile Tyr Ile Ser Phe Met
      20           25           30
Val Leu Lys Thr Ile Leu Gly Leu Ser His Arg Gly Val Arg Ser Tyr
      35           40           45
Pro Met Lys Ser Phe
      50

```

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

364

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439

```

Met Gln Asp Leu Pro Pro Cys Pro Lys Arg Asn Asp Ala Tyr Thr Tyr
1      5      10      15
His Asp Gly Thr Gln Phe Val Cys Ser Ser Cys Leu Tyr Glu Trp Asn
      20      25      30
Gly Asn Glu Ile Ser Asn Glu Glu Leu Ile Val Lys Asp Cys His Asn
      35      40      45
Asn Leu Leu Gln Asn Gly Asp Ser Val Ile Leu Ile Lys Asp Leu Lys
      50      55      60
Val Lys Gly Ser Ser Leu Val Leu Lys Lys Gly Thr Lys Ile Lys Asn
65      70      75      80
Ile Lys Leu Val Asn Ser Asp His Asn Val Asp Cys Lys Val Glu Gly
      85      90      95
Gln Ser Leu Ser Leu Lys Ser Glu Phe Leu Lys Lys Ala
      100      105

```

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440

```

Val Asp Gly Ala Ile Ile Thr Gly Asn Tyr Ala Leu Gln Ala Lys Leu
1      5      10      15
Thr Gly Ala Leu Phe Ser Glu Asp Lys Asp Ser Pro Tyr Ala Asn Leu
      20      25      30
Val Ala Ser Arg Glu Asp Asn Ala Gln Asp Glu Ala Ile Lys Ala Leu
      35      40      45
Ile Glu Ala Leu Gln Ser Glu Lys Thr Arg Lys Phe Ile Leu Asp Thr
      50      55      60
Tyr Lys Gly Ala Ile Ile Pro Ala Phe
65      70

```

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

365

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441

```

Val Phe Thr Met Leu Val Leu Val Leu Ser Asp Asn Phe Leu Gly Leu
1           5           10           15
Phe Ile Gly Trp Glu Gly Val Gly Leu Cys Ser Tyr Leu Leu Ile Gly
20           25           30
Phe Trp Tyr His Lys Lys Ser Ala Asn Asn Ala Ser Ile Glu Ala Phe
35           40           45
Val Met Asn Arg Ile Thr Asp Leu Gly Met Leu Met Gly Ile Ile Leu
50           55           60
Ile Phe Trp Asn Phe Gly Thr Leu Gln Tyr Lys Glu Val Phe Ser Met
65           70           75           80
Leu Asn Asn Ala Asp Tyr Ser Met Leu Phe Tyr Ile Ser Val Phe Leu
85           90           95
Phe Ile Gly Ala Met Gly Lys Ser Ala Gln Phe Pro Met His Thr Trp
100          105          110
Leu Ala Asn Ala Met Glu Gly Pro Thr Pro Val Ser Ala Leu Ile His
115          120          125
Ala Thr Thr Met Val Thr Ala Gly Val Tyr Leu Ile Ile Arg Ala Asn
130          135          140
Pro Leu Tyr Ser Ala Val Phe Glu Val Gly Tyr Phe Ile Ala Cys Leu
145          150          155          160
Gly Ala Phe Val Ala Leu Phe Gly Ala Ser Met Ala Leu Val Asn Lys
165          170          175
Asp Leu Lys Arg Ile Val Glu Tyr Ser Thr Leu Ser Gln Leu Gly Leu
180          185          190
Tyr Val Cys Ser Gly Arg Ala Trp Gly Leu Cys Asp Arg Ala Phe Pro
195          200          205
Pro Leu Tyr Ala Cys Val Leu Gln Ile Pro Pro Phe Leu Arg Leu Arg
210          215          220
Gln Cys His Ala Cys Asp Gly Arg Gln Ser Gly Tyr Tyr
225          230          235

```

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

366

(B) LOCATION 1...91

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442

Val	Cys	Leu	Gly	Leu	Ala	Asp	Val	Met	Val	Val	Leu	Ser	Leu	His	Leu
1				5					10					15	
Asn	Leu	Asn	Pro	Thr	Asn	Pro	Lys	Trp	Leu	Asn	Arg	Asp	Arg	Leu	Val
			20					25					30		
Phe	Ser	Gly	Gly	His	Ala	Ser	Ala	Leu	Val	Tyr	Ser	Leu	Leu	His	Leu
		35					40					45			
Trp	Gly	Phe	Asp	Leu	Ser	Leu	Asp	Asp	Leu	Lys	Arg	Phe	Arg	Gln	Leu
	50					55					60				
His	Ser	Lys	Thr	Pro	Gly	His	Pro	Glu	Leu	His	His	Thr	Glu	Gly	Ile
65					70					75					80
Glu	Ile	Thr	Thr	Unk	Phe	Arg	Ala	Arg	Phe	Cys					
				85					90						

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...91

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442

Val	Cys	Leu	Gly	Leu	Ala	Asp	Val	Met	Val	Val	Leu	Ser	Leu	His	Leu
1				5					10					15	
Asn	Leu	Asn	Pro	Thr	Asn	Pro	Lys	Trp	Leu	Asn	Arg	Asp	Arg	Leu	Val
			20					25					30		
Phe	Ser	Gly	Gly	His	Ala	Ser	Ala	Leu	Val	Tyr	Ser	Leu	Leu	His	Leu
		35					40					45			
Trp	Gly	Phe	Asp	Leu	Ser	Leu	Asp	Asp	Leu	Lys	Arg	Phe	Arg	Gln	Leu
	50					55					60				
His	Ser	Lys	Thr	Pro	Gly	His	Pro	Glu	Leu	His	His	Thr	Glu	Gly	Ile
65					70					75					80
Glu	Ile	Thr	Thr	Unk	Phe	Arg	Ala	Arg	Phe	Cys					
				85					90						

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

367

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...97

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443

```

Met Met Ile Thr Lys Gln Ser Tyr Gln Arg Phe Ala Leu Met Arg Val
1           5           10           15
Phe Val Phe Ser Leu Ser Ala Phe Ile Phe Asn Thr Thr Glu Phe Val
          20           25           30
Pro Val Ala Leu Leu Ser Asp Ile Ala Lys Ser Phe Glu Met Glu Ser
          35           40           45
Ala Thr Val Gly Leu Met Ile Thr Ala Tyr Ala Trp Val Val Ser Leu
          50           55           60
Gly Ser Leu Pro Leu Met Leu Leu Ser Ala Lys Ile Glu Arg Lys Arg
65           70           75           80
Leu Leu Leu Phe Leu Phe Ala Leu Phe Ile Phe Ser His Ile Leu Ser
          85           90           95
Arg

```

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444

```

Met Lys Leu Arg Ala Ser Val Leu Ile Gly Val Ala Ile Leu Cys Leu
1           5           10           15
Ile Leu Ser Ala Cys Ser Asn Tyr Ala Lys Lys Val Val Lys Gln Lys
          20           25           30
Asn His Val Tyr Thr Pro Val Tyr Asn Glu Leu Ile Glu Lys Tyr Ser
          35           40           45
Glu Ile Pro Leu Asn Asp Lys Leu Lys Asp Thr Pro Phe Met Val Gln
          50           55           60
Val Lys Leu Pro Asn Tyr Lys Asp Tyr Leu Leu Asp Asn Lys Gln Val
65           70           75           80
Val Leu Thr Phe Lys Leu Val His His Ser Lys Lys Ile Thr Leu Ile
          85           90           95
Gly Asp Ala Asn Lys Ile Leu Gln Tyr Lys Asn Tyr Phe Gln Ala Asn
          100          105          110
Gly Ala Arg Ser Asp Ile Asp Phe Tyr Leu Gln Pro Thr Leu Asn Gln
          115          120          125
Lys Gly Val Val Met Ile Ala Ser Asn Tyr Asn Asp Asn Pro Asn Asn
          130          135          140
Lys Glu Lys Pro Gln Thr Phe Asp Val Leu Gln Gly Ser Gln Pro Met
145          150          155          160
Leu Gly Ala Asn Thr Lys Asn Leu His Gly Tyr Asp Val Ser Gly Ala
          165          170          175

```

368

```

Asn Asn Lys Gln Val Ile Asn Glu Val Ala Arg Glu Lys Ala Gln Leu
      180      185      190
Glu Lys Ile Asn Gln Tyr Tyr Lys Thr Leu Leu Gln Asp Lys Glu Gln
      195      200      205
Glu Tyr Thr Thr Arg Lys Asn Asn Gln Arg Glu Ile Leu Glu Thr Leu
      210      215      220
Ser Asn Arg Ala Gly Tyr Gln Met Arg Gln Asn Val Ile Ser Ser Glu
      225      230      235      240
Ile Phe Lys Asn Gly Asn Leu Asn Met Gln Ala Lys Glu Glu Glu Val
      245      250      255
Arg Glu Lys Leu Gln Glu Glu Arg Glu Asn Glu Tyr Leu Arg Asn Gln
      260      265      270
Ile Arg Ser Leu Leu Ser Gly Lys
      275      280

```

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445

```

Met Thr Thr Pro Met Ile Ile Ile Ser Leu Glu Met Gly Leu Ser Leu
1      5      10      15
Val Pro Met Arg Gln Cys Leu Val Cys Gln Ala Leu Ala Arg Ser Ile
      20      25      30
Ser Trp Asn Gly Leu Gly Gly Asn Val Arg Asn Thr Lys Val Tyr Gly
      35      40      45
Lys Phe Ala Ala Tyr His His Leu Gln Lys Tyr Leu Leu Ile Asp Leu
      50      55      60
Ile Ala Arg Phe Lys Thr Gln Gly Gly Tyr Ile Phe Arg Tyr Asn Thr
      65      70      75      80
Asp Asp Tyr Leu Pro Leu Asn Ser Thr Phe Tyr Met Gly Gly Val Thr
      85      90      95
Thr Val Arg Gly Phe Arg Asn Gly Ser Ile Thr Pro Lys Asp Glu Phe
      100      105      110
Gly Leu Trp Leu Gly Gly Asp Gly Ile Phe Thr Unk Ser Thr Glu Leu
      115      120      125
Ser Tyr Gly Val Leu Lys Ala Ala Lys Met Arg Leu Ala Trp Phe Phe
      130      135      140
Asp Phe Gly Phe Leu Thr Phe Unk Thr Pro Thr Arg Gly Ser Phe Phe
      145      150      155      160
Tyr Asn Ala Unk Thr Thr Thr Ala Asn Phe Lys Asp Tyr Unk Val Val
      165      170      175
Gly Unk Unk Phe Glu Unk Ala Thr Trp Arg Ala
      180      185

```

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

369

(A) LENGTH: 187 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445

```

Met Thr Thr Pro Met Ile Ile Ile Ser Leu Glu Met Gly Leu Ser Leu
1          5          10          15
Val Pro Met Arg Gln Cys Leu Val Cys Gln Ala Leu Ala Arg Ser Ile
          20          25          30
Ser Trp Asn Gly Leu Gly Gly Asn Val Arg Asn Thr Lys Val Tyr Gly
          35          40          45
Lys Phe Ala Ala Tyr His His Leu Gln Lys Tyr Leu Leu Ile Asp Leu
          50          55          60
Ile Ala Arg Phe Lys Thr Gln Gly Gly Tyr Ile Phe Arg Tyr Asn Thr
          65          70          75          80
Asp Asp Tyr Leu Pro Leu Asn Ser Thr Phe Tyr Met Gly Gly Val Thr
          85          90          95
Thr Val Arg Gly Phe Arg Asn Gly Ser Ile Thr Pro Lys Asp Glu Phe
          100         105         110
Gly Leu Trp Leu Gly Gly Asp Gly Ile Phe Thr Unk Ser Thr Glu Leu
          115         120         125
Ser Tyr Gly Val Leu Lys Ala Ala Lys Met Arg Leu Ala Trp Phe Phe
          130         135         140
Asp Phe Gly Phe Leu Thr Phe Unk Thr Pro Thr Arg Gly Ser Phe Phe
          145         150         155         160
Tyr Asn Ala Unk Thr Thr Thr Ala Asn Phe Lys Asp Tyr Unk Val Val
          165         170         175
Gly Unk Unk Phe Glu Unk Ala Thr Trp Arg Ala
          180         185

```

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446

```

Met Trp Leu Asp His Ile Ala Lys Glu Ile Arg Ser Leu Val Glu Asn
1          5          10          15

```

SUBSTITUTE SHEET (RULE 26)

370

Asp Ile Glu Val Gly Ile Val Ile Gly Gly Gly Asn Ile Ile Arg Gly
 20 25 30
 Val Ser Ala Ala Leu Gly Gly Ile Ile Arg Arg Thr Ser Gly Asp Tyr
 35 40 45
 Met Gly Met Leu Ala Thr Val Ile Lys Arg
 50 55

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...85

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447

Val His Asn Phe His Trp Asn Val Lys Gly Thr Asp Phe Phe Asn Val
 1 5 10 15
 His Lys Ala Thr Glu Glu Ile Tyr Glu Gly Phe Ala Asp Met Phe Asp
 20 25 30
 Asp Leu Ala Glu Arg Ile Val Gln Leu Gly His His Pro Leu Val Thr
 35 40 45
 Leu Ser Glu Ala Ile Lys Leu Thr Arg Val Lys Glu Glu Thr Lys Thr
 50 55 60
 Ser Phe His Ser Lys Asp Ile Phe Lys Glu Ile Leu Glu Asp Tyr Lys
 65 70 75 80
 His Leu Glu Lys Glu
 85

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448

Met Asn Lys Thr Ile Lys Ala Ala Ala Leu Ala Tyr Asn Met Gly Gln
 1 5 10 15
 Asp His Ala Pro Lys Val Ile Ala Ser Gly Val Gly Glu Val Ala Lys

371

```

      20      25      30
Arg Ile Ile Gln Lys Ala Lys Glu Tyr Asp Ile Ala Leu Phe Ser Asn
      35      40      45
Pro Met Leu Val Asp Ser Leu Leu Lys Val Glu Leu Asp Cys Ala Ile
      50      55      60
Pro Glu Glu Leu Tyr Glu Ser Val Val Gln Val Phe Leu Trp Leu Asn
      65      70      75      80
Ser Val Glu Asn Asn Ala Gln Met Ser Lys
      85      90

```

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449

```

Met Gln Ala Leu Lys Ser Leu Leu Glu Val Ile Thr Lys Leu Gln Asn
1      5      10      15
Leu Gly Gly Tyr Leu Met His Ile Ala Ile Phe Ile Ile Phe Ile Trp
      20      25      30
Ile Gly Gly Leu Lys Phe Val Pro Tyr Glu Ala Glu Gly Ile Ala Pro
      35      40      45
Phe Val Unk Asn Ser Pro Phe Phe Ser Phe Met Tyr Lys Phe Glu Lys
      50      55      60
Pro Ala Tyr Lys Gln His Lys Met Ser Glu Ser Gln Ser Met Gln Glu
      65      70      75      80
Glu Met Gln Asp Asn Pro Lys Ile Val Glu Asn Lys Unk Trp His Lys
      85      90      95
Glu Asn Arg Thr Ser Phe Ser Gly
      100

```

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...104

372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449

```

Met Gln Ala Leu Lys Ser Leu Leu Glu Val Ile Thr Lys Leu Gln Asn
1          5          10          15
Leu Gly Gly Tyr Leu Met His Ile Ala Ile Phe Ile Ile Phe Ile Trp
20          25          30
Ile Gly Gly Leu Lys Phe Val Pro Tyr Glu Ala Glu Gly Ile Ala Pro
35          40          45
Phe Val Unk Asn Ser Pro Phe Phe Ser Phe Met Tyr Lys Phe Glu Lys
50          55          60
Pro Ala Tyr Lys Gln His Lys Met Ser Glu Ser Gln Ser Met Gln Glu
65          70          75          80
Glu Met Gln Asp Asn Pro Lys Ile Val Glu Asn Lys Unk Trp His Lys
85          90          95
Glu Asn Arg Thr Ser Phe Ser Gly
100

```

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450

```

Met Gly Lys Ile Ser Ala His Leu Ala His Glu Ile Arg Asn Pro Val
1          5          10          15
Gly Ser Ile Ser Leu Leu Ala Ser Val Leu Leu Lys His Ala Asn Glu
20          25          30
Lys Thr Lys Pro Ile Val Val Glu Leu Gln Lys Ala Leu Trp Arg Val
35          40          45
Glu Arg Ile Ile Lys Ala Thr Leu Leu Phe Ser Lys Gly Ile Gln Ala
50          55          60
Asn Arg Thr Lys Gln Ser Leu Lys Thr Leu Glu Ser Asp Leu Lys Glu
65          70          75          80
Ala Leu Asn Cys Tyr Thr Tyr Ser Lys Asp Ile Asp Phe Leu Phe Asn
85          90          95
Phe Ser Asp Glu Glu Gly Phe Phe Asp Phe Asp Leu Met Gly Ile Val
100          105          110
Leu Gln Asn Phe Leu Tyr Asn Ala Ile Asp Ala Ile Glu Ala Leu Glu
115          120          125
Glu Ser Glu Gln Gly Gln Val Lys Ile Glu Ala Phe Ile Gln Asn Glu
130          135          140
Phe Ile Val Phe Thr Ile Ile Asp Asn Gly Lys Glu Val Glu Asn Lys
145          150          155          160
Ser Ala Leu Phe Glu Pro Phe Glu Thr Thr Lys Leu
165          170

```

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

373

(A) LENGTH: 212 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451

Val	Ser	Glu	Phe	His	Gln	Val	Tyr	Asp	Pro	Leu	Gly	Asn	Ile	Trp	Leu
1				5					10				15		
Ser	Ala	Leu	Val	Ala	Leu	Leu	Pro	Ile	Leu	Leu	Phe	Phe	Leu	Ser	Leu
		20						25					30		
Met	Val	Phe	Lys	Leu	Lys	Gly	Tyr	Thr	Ala	Ala	Phe	Leu	Ser	Val	Ala
		35					40					45			
Leu	Ser	Ala	Ile	Ile	Ala	Val	Leu	Val	Tyr	Lys	Met	Pro	Val	Ser	Met
		50				55					60				
Val	Gly	Ser	Ser	Phe	Leu	Tyr	Gly	Phe	Leu	Tyr	Gly	Leu	Trp	Leu	Phe
65				70					75					80	
Ala	Trp	Ile	Ile	Ile	Ala	Ala	Ile	Phe	Leu	Tyr	Lys	Leu	Ser	Val	Lys
			85					90						95	
Ser	Gly	Tyr	Phe	Glu	Ile	Leu	Lys	Glu	Ser	Val	Gln	Ser	Ile	Thr	Leu
			100					105					110		
Asp	His	Arg	Ile	Leu	Val	Ile	Leu	Ile	Gly	Phe	Cys	Phe	Gly	Ser	Phe
		115						120				125			
Leu	Glu	Gly	Ala	Ile	Gly	Phe	Gly	Gly	Pro	Ile	Ala	Ile	Thr	Ala	Ala
		130				135					140				
Ile	Leu	Val	Gly	Leu	Gly	Leu	Ser	Pro	Leu	Tyr	Ser	Ala	Gly	Leu	Cys
145				150						155				160	
Leu	Ile	Ala	Asn	Thr	Ala	Pro	Val	Ala	Phe	Gly	Ala	Val	Gly	Ile	Pro
			165					170						175	
Ile	Ser	Ala	Met	Ala	Ser	Ala	Val	Gly	Val	Pro	Ala	Ile	Leu	Ile	Ser
			180					185					190		
Ala	Met	Thr	Gly	Lys	Ile	Leu	Phe	Phe	Val	Ser	Leu	Leu	Val	Pro	Phe
		195				200						205			
Phe	Ile	Val	Phe												
			210												

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...182

374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452

```

Met Glu Ile Lys Met Ala Lys Asp Tyr Gly Phe Cys Phe Gly Val Lys
1      5      10      15
Arg Ala Ile Gln Ile Ala Glu Lys Asn Gln Asn Ser Leu Ile Phe Gly
      20      25      30
Ser Leu Ile His Asn Ala Lys Glu Ile Asn Arg Leu Glu Lys Asn Phe
      35      40      45
Asn Val Lys Ile Glu Glu Asp Pro Lys Lys Ile Pro Lys Asn Lys Ser
      50      55      60
Val Ile Ile Arg Thr His Gly Ile Pro Lys Gln Asp Leu Glu Tyr Leu
      65      70      75      80
Lys Asn Lys Gly Val Lys Ile Thr Asp Ala Thr Cys Pro Tyr Val Ile
      85      90      95
Lys Pro Gln Gln Ile Val Glu Ser Met Ser Lys Glu Gly Tyr Gln Ile
      100     105     110
Val Leu Phe Gly Asp Ile Asn His Pro Glu Val Lys Gly Val Ile Ser
      115     120     125
Tyr Ala Thr Asn Gln Ala Leu Val Gly Asn Ser Leu Glu Glu Leu Gln
      130     135     140
Glu Lys Lys Leu Gln Arg Lys Val Ala Leu Val Ser Gln Thr Thr Gln
      145     150     155     160
Ala Asn Pro Lys Thr Leu Ala Asn Arg Phe Leu Phe Gly Gly Unk Cys
      165     170     175
Thr Glu Val Arg Ile Phe
      180

```

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear.

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453

```

Met Asp His Glu Phe Leu Ile Thr Met Arg Leu Ser Phe Ser Leu Ala
1      5      10      15
Leu Ile Thr Thr Leu Ile Leu Leu Pro Ile Gly Ile Phe Leu Gly Tyr
      20      25      30
Phe Leu Ser Leu Lys Arg Asn Leu Leu Thr Ser Leu Thr Glu Thr Leu
      35      40      45
Val Tyr Met Pro Leu Val Leu Pro Pro Ser Val Leu Gly Phe Tyr Leu
      50      55      60
Leu Leu Ile Phe Ser Pro Ser Ser Phe Leu Gly Ala Phe Leu Gln Asp
      65      70      75      80
Val Leu Asn Val Lys Leu Val Phe Ser Phe Gln Gly Leu Ile Leu Gly
      85      90      95
Ser Val Ile Phe Ser Leu Pro Phe Met Val Ser Pro Ile Lys Ser Ala
      100     105     110
Leu Ile Ser Leu Pro Thr Ser Leu Lys Glu Ala Ser Tyr Ser Leu Gly
      115     120     125
Lys Gly Glu Tyr Tyr Thr Leu Phe Phe Val Leu Leu Pro Asn Ile Lys

```

375

130	135	140
Pro Ser Val Leu Met Ala Ile Ile Thr Thr Phe Met His Thr Ile Gly		
145	150	155
Glu Phe Gly Val Val Met Met Leu Gly Gly Asp Ile Leu Gly Glu Thr		160
	165	170
Arg Val Ala Ser Ile Thr Ile Phe Asn Glu Ala Glu Ala Leu Asn Tyr		175
	180	185
Ser Lys Ala Ser Gln Tyr Ala Leu Thr Leu Thr Leu Ile Ser Phe Ser		190
	195	200
Leu Leu Phe Val Thr Leu Phe Leu Asn Lys Lys Gln Ser Ser Phe Leu		205
210	215	220

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454

Met His Pro Ile Met Phe Ala Tyr Ile Ala Asn Ala Leu Ala Gln Ala		
1	5	10
Arg Lys Ile Asn Gly Thr Leu Cys Met Ala Phe Gln Lys Ile Ser Gln		15
	20	25
Val Lys Glu Leu Gly Ile Asp Lys Ala Lys Ser Leu Ile Gly Asn Leu		30
	35	40
Ser Gln Val Ile Ile Tyr Pro Thr Lys Asp Thr Asp Glu Leu Ile Glu		45
	50	55
Cys Gly Val Pro Leu Ser Asp Ser Glu Ile Asn Phe Leu His Asn Thr		60
	65	70
Asp Met Arg Ala Arg Gln Val Leu Val Lys Asn Ile Val Thr Asn Ala		75
	80	85
Ser Ala Phe Ile Glu Ile Asp Leu Lys Lys Ile Cys Lys Asn Tyr Phe		90
	95	100
Ile Phe Leu Ile Ala Met Leu Val Ile Glu Lys Ser Ser Met Ile Leu		105
	110	115
Lys Lys Gln	120	125
130		

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

SUBSTITUTE SHEET (RULE 26)

376

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455

```

Met Cys Leu Thr Gly Gly Leu Met Arg Trp Leu Lys Ser Val Lys Pro
1          5          10          15
Glu Arg Ile Leu His Ser Val Val Glu Phe Val Asp Ile Ala Gly Leu
          20          25          30
Ile Lys Gly Ala Ser Lys Gly Glu Gly Leu Gly Asn Gln Phe Leu Ala
          35          40          45
Asn Ile Lys Glu Cys Glu Val Ile Leu Gln Val Val Arg Cys Phe Glu
          50          55          60
Asp Asp Asn Asn His Ala Cys Glu Arg
65          70

```

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...92

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456

```

Met His Val Ala Cys Leu Leu Ala Leu Gly Asp Asn Leu Ile Thr Leu
1          5          10          15
Ser Leu Leu Lys Glu Ile Ala Ser Lys Lys Gln Gln Gln Ser Leu Lys Ile
          20          25          30
Leu Gly Thr His Leu Thr Leu Lys Ile Ala Lys Leu Leu Glu Cys Glu
          35          40          45
Lys His Phe Glu Ile Ile Pro Val Phe Glu Asn Ile Pro Ala Phe Tyr
          50          55          60
Asp Leu Lys Lys Gln Gly Val Phe Trp Ala Met Lys Asp Phe Leu Trp
65          70          75          80
Leu Leu Lys Gln Leu Lys Asn Ile Lys Ser Asn Val
          85          90

```

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

377

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457

```

Met Lys Lys Lys Pro Leu Met Trp Arg Ile Cys Ala Leu Arg Arg Leu
1      5      10      15
Leu Leu Gly Phe Lys Arg Glu Arg Glu Leu Leu Ser Phe Ala Lys His
20      25      30
Trp Asn Ile Pro Thr Ile Val Val Phe Thr His Thr Gln Ala Glu Ala
35      40      45
Gly Asp Ala Phe Val Gln Glu Thr Lys Gly Ile Ile Asp Glu Glu Trp
50      55      60
Gly Phe Lys Gly Phe Val Arg Ala Tyr Val Arg Val Asn Ser Val Ala
65      70      75      80
Phe Ser Phe Arg Gly Leu Lys Val Pro Val Glu Gly Leu Glu Glu Leu
85      90      95
Val Asp Glu Thr Lys Lys Cys Leu Ser Asp Ala Glu Lys Asn Lys Lys
100     105     110
Arg His Phe Leu Ser Ile Gln Arg Val Lys Ile Gln Glu Arg Lys Gln
115     120     125
Ala Met Ile Glu Glu Cys Lys Thr Ile Ile His Val Ala Ser Gly Ala
130     135     140
Ala Gly Val Ala Gly Leu Ile Pro Ile Pro Phe Ser Asp Ala Leu Ala
145     150     155     160
Ile Ala Pro Ile Gln Ala Gly Met Ile Tyr Lys Met Asn Asp Ala Phe
165     170     175
Gly Met Asp Leu Asp Lys Ser Val Gly Ala Ser Leu Val Ala Gly Leu
180     185     190
Leu Gly Val Asn Cys Arg Ala Ser Gly Glu Asp Ser Arg
195     200     205

```

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...41

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458

```

Val Leu Gly Val Unk Asn Leu Arg Gly Asn Val Phe Pro Leu Ile Ser
1      5      10      15
Leu Arg Leu Lys Phe Gly Leu Lys Ala Glu Lys Gln Asn Lys Asp Thr
20      25      30
Arg Tyr Leu Val Val Arg His Asn Asp
35      40

```

378

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459

```

Val Lys Ser Val Phe Ser Glu Glu Lys Glu Thr Pro Val Thr Lys Glu
1      5      10      15
Asn Gly Ser Tyr Leu Ile Ala Tyr Asp Pro Leu Asp Gly Ser Ser Val
20     25     30
Met Glu Ala Asn Phe Leu Val Gly Thr Ile Ile Gly Val Tyr Glu Lys
35     40     45
Asp Tyr Lys Ala Gln Asn Leu Val Ala Ser Leu Tyr Val Val Phe Gly
50     55     60
His Lys Ile Glu Leu Val Val Ala Leu Glu Glu Val Tyr Arg Tyr Ala
65     70     75     80
Phe Tyr Gln Asn Lys Phe His Phe Ile Glu Thr Ile Val Leu Glu Asn
85     90     95
Lys Gly Lys Ile Ile Ala Ser Gly Gly Asn Gln Lys Asp Phe Ser Leu
100    105    110
Gly Leu Lys Lys Ala Leu Glu Gly Phe Phe Ala Glu Asn Tyr Arg Leu
115    120    125
Arg Tyr Ser Gly Ser Met Val Ala Asp Val His His Val Leu Val Lys
130    135    140
Lys Gly Gly Met Phe Ser Tyr Pro Gln Lys Lys Leu Arg Lys Leu Phe
145    150    155    160
Glu Val Phe Pro Leu Ala Leu Met Val Glu Lys Ala Lys Gly Glu Ala
165    170    175
Phe Tyr Phe Asp Lys Gly Val Lys Lys Arg Leu Leu Asp Gln Ser Val
180    185    190
Glu Ser Tyr His Glu Lys Ser Glu Cys Tyr Leu Ala Ser Pro His Glu
195    200    205
Ala Gln Ile Leu Glu Lys His Leu Lys Gly Glu
210    215

```

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

379

(A) NAME/KEY: misc_feature
(B) LOCATION 1...188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460

```

Met Lys Ser Ile Gly Glu Val Met Ala Ile Gly Gly Asn Phe Leu Glu
1      5      10      15
Ala Leu Gln Lys Ala Leu Cys Ser Leu Glu Asn Asn Trp Leu Gly Phe
20      25      30
Glu Ser Leu Ser Lys Asp Leu Glu Ala Ile Lys Lys Glu Ile Arg Arg
35      40      45
Pro Asn Pro Lys Arg Leu Leu Tyr Ile Ala Asp Ala Phe Arg Leu Gly
50      55      60
Val Ser Val Asp Glu Val Phe Glu Leu Cys Gln Ile Asp Arg Trp Phe
65      70      75      80
Leu Ser Gln Ile Gln Lys Leu Val Lys Ala Glu Glu Gly Ile Asn Ser
85      90      95
Ser Val Leu Thr Asp Ala Lys Lys Leu Arg Gly Leu Lys Asn Leu Gly
100     105     110
Phe Ser Asp Ala Arg Ile Ala Thr Lys Ile Lys Glu Asn Glu Asn Leu
115     120     125
Glu Val Ser Pro Phe Glu Val Glu Leu Ala Arg Ser Asn Leu Gln Ile
130     135     140
Ala Pro His Phe Glu Glu Val Asp Thr Cys Ala Ala Glu Phe Leu Ser
145     150     155     160
Leu Thr Leu Ile Cys Ile Pro Pro Met Pro Leu Thr Leu Cys Pro Leu
165     170     175
Leu Glu Thr Asn Lys Lys Asn Lys Lys Arg Lys Ser
180     185

```

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461

```

Met Phe Gly Asn Lys Gln Leu Gln Leu Gln Ile Ser Gln Lys Asp Ser
1      5      10      15
Glu Ile Ala Glu Leu Lys Lys Glu Val Asn Leu Tyr Gln Ser Leu Leu
20      25      30
Asn Leu Cys Leu His Glu Gly Phe Val Gly Ile Lys Asn Asn Lys Val
35      40      45
Val Phe Lys Ser Gly Asn Leu Ala Ser Leu Asn Asn Leu Glu Glu Gln
50      55      60
Ser Val His Phe Lys Glu Asn Ala Glu Ser Val Asn Leu Gln Gly Val
65      70      75      80
Ser Tyr Ser Leu Lys Ser Gln Asn Ile Asp Gly Val Gln Tyr Phe Ser
85      90      95
Leu Ala Lys Lys Thr Gly Gly Val Gly Glu Tyr His Lys Asn Asp Leu
100     105     110

```

380

```

Phe Lys Thr Phe Cys Thr Ser Leu Lys Glu Gly Leu Glu Asn Ala Gln
      115              120              125
Glu Ser Met Gln Tyr Phe His Gln Glu Thr Gly Leu Leu Leu Asn Ala
      130              135              140
Ala Lys Asn Gly Glu Glu His Ser Asn Glu Gly Leu Ile Thr Val Asn
145              150              155              160
Lys Thr Gly Gln Asp Ile Glu Ser Leu Tyr Glu Lys Met Gln Asn Ala
      165              170              175
Thr Ser Leu Ala Asp Ser Leu Asn Gln Arg Ser Asn Glu Ile Thr Gln
      180              185              190
Val Ile Ser Leu Ile Asp Asp Ile Ala Glu Gln Thr Asn Leu Leu Ala
      195              200              205
Leu Asn Ala Ala Ile Glu Ala Ala Arg Ala Val Asn Met Ala Glu Gly
      210              215              220
Leu Arg Trp Trp Leu Met Arg
225              230

```

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462

```

Met Trp Ile Met Ser Ser Leu Ser Ser Ser Phe Phe His Ser Leu Phe
1              5              10              15
Phe Ile Lys Ser Asn Pro Gly Gln Leu Leu Lys Gly Trp Gly Ser Lys
      20              25              30
Ile Phe Phe Ile Asn Arg Lys Phe Val Leu Ala Gln Tyr Asn Pro Ser
      35              40              45
Val Ser Ile Phe Ile Leu Leu Asn Arg Val Phe Gly Val Gly Val
      50              55              60

```

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...182

381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463

```

Met Gln Phe Glu Glu Met Lys Glu Leu Ala His Gln Ile Gly Val Phe
1           5           10           15
Tyr His Val Gly Val Asp Gly Ile Ala Leu Phe Leu Leu Leu Leu Asn
          20           25           30
Ala Ile Val Val Leu Leu Ser Val Val Tyr Val Lys Glu Arg Arg Lys
          35           40           45
Asp Phe Val Ile Cys Leu Leu Leu Leu Unk Gly Ile Leu Met Gly Val
50           55           60
Phe Ser Ser Leu Asn Val Ile Phe Phe Tyr Ala Phe Trp Glu Ile Ser
65           70           75           80
Leu Leu Pro Val Leu Tyr Leu Ile Gly Arg Phe Gly Arg Asn Asn Lys
          85           90           95
Ile Tyr Ser Gly Met Lys Phe Phe Leu Tyr Thr Phe Leu Ala Ser Leu
          100          105          110
Cys Met Leu Leu Gly Ile Leu Tyr Ile Gly Tyr Asp Tyr Ala Asn Asn
          115          120          125
Tyr Gly Met Met Ser Phe Asp Ile Leu Asp Trp Tyr Gln Leu Asn Phe
130          135          140
Ser Ser Gly Ile Lys Thr Trp Leu Phe Val Ala Phe Leu Ile Gly Ile
145          150          155          160
Ala Val Lys Ile Pro Leu Phe Pro Phe Thr His Gly Cys Leu Met Arg
          165          170          175
Ile Leu Thr Pro Pro Leu
          180

```

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463

```

Met Gln Phe Glu Glu Met Lys Glu Leu Ala His Gln Ile Gly Val Phe
1           5           10           15
Tyr His Val Gly Val Asp Gly Ile Ala Leu Phe Leu Leu Leu Leu Asn
          20           25           30
Ala Ile Val Val Leu Leu Ser Val Val Tyr Val Lys Glu Arg Arg Lys
          35           40           45
Asp Phe Val Ile Cys Leu Leu Leu Leu Unk Gly Ile Leu Met Gly Val
50           55           60
Phe Ser Ser Leu Asn Val Ile Phe Phe Tyr Ala Phe Trp Glu Ile Ser
65           70           75           80
Leu Leu Pro Val Leu Tyr Leu Ile Gly Arg Phe Gly Arg Asn Asn Lys
          85           90           95
Ile Tyr Ser Gly Met Lys Phe Phe Leu Tyr Thr Phe Leu Ala Ser Leu
          100          105          110
Cys Met Leu Leu Gly Ile Leu Tyr Ile Gly Tyr Asp Tyr Ala Asn Asn
          115          120          125

```

382

```

Tyr Gly Met Met Ser Phe Asp Ile Leu Asp Trp Tyr Gln Leu Asn Phe
 130          135          140
Ser Ser Gly Ile Lys Thr Trp Leu Phe Val Ala Phe Leu Ile Gly Ile
145          150          155          160
Ala Val Lys Ile Pro Leu Phe Pro Phe Thr His Gly Cys Leu Met Arg
          165          170          175
Ile Leu Thr Pro Pro Leu
          180

```

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464

```

Val Lys Lys Tyr Ala Glu Asp Phe Ile Thr Lys Asp Glu Val Lys Ser
 1          5          10          15
Leu Leu Glu Arg Leu Ala Lys Asp Tyr Pro Thr Ile Val Glu Glu Ser
          20          25          30
Lys Lys Ile Pro Thr Gly Ala Ile Arg Ser Val Leu Gln Ala Leu Leu
          35          40          45
His Glu Lys Ile Pro Ile Lys Asp Met Leu Thr Ile Leu Glu Thr Ile
          50          55          60
Thr Asp Ile Ala Pro Leu Val Gln Asn Asp Val Asn Ile Leu Thr Glu
          65          70          75          80
Gln Val Arg Ala Arg Leu Ser Arg Val Ile Thr Asn Ala Phe Lys Ser
          85          90          95
Glu Asp Gly Arg Leu Lys Phe Leu Thr Phe Ser Thr Asp Unk Glu Gln
          100          105          110
Phe Unk Ala Gln
          115

```

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...116

383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464

```

Val Lys Lys Tyr Ala Glu Asp Phe Ile Thr Lys Asp Glu Val Lys Ser
1      5      10      15
Leu Leu Glu Arg Leu Ala Lys Asp Tyr Pro Thr Ile Val Glu Glu Ser
20     25     30
Lys Lys Ile Pro Thr Gly Ala Ile Arg Ser Val Leu Gln Ala Leu Leu
35     40     45
His Glu Lys Ile Pro Ile Lys Asp Met Leu Thr Ile Leu Glu Thr Ile
50     55     60
Thr Asp Ile Ala Pro Leu Val Gln Asn Asp Val Asn Ile Leu Thr Glu
65     70     75     80
Gln Val Arg Ala Arg Leu Ser Arg Val Ile Thr Asn Ala Phe Lys Ser
85     90     95
Glu Asp Gly Arg Leu Lys Phe Leu Thr Phe Ser Thr Asp Unk Glu Gln
100    105    110
Phe Unk Ala Gln
115

```

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465

```

Val Gly Ala Asn Pro Val Pro His Ala Gln Ile Leu Gln Ser Val Val
1      5      10      15
Asp Asp Leu Lys Glu Lys Gly Ile Lys Leu Val Ile Val Ser Phe Thr
20     25     30
Asp Tyr Val Leu Pro Asn Leu Ala Leu Asn Asp Gly Ser Leu Asp Ala
35     40     45
Asn Tyr Phe Gln His Arg Pro Tyr Leu Asp Arg Phe Asn Leu Asp Arg
50     55     60
Lys Met His Leu Val Gly Leu Ala Asn Ile His Val Glu Pro Leu Arg
65     70     75     80
Phe Tyr Ser Gln Lys Ile Thr Asp Ile Lys Asn Leu Lys Lys Gly Ser
85     90     95
Val Ile Ala Val Pro Asn Asp Pro Ala Asn Gln Gly Arg Ala Leu Ile
100    105    110
Leu Leu His Lys Gln Gly Leu Ile Ala Leu Lys Asp Pro Ser Asn Leu
115    120    125
Tyr Ala Thr Glu Phe Asp Ile Val Lys Asn Pro Tyr Asn Ile Lys Ile
130    135    140
Lys Pro Leu Glu Ala Ala Val Ile Ala
145    150

```

(2) INFORMATION FOR SEQ ID NO:466:

384

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...43

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466

```

Met Gly Leu Val Ala Ser Gly Ile Asn Asp Glu Glu Leu Leu Lys Trp
1           5           10           15
Leu Gln Ala Phe Gly Leu Lys Met Gly Leu Cys Phe Gln Val Leu Asp
          20           25           30
Asp Ile Ile Asp Val Thr Gln Asp Glu Lys Glu
          35           40

```

(2) INFORMATION FOR SEQ ID NO:467:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 240 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467

```

Met Met Lys Asn Lys Arg Ser Gln Asn Ser Pro Tyr Val Thr Pro Asp
1           5           10           15
Asn Pro Tyr Leu Thr Leu Glu Lys Ala Leu Gly Tyr Ser Phe Lys Asp
          20           25           30
Lys Arg Leu Leu Glu Gln Ala Leu Thr His Lys Ser Cys Lys Leu Ala
          35           40           45
Leu Asn Asn Glu Arg Leu Glu Phe Leu Gly Asp Ala Val Leu Gly Leu
          50           55           60
Val Ile Gly Glu Leu Leu Tyr His Lys Phe Unk Unk Unk Asp Gly Gly
          65           70           75           80
Lys Leu Ser Lys Leu Arg Ala Ser Ile Val Ser Ala His Gly Phe Thr
          85           90           95
Lys Leu Ala Lys Ala Ile Ala Leu Gln Asp Tyr Leu Arg Val Ser Ser
          100          105          110
Ser Glu Glu Ile Ser Lys Gly Arg Glu Lys Pro Ser Ile Leu Ser Ser
          115          120          125
Ala Phe Glu Ala Leu Met Ala Gly Val Tyr Leu Glu Ala Gly Leu Ala
          130          135          140
Lys Val Arg Lys Ile Ile Gln Asn Leu Leu Asn Arg Ala Tyr Lys Arg

```

SUBSTITUTE SHEET (RULE 26)

385

145		150		155		160									
Leu	Asp	Leu	Glu	His	Leu	Phe	Met	Asp	Tyr	Lys	Thr	Ala	Leu	Gln	Glu
		165		170		175									
Leu	Thr	Gln	Unk	Gln	Phe	Cys	Val	Ile	Pro	Thr	Tyr	Gln	Leu	Leu	Gln
		180		185		190									
Glu	Lys	Gly	Pro	Asp	His	His	Lys	Glu	Phe	Glu	Met	Ala	Leu	Tyr	Ile
		195		200		205									
Gln	Asp	Lys	Met	Tyr	Ala	Thr	Ala	Lys	Gly	Lys	Ser	Lys	Lys	Glu	Ala
		210		215		220									
Glu	Gln	Gln	Cys	Ala	Tyr	Gln	Ala	Leu	Gln	Asn	Leu	Arg	Lys	Pro	Asn
		225		230		235									240

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467

Met	Met	Lys	Asn	Lys	Arg	Ser	Gln	Asn	Ser	Pro	Tyr	Val	Thr	Pro	Asp
1				5				10						15	
Asn	Pro	Tyr	Leu	Thr	Leu	Glu	Lys	Ala	Leu	Gly	Tyr	Ser	Phe	Lys	Asp
		20					25						30		
Lys	Arg	Leu	Leu	Glu	Gln	Ala	Leu	Thr	His	Lys	Ser	Cys	Lys	Leu	Ala
		35			40							45			
Leu	Asn	Asn	Glu	Arg	Leu	Glu	Phe	Leu	Gly	Asp	Ala	Val	Leu	Gly	Leu
		50			55					60					
Val	Ile	Gly	Glu	Leu	Leu	Tyr	His	Lys	Phe	Unk	Unk	Asp	Gly	Gly	
		65		70				75					80		
Lys	Leu	Ser	Lys	Leu	Arg	Ala	Ser	Ile	Val	Ser	Ala	His	Gly	Phe	Thr
		85			90								95		
Lys	Leu	Ala	Lys	Ala	Ile	Ala	Leu	Gln	Asp	Tyr	Leu	Arg	Val	Ser	Ser
		100			105							110			
Ser	Glu	Glu	Ile	Ser	Lys	Gly	Arg	Glu	Lys	Pro	Ser	Ile	Leu	Ser	Ser
		115			120							125			
Ala	Phe	Glu	Ala	Leu	Met	Ala	Gly	Val	Tyr	Leu	Glu	Ala	Gly	Leu	Ala
		130			135					140					
Lys	Val	Arg	Lys	Ile	Ile	Gln	Asn	Leu	Leu	Asn	Arg	Ala	Tyr	Lys	Arg
		145		150				155						160	
Leu	Asp	Leu	Glu	His	Leu	Phe	Met	Asp	Tyr	Lys	Thr	Ala	Leu	Gln	Glu
		165			170									175	
Leu	Thr	Gln	Unk	Gln	Phe	Cys	Val	Ile	Pro	Thr	Tyr	Gln	Leu	Leu	Gln
		180			185								190		
Glu	Lys	Gly	Pro	Asp	His	His	Lys	Glu	Phe	Glu	Met	Ala	Leu	Tyr	Ile
		195			200						205				
Gln	Asp	Lys	Met	Tyr	Ala	Thr	Ala	Lys	Gly	Lys	Ser	Lys	Lys	Glu	Ala
		210		215							220				
Glu	Gln	Gln	Cys	Ala	Tyr	Gln	Ala	Leu	Gln	Asn	Leu	Arg	Lys	Pro	Asn
		225		230				235							240

386

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468

```

Met Gly Phe Asn Arg Leu Val Asp Arg Asp Ile Asp Lys Asp Asn Pro
 1           5           10           15
Arg Thr Lys Asn Arg Pro Ser Val Asp Gly Arg Ile Ser Val Lys Gly
          20           25           30
Met Val Ile Phe Ser Val Ser Asn Ala Leu Leu Phe Val Gly Val Ser
          35           40           45
Tyr Phe Ile Asn Pro Leu Ala Phe Lys Leu Ser Leu Pro Phe Leu Ile
 50           55           60
Ile Leu Gly Gly Tyr Ser Tyr Phe Lys Arg Phe Ser Ser Leu Ala His
 65           70           75           80
Phe Val Val Gly Leu Ala Leu Gly Leu Ala Pro Ile Ala Gly Ser Val
          85           90           95
Ala Val Leu Gly Asp Ile Pro Leu Trp Asn Val Phe Leu Ala Leu Gly
          100          105          110
Val Met Leu Trp Val Ala Gly Phe Asp Leu Leu Tyr Ser Leu Gln Asp
          115          120          125
Met Glu Phe Asp Lys Glu Arg Gly Leu Phe Ser Ile Pro Ser Gln Leu
          130          135          140
Gly Glu Lys Trp Cys Leu Asn Leu Ser Arg Leu Ser His Leu Val Ala
          145          150          155          160
Leu Ile Cys Trp Leu Cys Phe Val Lys Cys Tyr His Gly Gly Leu Phe
          165          170          175
Ala Tyr Leu Gly Leu Gly Val Ser Ala Leu Ile Leu Leu Tyr Glu Gln
          180          185          190
Ile Leu Val Ala Arg Asp Tyr Lys Asn Ile Pro Lys Ser Leu Phe Cys
          195          200          205
Glu

```

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

387

(A) NAME/KEY: misc_feature
(B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469

Val	Glu	Gln	Asn	Lys	Ile	Ile	Lys	Leu	Phe	Thr	Val	Ala	Thr	Met	Ala
1			5					10						15	
Met	Met	Pro	Pro	Thr	Leu	Ile	Gly	Thr	Ile	Asn	Gly	Met	Asn	Phe	Lys
		20					25				30				
Phe	Met	Pro	Glu	Leu	Glu	Trp	Gln	Tyr	Gly	Tyr	Leu	Phe	Ala	Leu	Ile
		35				40					45				
Val	Met	Ala	Ile	Ser	Thr	Ile	Leu	Pro	Val	Ile	Tyr	Phe	Lys	Lys	Lys
	50				55				60						
Gly	Leu	Val	Val	Ala	Phe	His	Gly	Ile	Phe	Ile	Leu	Thr	Leu	Arg	Arg
65				70				75						80	
Ser	Phe	Tyr	Thr	Ala	Trp	His	Ser	Leu	Leu	Gly	Tyr	Ala	Thr	Leu	
			85					90						95	

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470

Leu	Leu	Val	Leu	Leu	Asn	Leu	Lys	Unk	Thr	Pro	Asn	Leu	Met	Trp	Pro
1			5					10						15	
Leu	Asp	Ile	Ile	Val	Val	Val	Ala	Trp	Val	Leu	Trp	Gly	Val	Asn	Met
		20					25				30				
Phe	Gly	Ser	Met	Ser	Val	Arg	Arg	Glu	Asn	Thr	Ile	Tyr	Val	Ser	Leu
		35				40					45				
Trp	Tyr	Tyr	Ile	Ala	Thr	Tyr	Val	Gly	Ile	Ala	Val	Met	Tyr	Ile	Phe
	50				55				60						
Asn	Asn	Leu	Ser	Ile	Pro	Thr	Tyr	Phe	Val	Ala	Asp	Met	Gly	Ser	Val
65				70				75						80	
Trp	His	Unk	Ile	Ser	Met	Tyr	Ser	Gly	Ser	Asn	Asp	Ala	Leu	Ile	Gln
		85					90						95		
Trp	Trp	Trp	Gly	His	Asn	Ala	Val	Ala	Phe	Val	Phe	Thr	Ser	Gly	Val
		100					105					110			
Ile	Gly	Thr	Ile	Tyr	Tyr	Phe	Leu	Pro	Lys	Glu	Ser	Gly	Gln	Pro	Ile
		115				120					125				
Phe	Ser	Tyr	Lys	Leu	Thr	Leu	Phe	Ser	Phe	Trp	Ser	Leu	Met	Phe	Val
	130				135				140						
Tyr	Ile	Trp	Ala	Gly	Gly	His	His	Leu	Ile	Tyr	Ser	Thr	Val	Unk	Asp
145			150				155							160	
Unk	Val	Gln	Thr	Leu	Ser	Ser	Unk	Phe	Ser	Val	Val	Leu	Ile	Leu	Pro
		165					170						175		
Ser	Unk	Gly	Thr	Ala	Ile	Asn	Met	Leu	Leu	Unk	Met	Arg	Gly	Gln	Trp
		180					185					190			
His	Gln	Unk	Lys	Glu	Ser	Pro	Leu	Ile	Lys	Phe	Leu	Val	Leu	Ala	Ser
		195				200						205			

SUBSTITUTE SHEET (RULE 26)

388

Thr Phe Tyr Met Leu Ser Thr Leu Glu Gly Ser Ile Gln Ala Ile Lys
 210 215 220
 Ser Val Asn Ala
 225

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470

Leu Leu Val Leu Leu Asn Leu Lys Unk Thr Pro Asn Leu Met Trp Pro
 1 5 10 15
 Leu Asp Ile Ile Val Val Val Ala Trp Val Leu Trp Gly Val Asn Met
 20 25 30
 Phe Gly Ser Met Ser Val Arg Arg Glu Asn Thr Ile Tyr Val Ser Leu
 35 40 45
 Trp Tyr Tyr Ile Ala Thr Tyr Val Gly Ile Ala Val Met Tyr Ile Phe
 50 55 60
 Asn Asn Leu Ser Ile Pro Thr Tyr Phe Val Ala Asp Met Gly Ser Val
 65 70 75 80
 Trp His Unk Ile Ser Met Tyr Ser Gly Ser Asn Asp Ala Leu Ile Gln
 85 90 95
 Trp Trp Trp Gly His Asn Ala Val Ala Phe Val Phe Thr Ser Gly Val
 100 105 110
 Ile Gly Thr Ile Tyr Tyr Phe Leu Pro Lys Glu Ser Gly Gln Pro Ile
 115 120 125
 Phe Ser Tyr Lys Leu Thr Leu Phe Ser Phe Trp Ser Leu Met Phe Val
 130 135 140
 Tyr Ile Trp Ala Gly Gly His His Leu Ile Tyr Ser Thr Val Unk Asp
 145 150 155 160
 Unk Val Gln Thr Leu Ser Ser Unk Phe Ser Val Val Leu Ile Leu Pro
 165 170 175
 Ser Unk Gly Thr Ala Ile Asn Met Leu Leu Unk Met Arg Gly Gln Trp
 180 185 190
 His Gln Unk Lys Glu Ser Pro Leu Ile Lys Phe Leu Val Leu Ala Ser
 195 200 205
 Thr Phe Tyr Met Leu Ser Thr Leu Glu Gly Ser Ile Gln Ala Ile Lys
 210 215 220
 Ser Val Asn Ala
 225

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

389

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...92
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:471

```

Met Phe Asp Ser Ile Val Tyr Phe Phe Asn Lys Ser Gly Phe Val Thr
1           5           10           15
Thr Leu Val Leu Val Trp Ile Ser Leu Tyr Leu Val Met Thr Leu Trp
          20           25           30
Val Phe Leu Tyr Lys Ser Ile Val Leu Lys Ile Glu Leu Arg Arg Glu
          35           40           45
Met Gln Ser Leu Ser Asn Ile Leu Asn Gly Ala Gln Asp Ala Pro Glu
          50           55           60
His Phe Met Phe Asn Lys Lys Arg Asn Asp Glu Thr Lys Arg Tyr Ser
65           70           75           80
Asn Glu Leu Leu Gln Asp Leu Glu Thr Pro Gly Ser
          85           90

```

(2) INFORMATION FOR SEQ ID NO:472:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...96

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472

```

Met Ala Met Leu Tyr Cys Met Arg Leu Leu Met Pro Ile Leu Gly Ala
1           5           10           15
Ile Lys Gly Gly Asp Ile Gly Glu Trp Phe Pro Asp Asn Asp Pro Lys
          20           25           30
Tyr Lys Asn Ala Ser Ser Lys Glu Leu Leu Lys Ile Val Leu Asp Phe
          35           40           45
Ser Gln Ser Ile Gly Phe Glu Leu Leu Glu Met Gly Ala Thr Ile Phe
          50           55           60
Ser Glu Ile Pro Lys Ile Thr Pro Tyr Lys Pro Ala Ile Leu Glu Asn
65           70           75           80
Leu Ser Gln Leu Leu Gly Leu Glu Lys Ser Gln Ile Ser Leu Lys Ala
          85           90           95

```

(2) INFORMATION FOR SEQ ID NO:473:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1178 amino acids

SUBSTITUTE SHEET (RULE 26)

390

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473

```

Met Ile Pro Asn Leu Asp Ile Glu Gly Glu Thr Met Thr Asn Glu Ala
1      5      10      15
Ile Asn Gln Gln Pro Gln Thr Glu Ala Ala Phe Asn Pro Gln Gln Phe
20     25     30
Ile Asn Asn Leu Gln Val Ala Phe Ile Lys Val Asp Asn Val Val Ala
35     40     45
Ser Phe Asp Pro Asn Gln Lys Pro Ile Val Asp Lys Asn Asp Arg Asp
50     55     60
Asn Arg Gln Ala Phe Glu Lys Ile Ser Gln Leu Arg Glu Glu Phe Ala
65     70     75     80
Asn Lys Ala Ile Lys Asn Pro Thr Lys Lys Asn Gln Tyr Phe Ser Ser
85     90     95
Phe Ile Ser Lys Ser Asn Asp Leu Ile Asp Lys Asp Asn Leu Ile Asp
100    105    110
Thr Gly Ser Ser Ile Lys Ser Phe Gln Lys Phe Gly Thr Gln Arg Tyr
115    120    125
Gln Ile Phe Met Asn Trp Val Ser His Gln Asn Asp Pro Ser Lys Ile
130    135    140
Asn Thr Gln Lys Ile Arg Gly Phe Met Glu Asn Ile Ile Gln Pro Pro
145    150    155    160
Ile Ser Asp Asp Lys Glu Lys Ala Glu Phe Leu Arg Ser Ala Lys Gln
165    170    175
Ala Phe Ala Gly Ile Ile Ile Gly Asn Gln Ile Arg Ser Asp Gln Lys
180    185    190
Phe Met Gly Val Phe Asp Glu Ser Leu Lys Glu Arg Gln Glu Ala Glu
195    200    205
Lys Asn Gly Glu Pro Asn Gly Asp Pro Thr Gly Gly Asp Trp Leu Asp
210    215    220
Ile Phe Leu Ser Phe Val Phe Asn Lys Lys Gln Ser Ser Asp Leu Lys
225    230    235    240
Glu Thr Leu Asn Gln Glu Pro Val Pro His Val Gln Pro Asp Val Ala
245    250    255
Thr Thr Thr Thr Asp Ile Gln Ser Leu Pro Pro Glu Ala Arg Asp Leu
260    265    270
Leu Asp Glu Arg Gly Asn Phe Ser Lys Phe Thr Leu Gly Asp Met Asn
275    280    285
Met Leu Asp Val Glu Gly Val Ala Asp Ile Asp Pro Asn Tyr Lys Phe
290    295    300
Asn Gln Leu Leu Ile His Asn Asn Ala Leu Ser Ser Val Leu Met Gly
305    310    315    320
Ser His Asn Gly Ile Glu Pro Glu Lys Val Ser Leu Leu Tyr Gly Asn
325    330    335
Asn Gly Gly Pro Glu Ala Arg His Asp Trp Asn Ala Thr Val Gly Tyr
340    345    350
Lys Asn Gln Arg Gly Asp Asn Val Ala Thr Leu Ile Asn Val His Met
355    360    365
Lys Asn Gly Ser Gly Leu Val Ile Ala Gly Gly Glu Lys Gly Ile Asn
370    375    380
Asn Pro Ser Phe Tyr Leu Tyr Lys Glu Asp Gln Leu Thr Gly Ser Gln

```

SUBSTITUTE SHEET (RULE 26)

391

385		390		395		400									
Arg	Ala	Leu	Ser	Gln	Glu	Ile	Gln	Asn	Lys	Val	Asp	Phe	Met	Glu	
				405				410						415	
Phe	Leu	Ala	Gln	Asn	Asn	Ala	Lys	Leu	Asp	Asn	Leu	Ser	Lys	Lys	Glu
			420					425					430		
Lys	Glu	Lys	Phe	Gln	Asn	Glu	Ile	Glu	Asp	Phe	Gln	Lys	Asp	Ser	Lys
		435					440					445			
Ala	Tyr	Leu	Asp	Ala	Leu	Gly	Asn	Asp	His	Ile	Ala	Phe	Val	Ser	Lys
	450					455					460				
Lys	Asp	Lys	Lys	His	Leu	Ala	Leu	Val	Ala	Glu	Phe	Gly	Asn	Gly	Glu
	465				470					475					480
Leu	Ser	Tyr	Thr	Leu	Lys	Asp	Tyr	Gly	Lys	Lys	Ala	Asp	Lys	Ala	Leu
			485					490							495
Asp	Arg	Glu	Ala	Lys	Thr	Thr	Leu	Gln	Gly	Ser	Leu	Lys	His	Asp	Gly
		500						505					510		
Val	Met	Phe	Val	Asp	Tyr	Ser	Asn	Phe	Lys	Tyr	Thr	Asn	Ala	Ser	Lys
		515					520					525			
Ser	Pro	Asp	Lys	Gly	Val	Gly	Ala	Thr	Asn	Gly	Val	Ser	His	Leu	Glu
	530					535					540				
Ala	Gly	Phe	Ser	Lys	Val	Ala	Val	Phe	Asn	Leu	Pro	Asn	Leu	Asn	Asn
	545				550				555						560
Leu	Ala	Ile	Thr	Ser	Val	Val	Arg	Gln	Asp	Leu	Glu	Asp	Lys	Leu	Ile
			565					570							575
Ala	Lys	Gly	Leu	Ser	Pro	Gln	Glu	Ala	Asn	Lys	Leu	Val	Lys	Asp	Phe
			580					585					590		
Leu	Ser	Ser	Asn	Lys	Glu	Leu	Val	Gly	Lys	Ala	Leu	Asn	Phe	Asn	Lys
		595				600						605			
Ala	Val	Ala	Glu	Ala	Lys	Asn	Thr	Gly	Asn	Tyr	Asp	Glu	Val	Lys	Gln
	610					615					620				
Ala	Gln	Lys	Asp	Leu	Glu	Lys	Ser	Leu	Lys	Lys	Arg	Glu	Arg	Leu	Glu
	625				630					635					640
Lys	Asp	Val	Ala	Lys	Asn	Leu	Glu	Ser	Lys	Ser	Gly	Asn	Lys	Asn	Lys
			645					650						655	
Met	Glu	Ala	Lys	Ser	Gln	Ala	Asn	Ser	Gln	Lys	Asp	Glu	Ile	Phe	Ala
		660						665					670		
Leu	Ile	Asn	Lys	Glu	Ala	Asn	Arg	Asp	Ala	Arg	Ala	Ile	Ala	Tyr	Ala
		675					680					685			
Gln	Asn	Leu	Lys	Gly	Ile	Lys	Arg	Glu	Leu	Ser	Asp	Lys	Leu	Glu	Asn
	690					695					700				
Ile	Asn	Lys	Asp	Leu	Lys	Asp	Phe	Ser	Lys	Ser	Phe	Asp	Glu	Phe	Lys
	705				710					715					720
Asn	Gly	Lys	Asn	Lys	Asp	Phe	Ser	Lys	Ala	Glu	Glu	Thr	Leu	Lys	Ala
			725						730					735	
Leu	Lys	Gly	Ser	Val	Lys	Asp	Leu	Gly	Ile	Asn	Pro	Glu	Trp	Ile	Ser
		740						745					750		
Lys	Val	Glu	Asn	Leu	Asn	Ala	Ala	Leu	Asn	Glu	Phe	Lys	Asn	Gly	Lys
		755				760					765				
Asn	Lys	Asp	Phe	Ser	Lys	Val	Thr	Gln	Ala	Lys	Ser	Asp	Leu	Glu	Asn
		770				775					780				
Ser	Ile	Lys	Asp	Val	Ile	Asn	Gln	Lys	Ile	Thr	Asp	Lys	Val	Asp	
	785				790				795						800
Asn	Leu	Asn	Gln	Ala	Val	Ser	Val	Ala	Lys	Ala	Thr	Gly	Asp	Phe	Ser
			805					810						815	
Gly	Val	Glu	Gln	Ala	Leu	Ala	Asp	Leu	Lys	Asn	Phe	Ser	Lys	Glu	Gln
		820						825					830		
Leu	Ala	Gln	Gln	Ala	Gln	Lys	Asn	Glu	Asp	Phe	Asn	Thr	Gly	Lys	Asn
		835					840					845			
Ser	Ala	Leu	Tyr	Gln	Ser	Val	Lys	Asn	Gly	Val	Asn	Gly	Thr	Leu	Val
		850				855					860				
Gly	Asn	Gly	Leu	Ser	Lys	Ala	Glu	Ala	Thr	Thr	Leu	Ser	Lys	Asn	Phe
	865				870				875						880
Ser	Asp	Ile	Lys	Lys	Glu	Leu	Asn	Ala	Lys	Leu	Gly	Asn	Phe	Asn	Asn
			885					890						895	
Asn	Asn	Asn	Asn	Gly	Leu	Glu	Asn	Ser	Thr	Glu	Pro	Ile	Tyr	Thr	Gln
			900					905						910	

SUBSTITUTE SHEET (RULE 26)

392

Val Ala Lys Lys Val Lys Ala Lys Ile Asp Arg Leu Asp Gln Ile Ala
 915 920 925
 Ser Gly Leu Gly Asp Val Gly Gln Ala Ala Ser Phe Leu Leu Lys Arg
 930 935 940
 His Asp Lys Val Asp Asp Leu Ser Lys Val Gly Leu Ser Ala Asn His
 945 950 955 960
 Glu Pro Ile Tyr Ala Thr Ile Asp Asp Leu Gly Gly Pro Phe Pro Leu
 965 970 975
 Lys Arg His Asp Lys Val Asp Asp Leu Ser Lys Val Gly Leu Ser Arg
 980 985 990
 Glu Gln Lys Leu Thr Gln Lys Ile Asp Asn Leu Asn Gln Ala Val Ser
 995 1000 1005
 Glu Ala Lys Ala Ser His Phe Asp Asn Leu Asp Gln Met Ile Asp Lys
 1010 1015 1020
 Leu Lys Asp Ser Thr Lys Lys Asn Val Val Asn Leu Tyr Val Glu Ser
 1025 1030 1035 1040
 Ala Lys Lys Val Pro Thr Ser Leu Ser Ala Lys Leu Asp Asn Tyr Ala
 1045 1050 1055
 Thr Asn Ser His Thr Arg Ile Asn Ser Asn Val Lys Asn Gly Thr Ile
 1060 1065 1070
 Asn Glu Lys Ala Thr Gly Met Leu Thr Gln Lys Asn Ser Glu Trp Leu
 1075 1080 1085
 Lys Leu Val Asn Asp Lys Ile Val Ala His Asn Val Gly Ser Ala Pro
 1090 1095 1100
 Leu Ser Ala Tyr Asp Lys Ile Gly Phe Asn Gln Lys Asn Met Lys Asp
 1105 1110 1115 1120
 Tyr Ser Asp Ser Phe Lys Phe Ser Thr Arg Leu Ser Asn Ala Val Lys
 1125 1130 1135
 Asp Ile Lys Ser Gly Phe Val Gln Phe Leu Thr Asn Ile Phe Ser Met
 1140 1145 1150
 Gly Ser Tyr Ser Leu Met Lys Ala Ser Val Glu His Gly Val Lys Asn
 1155 1160 1165
 Thr Asn Thr Lys Gly Gly Phe Gln Lys Ser
 1170 1175

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474

Met Lys Ala Pro Ser Gln Unk Asp Leu Lys Lys Ile Leu Gly Ile Glu
 1 5 10 15
 Glu Val Ile Unk Ser Thr Ser Pro Met Glu Leu Arg Leu Ala Asn
 20 25 30
 Gln Lys Leu Gly Asn Arg Phe Ile Lys Thr Leu Gln Ala Met Asn Glu
 35 40 45
 Leu Asp Met Gly Ala Phe Phe Asn Ala Tyr Ala Gln Thr Thr Lys Asp
 50 55 60
 Pro Thr His Ala Thr Ser Tyr Gly Val Phe Ala Ala Ser Leu Asn Met

393

```

65          70          75          80
Glu Leu Lys Lys Ala Leu Arg His Tyr Leu Tyr Ala Gln Thr Ser Asn
      85          90          95
Met Val Ile Asn Cys Val Lys Ser Val Pro Leu Ser Gln Asn Asp Gly
      100        105        110
Gln Lys Ile Leu Leu Ser Leu Gln Ser Pro Phe Asn Gln Leu Ile Glu
      115        120        125
Lys Thr Leu Glu Leu Asp Glu Ser His Leu Cys Ala Ala Ser Val Gln
      130        135        140
Asn Asp Ile Lys Ala Met Gln His Glu Ser Leu Tyr Ser Arg Leu Tyr
145          150          155          160
Met Ser

```

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474

```

Met Lys Ala Pro Ser Gln Unk Asp Leu Lys Lys Ile Leu Gly Ile Glu
1          5          10          15
Glu Val Ile Unk Unk Ser Thr Ser Pro Met Glu Leu Arg Leu Ala Asn
      20          25          30
Gln Lys Leu Gly Asn Arg Phe Ile Lys Thr Leu Gln Ala Met Asn Glu
      35          40          45
Leu Asp Met Gly Ala Phe Phe Asn Ala Tyr Ala Gln Thr Thr Lys Asp
      50          55          60
Pro Thr His Ala Thr Ser Tyr Gly Val Phe Ala Ala Ser Leu Asn Met
65          70          75          80
Glu Leu Lys Lys Ala Leu Arg His Tyr Leu Tyr Ala Gln Thr Ser Asn
      85          90          95
Met Val Ile Asn Cys Val Lys Ser Val Pro Leu Ser Gln Asn Asp Gly
      100        105        110
Gln Lys Ile Leu Leu Ser Leu Gln Ser Pro Phe Asn Gln Leu Ile Glu
      115        120        125
Lys Thr Leu Glu Leu Asp Glu Ser His Leu Cys Ala Ala Ser Val Gln
      130        135        140
Asn Asp Ile Lys Ala Met Gln His Glu Ser Leu Tyr Ser Arg Leu Tyr
145          150          155          160
Met Ser

```

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

394

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475

```

Met Lys Ala Leu Lys Thr Phe Leu Lys Lys Ser Leu Ile Leu Leu Leu
1      5      10      15
Ala Ile Ala Leu Asn His Leu Asn Ala Val Ala Met Ile Val Asp Asn
20      25      30
Pro Thr Gln Asn Ala Trp Asn Gly Ala Lys Arg Ala Trp Asp Glu Ser
35      40      45
Lys Trp Ala Lys His Leu Ala Thr Ile Thr Glu Arg Ile Lys Leu Ala
50      55      60
Gln Asp Thr Leu Asp Arg Ala Asn Gln Thr Leu Asn Ser Ile Asn Lys
65      70      75      80
Val Asn Asp Val Leu Asn Lys Thr Asn Gln Phe Leu Thr Gly Ser Ile
85      90      95
Leu Ser Ile Pro Asn Pro Met Gln Tyr Val Glu Lys Ile Gln Ser Phe
100     105     110
Ala Lys Gln Val Gln Ala Asn Thr Glu Arg Ile Lys Glu Asn Ala Gln
115     120     125
Asn Tyr Asp Ile Arg Asn Gln Ile Ala Ala Lys Arg Ile Ser Glu Lys
130     135     140
Cys Pro Glu Leu Asn Trp Asp Val Ser Gln Asp Ala Ser Pro Thr Glu
145     150     155     160
Lys Asn Leu His Gln Phe Phe Thr Ser Lys Gly Lys Glu Ser Ala Asn
165     170     175
Thr Lys Ala Leu Lys Asp Phe Ala Asn Ala Ile Gly Asn Thr Gln Ile
180     185     190
Ser Thr Ala Asn Asp Leu Gly Ala Gly Leu Arg Gly Arg Ala Leu Leu
195     200     205
Glu Tyr Ile Cys Ile Gln Lys Gly Asn Leu Glu Ala Ala Lys Lys Ile
210     215     220
Gln Leu Leu Asp Ser Gln Met Thr Leu Ala Leu Leu Asn Asn Asp Tyr
225     230     235     240
Thr Ala Tyr Glu Lys Leu Arg Ala Glu Lys Glu Glu Leu Lys Arg Gln
245     250     255
Ile Ala Ser Asn Val Tyr Ala Lys Val Lys Gln Leu Val Val Ala Ser
260     265     270
Gln Asp Arg Ala Phe Ser Gln Met Asp Asn Glu Leu Gly Val Lys Thr
275     280     285
Phe Gly Phe Asn Asp Glu Asn Val Lys Lys Gly Tyr Cys Lys Lys Glu
290     295     300
Asn Arg Asn Gly Lys Ser Glu Cys Ile Pro Asn Met Leu Asn Val Asn
305     310     315     320
Arg Leu Lys Ala Gln Phe Asp Glu Leu Asn Leu Asp Tyr Ser Arg Asp
325     330     335
Ile Ala Gly Lys Lys Gly Glu Ala Ala Ala Lys Val Phe Asn Asp Tyr
340     345     350
Lys His Arg Phe Gln Gln Leu Ser Val Glu Thr Ala Leu Glu Ile Ala
355     360     365
Gln Asn Leu Ser Phe Met Asn Lys Thr Leu Gly Leu Met Val Gln Met
370     375     380
Gln Ser Tyr Ala Phe Lys Gln Gln Met Gly Tyr Phe Glu Asp Ile Ile
385     390     395     400
Pro Ala Asp Ala Leu Lys Asp Asp Lys Glu His Gln Glu Asn Leu Glu

```

SUBSTITUTE SHEET (RULE 26)

395

```

          405          410          415
Gln Lys Gln Gln Glu Ile Glu Lys Val Tyr Arg Ala Lys Leu Asp Ala
          420          425          430
Tyr Gly Phe Pro Asn Gly Ser Val Gly Lys Ala Ser Gly Val Asn Ser
          435          440          445
Asn Ser Asn Asn Glu Ala Pro Ser Ser Asp Asn Ile Gln Ser Phe Asn
          450          455          460
Pro Tyr
465

```

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...59

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476

```

Met Ala Phe Ile Leu Thr Thr Asn Leu Phe Ile Lys Ser Phe Thr Asn
1          5          10          15
Ser Ile Arg Ile Thr Gly Cys Ile Ile Ser Pro Asn Val Phe Phe Ala
          20          25          30
Tyr Glu Phe Cys Ala Leu Gly Phe Arg Lys Gly Gly Leu Ile Leu Asp
          35          40          45
Asn Phe Ser Lys Phe Val Ser His Arg Leu Gln
50          55

```

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...59

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476

```

Met Ala Phe Ile Leu Thr Thr Asn Leu Phe Ile Lys Ser Phe Thr Asn
1          5          10          15
Ser Ile Arg Ile Thr Gly Cys Ile Ile Ser Pro Asn Val Phe Phe Ala
          20          25          30

```

396

Tyr Glu Phe Cys Ala Leu Gly Phe Arg Lys Gly Gly Leu Ile Leu Asp
 35 40 45
 Asn Phe Ser Lys Phe Val Ser His Arg Leu Gln
 50 55

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477

Val Arg Phe Phe Ile Phe Leu Ile Leu Ile Cys Pro Leu Ile Cys Pro
 1 5 10 15
 Leu Met Ser Ala Asp Ser Ala Leu Pro Ser Val Asn Leu Ser Leu Asn
 20 25 30
 Ala Pro Ser Asp Pro Lys Gln Leu Val Thr Thr Leu Asn Val Ile Ala
 35 40 45
 Leu Leu Thr Leu Leu Val Leu Ala Pro Ser Leu Ile Leu Val Met Thr
 50 55 60
 Ser Phe Thr Arg Leu Ile Val Val Phe Ser Phe Leu Arg Thr Ala Leu
 65 70 75 80
 Gly Thr Gln Gln Thr Pro Pro Thr Gln Ile Leu Val Ser Leu Ser Leu
 85 90 95
 Ile Leu Thr Phe Phe Ile Met Glu Pro Ser Leu Lys Lys Ala Tyr Asp
 100 105 110
 Thr Gly Ile Lys Pro Tyr Met Asp Lys Lys Ile Ser Tyr Thr Glu Ala
 115 120 125
 Phe Glu Lys Ser Thr Leu Pro Phe Lys Glu Phe Met Leu Lys Asn Thr
 130 135 140
 Arg Glu Lys Asp Leu Ala Leu Phe Phe Arg Ile Arg Asn Leu Pro Asn
 145 150 155 160
 Pro Lys Thr Pro Asp Asp Val Ser Leu Ser Val Leu Ile Pro Ala Phe
 165 170 175
 Met Ile Ser Glu Leu Lys Thr Ala Phe Gln Ile Gly Phe Leu Leu Tyr
 180 185 190
 Leu Pro Phe Leu Val Ile Asp Met Val Ile Ser Ser Ile Leu Met Ala
 195 200 205
 Met Gly Met Met Met Leu Pro Pro Val Met Ile Ser Leu Pro Phe Lys
 210 215 220
 Ile Leu Val Phe Ile Leu Val Asp Gly Phe Asn Leu Leu Thr Glu Asn
 225 230 235 240
 Leu Val Ala Ser Phe Lys Met Val
 245

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
 (B) TYPE: amino acid

397

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477

```

Val Arg Phe Phe Ile Phe Leu Ile Leu Ile Cys Pro Leu Ile Cys Pro
1      5      10      15
Leu Met Ser Ala Asp Ser Ala Leu Pro Ser Val Asn Leu Ser Leu Asn
20     25     30
Ala Pro Ser Asp Pro Lys Gln Leu Val Thr Thr Leu Asn Val Ile Ala
35     40     45
Leu Leu Thr Leu Leu Val Leu Ala Pro Ser Leu Ile Leu Val Met Thr
50     55     60
Ser Phe Thr Arg Leu Ile Val Val Phe Ser Phe Leu Arg Thr Ala Leu
65     70     75     80
Gly Thr Gln Gln Thr Pro Pro Thr Gln Ile Leu Val Ser Leu Ser Leu
85     90     95
Ile Leu Thr Phe Phe Ile Met Glu Pro Ser Leu Lys Lys Ala Tyr Asp
100    105    110
Thr Gly Ile Lys Pro Tyr Met Asp Lys Lys Ile Ser Tyr Thr Glu Ala
115    120    125
Phe Glu Lys Ser Thr Leu Pro Phe Lys Glu Phe Met Leu Lys Asn Thr
130    135    140
Arg Glu Lys Asp Leu Ala Leu Phe Phe Arg Ile Arg Asn Leu Pro Asn
145    150    155    160
Pro Lys Thr Pro Asp Asp Val Ser Leu Ser Val Leu Ile Pro Ala Phe
165    170    175
Met Ile Ser Glu Leu Lys Thr Ala Phe Gln Ile Gly Phe Leu Leu Tyr
180    185    190
Leu Pro Phe Leu Val Ile Asp Met Val Ile Ser Ser Ile Leu Met Ala
195    200    205
Met Gly Met Met Met Leu Pro Pro Val Met Ile Ser Leu Pro Phe Lys
210    215    220
Ile Leu Val Phe Ile Leu Val Asp Gly Phe Asn Leu Leu Thr Glu Asn
225    230    235    240
Leu Val Ala Ser Phe Lys Met Val
245

```

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

SUBSTITUTE SHEET (RULE 26)

398

(B) LOCATION 1...44

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478

```

Val Met Asp Ala Glu Asn Gly Glu Leu Leu Val Ala Gly Ser Tyr Pro
1      5      10      15
Glu Tyr Asn Leu Asn Asp Phe Val Gly Ile Ser Gln Asp Lys Trp
20      25      30
Gln Lys Leu Gln Asp Asp Ile Tyr Asn Pro Leu Leu
35      40

```

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 421 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479

```

Met Asn Phe Phe Asp Thr Leu Met Gly Met Phe Val Glu Pro Ser Gln
1      5      10      15
Lys Val Ala Lys Ser Leu Ala Glu His Val Gly Ser Phe Phe His Ala
20      25      30
Gln Leu Ile Leu Asn Thr Ile Ile Thr Ile Leu Phe Met Ile Trp Ala
35      40      45
Tyr Lys Arg Val Lys Glu Gly Asp Met Phe Glu Phe Lys Thr Ala Met
50      55      60
Gly Val Val Val Phe Ile Ala Phe Val Gly Phe Ile Asn Trp Gly Ile
65      70      75      80
Lys Asn Pro Asn Asp Phe Asn Thr Tyr Phe Ile Asn Thr Ile Phe Tyr
85      90      95
Pro Ser Glu Lys Leu Ala Ile Leu Ile Ala Gln Ser Leu Asn Asp Gly
100      105      110
Leu Glu Ile Pro Thr Asn Thr Asn Leu Ser Pro Ser Glu Ile Phe Ser
115      120      125
Ile Gly Asn Leu Ala Ser Ser Ala Tyr Ala Met Ile Val Asn Leu Trp
130      135      140
Asp Asn Ala Phe Asp Gly Ile Asn Met Phe Asn Trp Leu Thr Met Ile
145      150      155      160
Pro Lys Ile Ile Met Phe Phe Leu Val Ile Leu Gly Glu Leu Leu Phe
165      170      175
Leu Gly Leu Leu Leu Ile Ile Val Leu Leu Val Thr Ala Glu Ile Phe
180      185      190
Met Trp Ser Ala Leu Gly Leu Ile Val Leu Pro Leu Gly Leu Ile Pro
195      200      205
Gln Thr Lys Gly Met Leu Phe Ser Tyr Leu Lys Lys Leu Ile Ser Leu
210      215      220
Thr Leu Tyr Lys Pro Cys Met Met Leu Val Ala Phe Phe Asn Tyr Gly
225      230      235      240
Ile Ile Tyr Lys Val Asn Thr Leu Ile Pro Thr Lys His Glu Val Thr
245      250      255
Gln Gly Phe Tyr Gly Asn Ala Asp Lys Met Ala Asn Glu Gly Lys Ile

```

SUBSTITUTE SHEET (RULE 26)